Serge Morand
Jean-Pierre Dujardin
Régine Lefait-Robin
Chamnarn Apiwathnasorn *Editors*

Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia

Springer

Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia

Serge Morand • Jean-Pierre Dujardin
Régine Lefait-Robin • Chamnarn Apiwathnasorn
Editors

Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia

Springer

Editors
Serge Morand
CNRS ISEM - CIRAD AGIRs,
Centre d'Infectiologie Christophe
Mérieux du Laos
Vientiane, Laos

Jean-Pierre Dujardin
Institut de Recherches pour le
Développement, IRD, UMR17
IRD-CIRAD INTERTRYP
Montpellier, France

Régine Lefait-Robin
Haut Conseil de la santé publique, Ministère
des affaires sociales et de la santé
Paris, France

Chamnarn Apiwathnasorn
Department of Medical Entomolgy, Faculty
of Tropical Medicine
Mahidol University
Bangkok, Thailand

ISBN 978-981-287-526-6 ISBN 978-981-287-527-3 (eBook)
DOI 10.1007/978-981-287-527-3

Library of Congress Control Number: 2015944825

Springer Singapore Heidelberg New York Dordrecht London
© Springer Science+Business Media Singapore 2015
This work is subject to copyright. All rights are reserved by the Publisher, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilms or in any other physical way, and transmission or information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed.
The use of general descriptive names, registered names, trademarks, service marks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.
The publisher, the authors and the editors are safe to assume that the advice and information in this book are believed to be true and accurate at the date of publication. Neither the publisher nor the authors or the editors give a warranty, express or implied, with respect to the material contained herein or for any errors or omissions that may have been made.

Printed on acid-free paper

Springer Science+Business Media Singapore Pte Ltd. is part of Springer Science+Business Media (www.springer.com)

Acknowledgements

This book emerges from an international symposium organized in Bangkok in October 2011 at the Faculty of Tropical Medicine of Mahidol University and supported by the IRD, and its main objective was to join scholars in history, sociology, law, ecology, epidemiology, medical entomology, veterinary sciences, physicians and environmental sciences to present a multidisciplinary overview about the links between environment, biodiversity and human health, mostly through infectious diseases in Asia with most examples from Southeast Asia.

We thank also the French ANR for supporting the project BiodivHealthSEA (*Impacts and perceptions of global changes: Biodiversity and health in Southeast Asia*) and the French AFD-CNRS Bio-Asia for supporting the project PathoDivSEA (*Pathogen Diversity in Southeast Asia*).

Contents

Part III Global Changes, Land Use Changes and Vector-Borne Diseases

Part IV Monitoring and Data Acquisition

Part V Managing Health Risks

Chapter 1
Introduction to Socioecological Dimensions of Infectious Diseases and Health in Southeast Asia

Serge Morand, Jean-Pierre Dujardin, Régine Lefait-Robin, and Chamnarn Apiwathnasorn

Abstract Global changes affect host-pathogen interactions, through the modification of the epidemiological environment (climate, land use, biodiversity), leading to new and sometimes unexpected risks. Epidemics, emergence and re-emergence of infectious diseases are outcomes of these changes, and they constitute serious global threats for health. Although some local emergences have a potential for global threat (i.e. SARS, avian influenza, etc.), most of infectious diseases affect rural and poor populations particularly in developing countries, which are particularly vulnerable to the consequences of global change. Southeast Asia is both a hotspot of infectious emerging diseases of potential global pandemics and of biodiversity, particularly at threat due to dramatic changes in land use (Morand et al. 2014). These may explain why international organizations, developmental agencies and non-governmental conservationist organizations have specially focused on Southeast Asia. Infectious diseases are still a major concern in most Southeast-Asian countries (Coker et al. 2011).

Many aspects of the environments and the socio-economics are linked to infectious diseases and health. Now, it is time to evaluate in a multidisciplinary approach the socioecological dimensions of infectious diseases in Southeast Asia.

S. Morand (✉)
CNRS ISEM – CIRAD AGIRs, Centre d'Infectiologie Christophe Mérieux du Laos, Vientiane, Lao PDR
e-mail: serge.morand@univ-montp2.fr

J.-P. Dujardin
Institut de Recherches pour le Développement, IRD, UMR17 IRD-CIRAD INTERTRYP, Montpellier, France

R. Lefait-Robin
Haut Conseil de la santé publique, Ministère des affaires sociales et de la santé, Paris, France

C. Apiwathnasorn
Department of Medical Entomology, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_1

This book emerges from a symposium organized in Bangkok in October 2011 at the Faculty of Tropical Medicine of Mahidol University and supported by the IRD, and its main objective was to join scholars in history, sociology, law, ecology, epidemiology, medical entomology, veterinary sciences, physicians and environmental sciences to present a multidisciplinary overview about the links between environment, biodiversity and human health, mostly through infectious diseases.

The present book is organized in six parts, each comprising three chapters: (1) infectious diseases and societies; (2) health and socio-ecosystems; (3) global changes, land use changes and vector-borne diseases; (4) monitoring and data acquisition; (5) managing risks; and (6) developing strategies.

The first part of this book concerns infectious diseases and societies from historical times to present days. This part starts with Chap. 2 on how Chinese classics of medicine and medical records referred about epidemic febrile diseases. As Dominique Buchillet emphasizes along with famine due to crop failures and other calamities, epidemics exerted a heavy burden on Chinese populations throughout the ages. The chapter reviews the evolution of medical perceptions on epidemic diseases through these Chinese classics, stressing the importance of the growing awareness of variations in environments and the refashioning of discourses and practices relative to epidemic diseases in Chinese medicine.

In the third chapter, Malee Sitthikriengkrai and Chayan Vaddhanaphuti describe the history and responses to HIV/AIDS in Thailand from a sociocultural perspective. As persons living with HIV had a way to interpret the meaning of their problem, the authors show how they took power into their own hands through the formation of self-help groups and through redefining the way they lived with the disease.

Bernard Moizo in the fourth chapter discusses the issue of infectious diseases in relation to social and environmental global changes. Using the example of growing tourist activities as one possible agent of diseases spreading, the author suggests several ideas that could enhance the development of interdisciplinary approaches despite long-time obstacles.

The second part of this book deals with socio-ecosystems (water and soil) and health, putting the emphasis on environment. In Chap. 5, Séraphine Grellier and colleagues evaluate the contamination in trace metal element (TME) related to the Mae Thang Reservoir. They study the transfer of the TME between the different compartments in and downstream of the reservoir. In particular, they show that upstream areas contributed to bring TME in the Mae Thang Reservoir and that TME concentrations in fishes were thus affected and should be controlled. Finally, they conclude that accumulation of TME in soils of paddy field due to the use of pesticides and fertilizer may increase contamination of rice in the long term.

Chapter 6 concerns local community perception on water and health. Vincent Herbreteau and colleagues report the results of a questionnaire-based survey conducted to assess the exposure of households to potential water pollutions in order to better understand their behaviour regarding the use of water and recourse to health services. This study focusing in localities upstream and downstream of the Mae

Thang Reservoir (see Chap. 5) stresses both economic inequalities and lack of surveillance.

The last chapter (Chap. 7) of this first part reviews the results conducted on melioidosis, a tropical disease caused by a soil-dwelling bacterium *Burkholderia pseudomallei* transmitted from contaminated soil or surface water, in Laos during two intensive campaigns. An important finding emphasized by Yves Buisson and his colleagues is that, because a high proportion of water samples were positive downstream of a heavily contaminated terrestrial site, contamination by water runoff from land reservoirs is likely to be of epidemiological importance.

The third part of this book includes contributions on how climate change and land use change are affecting the ecology and distribution of mosquitoes and particularly those that are vectors of major infectious diseases such as malaria, dengue and chikungunya.

In Chap. 8, Ranjan Ramasamy and colleagues stress the importance of physiological adaptation of mosquitoes to brackish water. *Anopheles culicifacies* (vector of malaria) and *Aedes aegypti* and *Aedes albopictus* (vectors dengue and chikungunya) can develop in brackish water collections in coastal areas of South and Southeast Asia. They may cause serious new threats as their populations can expand in these coastal zones with climate change and rising sea levels due to global warming.

Hans J. Overgaard, Wannapa Suwonkerd and Jeffrey Hii describe in Chap. 9 the effect of land use on malaria vector density, species diversity and insecticide resistance in northern Thailand. They emphasize on the use of landscape analysis as a tool in vector control strategy development and show that an increase in landscape diversity, particularly forest fragmentation, reduces malaria vector diversity and density. Their chapter argues for an intersectoral collaboration between the public health and agricultural sectors, to develop and implement integrated pest and vector management (IPVM) strategies and insecticide resistance management plans.

In Chap. 10 Padikkala Kandiyil Sumodan and his colleagues compare the mosquito fauna in rubber plantations from Thailand and India and contrasted it with mosquito fauna in fragmented forests from Northern Thailand. They observed that in both rubber plantations and forests, *Aedes albopictus* was the most frequent mosquito. The use of geometric morphometrics tools allowed to distinguish the populations, potentially invasive, in rubber plantations from the ones, potentially native, in fragmented forests. Rubber plantations (RP) in Asia represent millions of artificial breeding sites for dangerous mosquitoes: they could be responsible for the drastic increase and recent planetary importance of *Aedes albopictus* populations.

Monitoring, data acquisition and also data banking are the subjects of the fourth part, which starts with Chap. 11 on the need to rescue epidemiological data. Marc Choisy and his colleagues presented the aims of modelling epidemiology and their roles for public health. They further emphasized how public health data that have been extensively collected in many parts of the world can be exploited in an efficient manner. With the support of Bill & Melinda Gates Foundation-funded Vaccine Modeling Initiative, they presented some achievement on dengue fever in Southeast Asia.

In Chap. 12, Edi Prifti and Jean-Daniel Zucker illustrate the growing applications of next-generation sequencing (NGS) technologies to human health. They discuss some of the challenges faced by metagenomic data acquisition and their subsequent analysis. The chapter concludes with the idea that there are significant benefits in building capacities for developing high-level scientific research in metagenomics in developing countries.

Claire Lajaunie and Serge Morand, in the last Chap. 13 of this fourth part, summarize some of the outcomes of the project Pathogen Diversity in Southeast Asia (PathodivSEA). They emphasize the importance of advancements in barcoding, biobanking and e-banking, which favour data, samples and knowledge sharing. A particular attention is given on the ethical and legal norms as well as industrial and economic standards that could overlap.

Three chapters are included in the fifth part dealing with the management of health risks.

Marion Bordier and her colleagues, in Chap. 14, describe the methods of prioritization of diseases as an essential tool for policymakers in charge of allocating resources for surveillance and control programmes. They present an innovative way based on the use of an electronic-based questionnaire, as a method to identify criteria allowing differentiations among zoonoses and their impacts in Southeast Asia.

In Chap. 15, Muriel Figuié and Stéphanie Desvaux document the logics underpinning the management practices of farmers facing an emerging disease. They explore how Vietnamese farmers responded when called upon to collaborate to the international fight against the virus H5N1. The results of their survey showed that local management of the disease did not (and cannot) fit with the precautionary approach promoted by the international community.

Alexandre Bouchot and Marion Bordier, in Chap. 16, present the strategy of one major actor of the international community, the World Organization for Animal Health (OIE). Among others, OIE promotes strong partnerships, notably with FAO and WHO, with regard to two topics that require a strong multi-sectoral collaboration at all levels because of their social, economical and ecological determinants: rabies and antimicrobial resistance.

The last part of this book includes contributions on new approaches for developing new strategies for health, societies and environment.

In the first chapter (Chap. 17) of this last part, Valérie Boisvert and her colleagues overview the concept of ecosystem services formed at the interface of science and policy, where it was grounded neither in ecological nor in economic theories. This concept is questioned on how a sustained market development can maintain a harmonious combination of human activities and environmental protection. Finally, the authors conclude that the notion of ecosystem services does not provide an adequate framework to deal with vulnerability and risk.

In Chap. 18, Angela Yang, Peter M. DiGeronimo and Alexandre Azevedo emphasize that the state of our ecosystems is integral to the conservation and sustainable management and that the health of the environment cannot be segregated from our own health. This needs to examine health from a global stance through holistic strategies as “One Health”.

In the last chapter (Chap. 19), Aurélie Binot and Serge Morand suggest that the lessons learnt from several community-based, participatory and adaptive management initiatives could be promoted in the frame of a "One Health" approach's implementation. This will improve risk communication and help turn rhetoric into reality.

We hope this book will be stimulating and that students and researchers in health in Southeast Asia (and more broadly in Asia) will find in it examples and encouragement to get a broad perspective, to integrate multidisciplinary approach and to favour cross-sectoral exchanges.

References

Coker RJ, Hunter BM, Rudge JW, Liverani M, Hanvoravongchai P (2011) Emerging infectious diseases in Southeast Asia: regional challenges to control. Lancet 377(9765):599–609

Morand S, Jittapalapong S, Supputamongkol Y, Abdullah MT, Huan TB (2014) Infectious diseases and their outbreaks in Asia-Pacific: biodiversity and its regulation loss matter. PLoS One 9(2):e90032

Part I
Infectious Diseases and Societies

Chapter 2
Climate, Environment and Epidemic Febrile Diseases: A View from Chinese Medicine

Dominique Buchillet

Abstract Chinese classics of medicine and medical records abound in reference to epidemic febrile diseases. Along with famine due to crop failures, droughts, floods and wars, they exerted a heavy burden on Chinese populations throughout the ages. The early classics of medicine (e.g. *Huang Di Nei Jing*, *Nan Jing*, *Shang Han Lun*, about 200 B.C.–220 A.D.) credited epidemic diseases to the invasion of the body by pathogenic cold and wind, classing them into the category of "cold damage disorders". With the creation of the "School of Warm Diseases" (Qing Dynasty, 1644–1911), a new conception of epidemic diseases emerged: distinction between "warm diseases" and "cold damage disorders", role of a warm "epidemic (or pestilential) *qi*" or "epidemic toxin" in their occurrence, body invasion through the mouth and nose, high contagiousness, specificity of the epidemic *qi* according to the species (human or animal) and the nature of the epidemic disease, favouring role of severe climatic and environmental conditions in their emergence, etc. This paper reviews the evolution of medical perceptions on epidemic diseases through Chinese classics of medicine. It stresses the importance of the growing awareness of variations in local and regional environments (with their climatic, epidemiological and medical specificities) in the refashioning of discourses and practices relative to epidemic diseases in Chinese medicine.

This paper was written when I was a member of the research unit UMR_D 190 "Emergence des Pathologies virales", Aix Marseille University, French Institute of Research for Development (IRD) and French School of Public Health (EHESP) (13005, Marseille, France) and located at the Center of Excellence for Vectors and Vector-Borne Diseases (CVVD), Faculty of Sciences, Mahidol University at Salaya, Thailand.

D. Buchillet (✉)
Medical Anthropologist (Retired), IRD-French Institute
of Research for Development, Marseille, France
e-mail: dominique.buchillet@gmail.com

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_2

2.1 Introduction

In the past, China was repeatedly struck by epidemic febrile diseases. Along with famine due to crop failures, droughts, floods, warfare and other social turbulences, they exerted a heavy burden on Chinese populations throughout the ages.[1] Prior to the Ming Dynasty (1638–1644), epidemic diseases (*yi* 疫 or *wen yi* 温疫, literally "warm epidemics") or also pestilence (*li* 疠) were credited to abnormal climatic conditions, in particular to excessive or unseasonable cold. In the late Ming Dynasty and early Qing Dynasty (1644–1911), a new conception of epidemic febrile diseases emerged: they are ascribed to heterogeneous pestilential *qi* (*li qi* 疠气) or to warm epidemic toxins (*wen du* 温毒) which exist in the environment and whose emergence is favoured by abnormal climatic and environmental conditions and/or social turbulences. After a brief consideration of some fundamental concepts in Chinese medicine,[2] this chapter reviews the evolution of medical perceptions on epidemic febrile diseases from the early classics of medicine to the foundation of the "School of Warm Diseases" in the nineteenth century.

2.2 *Qi*, *Yin-Yang*, *Wu Xing* ("Five Movements"), *Zang-Fu* ("Organs") and *Bing Yin* ("Aetiology")

2.2.1 Qi

In Chinese philosophy, *qi* 气[3] is the fundamental substance which, through its constant movements and changes, produces everything in the natural world. In medicine, it refers to a subtle matter with a strong vital force and in constant movement. It is the fundamental substance for the constitution of the human organism of which it maintains the vital activities. Each phase of life of the individual, from birth to decay and death, is connected to it. The *qi* of human beings originates from the congenital essence, food and water and from the inhaled air. Chinese medicine distinguishes various kinds of *qi* according to their origin, distribution and specific functions within the organism which, as a matter of fact, are different manifestations and functions of the individual *qi* once formed: *yuan qi* 元气 ("original *qi*") which is the driving force of the vital process. It derives from the congenital essence inherited from one's parents and depends for its development of the postnatal

---

[1] A first apprehension of the concept of warm diseases in Chinese medicine has been published in French in 2010 (see Buchillet 2010).

[2] On fundamental concepts in Chinese medicine in western languages, see Liu (1988), Zhen (1995), Marié (1997), Kaptchuk (2000) and Maciocia (1989).

[3] *Qi* has been translated in English as "vital energy", "energy", "vapour", etc. However, none of these translations are able to capture the different meanings of *qi* according to the Chinese thought. It is why I keep the original word in Chinese.

essence acquired from water and food. Its main function is to promote the growth and development of the organism, *zong qi* 宗气 (“ancestral *qi*”, also translated as “*qi* of the chest” because it gathers in the chest), which results from the combination of inhaled air and nutritive essences of food and water. It is transported by the spleen to the lungs and stimulates and regulates the rhythmic movements of respiration and heartbeat, *ying qi* 营气 (“constructive/nutritive *qi*”), which derives from the nutritive substances of food and water and produces, transforms, pushes and contains the blood in the blood vessels. It is a fundamental factor for the nourishment of the body, *wei qi* 卫气 (“defensive *qi*”) which circulates on the surface body, regulates sweating, warms up the organism and defends it against exogenous aggressions and *zheng qi* 正气 (“right *qi*”) which is the body’s healthy *qi* as opposed to the pathogenic one (*xie qi* 邪气). In Chinese medicine, the term *qi* is also used to refer to the physiological activities of body organ systems (*zang fu zhi qi* 脏腑之气, “organ *qi*”) and channels and network vessels (*jing luo zhi qi* 经络之气, “channels and network vessels *qi*”), to the seasonal (*liu qi* 六气, “six *qi*” or “six climatic configurations”) or abnormal (*liu yin* 六淫 or *liu xie qi* 六邪气, “six excesses” or “six climatic perversities”) climatic conditions, to an external pathogen which lurks within the organism (*fu qi* 伏气, “latent *qi*”) and, finally, to the second level of penetration of a warm-heat pathogen within the organism (*qi fen* 气分, “*qi* level”).

2.2.2 Yin-Yang

Yin 阴 and *yang* 阳 are two opposites but interdependent principles which reflect the inherent duality of beings and phenomena in the universe. Through their constant movements and mutations (opposition, divisibility, mutual control and balance, transformation into one another, etc.), they are the foundation of everything and every change in the universe. *Yin* and *yang* are relative (e.g. there is no absolute *yin* or *yang*) and interdependent (e.g. *yin* does not exist without *yang* and *yang* does not exist without *yin*). Furthermore, their relation is constantly changing, and, under certain circumstances, they may transform into one another. In Chinese philosophy, the theory of *yin-yang* is a way of explaining the nature and the universe. Initially, these two principles referred to the shady and sunny side of a slope. Later, the theory was applied to other domains: climate (cold/hot), season (autumn-winter/spring-summer), location (lower/upper, left/right, interior/exterior), orientation (north/south, west/east), movement of things and phenomena (passive/active, descending/ascending), gender (female/male), etc. In medicine, this theory pervades anatomy, physiology, aetiology, pathogeny and therapeutics: for example, the body surface and back are *yang*, while the interior and abdomen are *yin*; body organs are *yin* or *yang* according to their form, functions and depth within the body; a disease is *yang* when it is caused by external pathogens and *yin* when it is due to internal causes; drugs are also classified as *yin* or *yang* according to their nature, flavour and functions. Health is the balance of these two principles within the body, while pathology results from their imbalance. In the latter case, we speak of “excess” (*shi* 实) or of “deficiency” (or “vacuity” *xu* 虛) of *yin* or *yang*.

2.2.3 Wu Xing (“Five Movements”)

The theory of *wu xing* 五行 is a development of the *yin-yang* theory.[4] According to Chinese philosophy, events and phenomena within the universe result from the movement and mutation of five basic substances, namely, wood, fire, earth, metal and water. They correspond to phases of mutation of *qi* generated by the succession of *yin* and *yang*. Each movement has specific characteristics: wood (*mu* 木) bends and straights up, fire (*huo* 火) burns and rises, earth (*tu* 土) receives the seed and gives crops, metal (*jin* 金) is malleable and takes other shapes, and, finally, water (*shui* 水) moisturizes and flows downwards. These movements are interdependent and influence each other: we speak of promotion or subjugation. It is said, for example, that water promotes wood which promotes fire, etc., but water subjugates fire which subjugates metal, etc. Applied to medicine, this theory explains the physio-pathological relations between body organ systems.

2.2.4 Zang-Fu (“Organs”)

According to Chinese medicine, the human body is an integrated whole containing five *zang* organs 脏 (e.g. heart, lung, spleen, liver and kidney) and six *fu* organs 腑 (e.g. gallbladder, stomach, small and large intestines, urinary bladder and triple burner).[5] The *zang* organs are *yin* because they are perceived as being located deeper within the body and their common functions are to produce, transform, regulate and store fundamental substances (*qi*, blood, essence and body fluids). The *fu* organs are *yang* because of their more external location in the body. Their common functions are to receive and decompose parts of solid and liquid food that will be transformed into fundamental substances and to transport and excrete the waste. The *zang-fu* organs are interconnected by the system of channels and network vessels. They are conceived as complex and interdependent functional systems: each *zang* organ is

---

[4] In English, *wu xing* 五行 is often translated as “five elements” by analogy with the notion of “element” as a basic constituent of nature in the ancient Greek philosophy (Maciocia 1989). As *xing* literally means “movement” or “process” and as the theory of *wu xing* emphasizes movement and change, its translation as “five movements” appears more adequate.

[5] The *san jiao* 三焦 (triple burner or three burners) refers to three areas (or burners) of the body cavity which include the different organs with their functional activities: one distinguishes the upper (e.g. heart/pericardium and lungs), middle (e.g. stomach and spleen) and lower (e.g. liver, kidneys, bladders, small and large intestines, and the womb in women) burners. It is the way of circulation of the *qi* within the organism which stimulates the physiological activities of body organs and fluids.

coupled with a *fu* organ, a sense organ, a body tissue, a body fluid, an emotion, a sound and also a specific movement, climatic factor and season. The lung, for example, which is located in the upper part of the body cavity (or upper burner, see note 5), is related to the large intestine (*fu* organ), nose (sense organ), skin and body hair (body tissue), nasal secretions (body fluid), sadness (emotion), sob (sound), metal (movement), dryness (climatic factor) and autumn (season). Therefore, when Chinese medicine speaks of the lung, it refers to the system of the lung with all its connections and functions. The human body is thus conceived as a microcosm within the macrocosm of the universe. Z*ang-fu* organs are related on physio-pathological levels: their functions are interdependent, and a disease may pass from one organ system to another.

2.2.5 Bing Yin (“Aetiology”)

If health is the result of the balance of *yin* and *yang* within the organism, it also depends on the harmony of human beings with the natural world. Nature provides a favourable environment to the existence of human beings, and human organism regulates and adapts to the changes that occur in the environment. All environmental events (e.g. seasonal climatic conditions, unseasonable weather, environmental alteration, etc.) affect the individual, including his health state. When the organism fails to adapt, disease may appear.

In Chinese medicine, abnormal climatic changes may invade the body, causing diseases. Usually, wind (*feng* 风), cold (*han* 寒), summer heat (*shu* 暑), dryness (*zao* 燥), dampness (*shi* 湿) and fire/heat (*huo/re* 火/热)[6] are normal climatic factors related to specific seasons according to the theories of *yin-yang* and *wu xing*. They are collectively called the “six *qi*” or “six climatic configurations” (*liu qi* 六气). Wind usually occurs in spring although it may appear in other seasons; cold is associated with winter, summer heat with summer, dryness with late summer,[7] dampness with autumn and fire/heat with any other season. The six *qi* are necessary to the life and growth of human beings and normally do not cause disease. However, when they act out of their regular temporal sequence (e.g. heat during winter), manifest excessively or change abruptly (e.g. rapid alternation of cold and heat) and when body resistance is low, they may cause a disease. Becoming the “six excesses”

---

[6] The terms “fire” (*huo*) and “heat” (*re*) are often used interchangeably in works about Chinese medicine. They refer however to different realities. Firstly, there is a difference of degree between them (e.g. heat is lesser than fire). Secondly, fire as a pathogenic climatic factor refers either to summer heat (*shu*), to an extreme heat that may occur at any season or to the transformation into fire of another climatic perversity within the organism (e.g. cold contracted in winter may transform into heat and extreme heat may give way to fire). Finally, one distinguishes the “lesser fire” (*shao huo* 少火), which is essential to the physiological activity, from the “vigorous fire” (*zhuang huo* 壮火) or pathogenic fire which may injure the *qi*. It becomes an internal cause of disease (Marié 1997).

[7] Late summer is a period of ten days around the summer solstice.

(*liu yin* 六淫) or "six climatic perversities" (*liu xie qi* 六邪气), they are said to enter the organism through the skin and body hair or through the nose and mouth and to work their way inwards, causing various kinds of functional disorders. Wind is usually considered as the precursor of exogenous febrile diseases. It acts as a support and vehicle for the other excesses and also reinforces their virulence. The six excesses may change in nature according to the individual constitution: for example, pathogenic cold may turn into internal heat when individual constitution is characterized by an excess of *yang*. In some cases, they may stay latent within the organism and emerge later under another nature (see *infra*). Finally, they do not affect people in a similar way. This depends on the relative force or weakness of the individual *zheng qi* as opposed to that of the *xie qi* which is influenced by constitution, physical activity, alimentation, lifestyle, emotional state, etc., of the person. Body resistance (e.g. the strength of the individual *zheng qi*) is thus the determining factor in the emergence of a disease, while the pathogenic factor is only a contributing factor.

The six excesses manifest in the patient's body with different signs and symptoms. Some are common to every disease (e.g. fever and aversion to cold which express the invasion of the body by a pathogen), while others depend on the specific nature of the excess(es) involved. For example, due to its mobile and changing nature, wind manifests in the patient's body with inconstant and moving symptoms such as erratic pains, pruritus or cutaneous eruptions which change places, spasms, trembling, etc. While cold manifests with headaches, body pains, spasms (e.g. one quality of cold is to contract), etc., heat presents with high fever, sensation of hot body, sweating (e.g. heat opens the pores), aversion to heat and search for cold, redness of the face and eyes, etc. Given its tendency to damage body fluids, it can also produce thirst, dry tongue, rare dark urines, etc. When in excess, it may transform into fire and then concentrate on a specific spot of the body, giving way to ulcers, abscesses, furuncles, etc. In this case, Chinese medicine speaks of "heat toxin" (*re du* 热毒) or "warm toxin" (*wen du* 温毒) (see *infra*).

2.3 Epidemic Febrile Diseases in Early Classics of Medicine

According to early classics of medicine, exogenous febrile diseases (including epidemic febrile diseases) are due to abnormal climatic conditions. Actually,

> [They are] understood within the traditional system of cyclical change at the basis of the Chinese agrarian calendar. (Hanson 2011)

They are ranged in the general category of *shang han* 伤寒 ("cold damage disorders") whatever the nature of the causative climatic pathogen or the clinical manifestations of the disease. In this way, diseases presenting with a rapid evolution, pronounced signs and symptoms of heat and a tendency to damage the *yin* – and hence called "warm diseases" (*wen bing* 温病) or "heat diseases" (*re bing* 热病) –

belong to this category.[8] For example, Chap. 31 (paragraph 1) of the *Huang Di Nei Jing – Su Wen* 黄帝内经-素问 ("Classic of Internal Medicine of the Yellow Emperor – Plain Questions")[9] states that warm diseases belong to the category of cold damage disorders (*shang han* 伤寒).

Moreover, *Su Wen* 3 (paragraph 13) stresses that the exposition in winter to pathogenic cold may manifest in spring as a warm disease, and *Su Wen* 31 (paragraph 8) further specifies that pathogenic cold contracted in winter may manifest as a "warm disease" in spring or as a "heat disease" in summer. Therefore, pathogenic cold may stay latent (or lurk) within the organism and give way later to a disease of another kind. In this way, the so-called warm and heat diseases result from the transformation of pathogenic cold into warmth or heat within the organism. At that time, pathogenic cold and wind were understood as the main causes of exogenous febrile diseases (including epidemic febrile diseases), and warm diseases were considered a kind of cold damage disorders.

Su Wen 72 (paragraphs 7 and 8) refers to five kinds of seasonal febrile diseases which are related to the five movements (e.g. earth, water, metal, wood and fire), "easily pass between people" and manifest with the same degree of severity regardless of the person's age. It further states that persons with a strong *zheng qi* are not affected by them (see Van Nghi 1973/1991).

The absence of a clear distinction between cold damage disorders and warm diseases is also apparent in the *Nan Jing* 难经 ("Classic of Difficult Issues") written slightly later and which discusses certain theoretical problems presented by the *Nei Jing – Su Wen*. The 58th difficult issue distinguishes five "kinds of harm caused by cold": *zhong feng* 中风 ("wind stroke"), *shang han* 伤寒 ("cold damage disorder"), *shi re* 湿热 ("damp-heat attack"), *wen bing* 温病 ("warm disease") and *re bing* 热病 ("heat disease") (Unschuld 1986). In these two early classics of medicine, *shang han* refers to the category of exogenous febrile diseases brought on by unseasonable weather and also to a specific febrile disease caused by pathogenic cold. Nowadays, it only refers to diseases resulting from a cold injury. It is also the modern term for typhoid fever.

This conception was retaken by Zhang Ji (Zhang Zhong-Jing, 150–219) in his master essay *Shang Han Lun* 伤寒论 ("Treatise on Cold Damage Disorders")[10]

---

[8] Warmth is an attenuated form of heat. In works devoted to Chinese medicine, the denomination "warm diseases" (*wen bing*) refers interchangeably to warm and heat diseases.

[9] The *Huang Di Nei Jing* ("Classic of Internal Medicine of the Yellow Emperor") or, in short, *Nei Jing* ("Classic of Internal Medicine"), which is ascribed to the legendary emperor Huang Di, was probably compiled by unknown authors at different periods from the Warring States Period (475–221 B.C.) to the Eastern Han Dynasty (25–220 A.D.). It is a synthesis of the different currents of thought and clinical observations and experiences of these periods. It consists of two parts: *Su Wen* 素问 ("Plain Questions") which establishes the theoretical foundations of Chinese medicine and gives the descriptions of numerous diseases and *Ling Shu* 灵枢 ("Spiritual Pivot") which is more devoted to acupuncture and moxibustion. References to the *Huang Di Nei Jing – Su Wen* were borrowed from Van Nghi (1973/1991), Liu (2001), Unschuld (2003) and Kong (2010).

[10] The *Shang Han Lun* is part of Zhang Ji's original text entitled *Shang Han Za Bing Lun* 伤寒杂病论 ("Treatise on Cold Damage Disorders and Miscellaneous Diseases") that was lost during the

written in reaction to the series of deadly epidemics which swept out various provinces during the last decade of the Eastern Han Dynasty (25–220).[11] Zhang Ji was an official of Changsha, capital city of the Hunan province, which was then located in the "south" (nowadays, South Central China). In the preface of the *Treatise*, Zhang Ji alluded to the death of two-thirds of his clan members in less than ten years, seven out of ten from exogenous febrile diseases. This situation inspired him to study the characteristics of the epidemics which were sweeping out his province. Looking back on ancient medical texts and collecting the medicinal formulas of his contemporaries, he wrote the *Shang Han Lun* in which he provided a theoretical framework for the diagnosis and treatment of exogenous febrile diseases. Focusing on pathogenic cold and wind to which he credited these deadly epidemic diseases, Zhang Ji showed that exogenous febrile diseases may progress according to six stages within the organism, three *yang* and three *yin*, namely, the *tai yang* ("greater *yang*"), *yang ming* ("*yang* brightness"), *shao yang* ("lesser *yang*"), *tai yin* ("greater *yin*"), *shao yin* ("lesser *yin*") and *jue yin* ("attenuated *yin*") stages.[12] In the *san yang* (e.g. the three *yang* stages), the disease involves the six *fu* organs, while in the *san yin* (e.g. the three *yin* stages), it implicates the five *zang* organs. Only the *tai yang* stage (e.g. the first of the *yang* stages) is an exterior condition. Each stage is marked by specific syndromes. Syndromes (or "patterns", *zheng* 证) are specific constellations of signs (e.g. characteristics of the pulse, tongue form, colour and largeness, tongue moss characteristics, etc.) and symptoms (sensation of hot body, fever more or less high, thirst, sweating, aversion to cold or wind, headaches, agitation, fear of heat, etc.) which vary over the time during the course of the disease according to the relative strength or weakness of the pathogenic factor and to that of the individual *zheng qi*, the location of the disease within the organism and also the organ system affected. In the *san yang*, for example, the *zheng qi* is strong despite the predominance of the pathogenic factor, hence the symptoms of excess and heat; in the *san yin*, there is a gradual weakening of the *zheng qi*, hence the symptoms of cold and deficiency. Syndromes usually appear in an isolated way. In some cases, two or more syndromes may appear simultaneously. In addition, one syndrome may transform into another. Warm diseases are referred to in the *tai yang* stage where

---

numerous wars of the late Eastern Han Dynasty. Fragments of the original treatise have been found some decades later. The section devoted to cold damage disorders was arranged and edited by Wang Xi (Wang Shu-He, 210–285), a palace physician of the Western Jin Dynasty (220–265), into the book we know now as *Shang Han Lun* ("Treatise on Cold Damage Disorders"). The sections of the original manuscript devoted to the study of different types of diseases (including digestive, gynaecological and paediatric disorders) were rearranged later into the book entitled *Jin Kui Yao Lue* 金匮要略 ("Synopsis of Prescriptions of the Golden Chamber"). The citations in this article are borrowed from the translation of the *Shang Han Lun* by Mitchell et al. (see Shāng Hán Lùn 1999).

[11] 119 disasters including epidemic diseases have been reported during the late Eastern Han Dynasty (see Qu et al. 1994).

[12] It should be noted that *tai yang*, *yang ming*, *shao yang*, *tai yin*, *shao yin* and *jue yin* are the names of the six pairs of major channels to which one refers to in acupuncture and moxibustion. In the *Shang Han Lun*, they are referring to different stages of penetration of the exogenous pathogens within the organism and not to the channels.

Zhang Ji differentiated four syndromes: *zhong feng* 中风 ("wind stroke"), *shang han* 伤寒 ("cold damage disorder"), *wen bing* 温病 ("warm disease") and *feng wen* 风温 ("wind warmth"). *Wen bing* and *feng wen* are defined as follows:

> When in greater *yang* disease [there is] heat effusion and thirst, without aversion to cold, [this] is a warm disease. If, after sweating has been promoted, there is generalized scorching heat [e.g., sensation of hot body], this is called wind-warmth. (line 6; see Shāng Hán Lùn 1999)

As it can be seen, warm diseases and wind warmth are specific syndromes into the category of cold damage disorders. Zhang Ji developed a system of diagnosis and treatment of syndromes based on the six stages of progression of the disease within the organism. As he did not suggest any specific medicinal formulas for warm diseases, the latter have been treated during centuries according to the general principles established for cold damage disorders, e.g. mainly by warm and acrid substances.[13]

In the *Zhu Bing Yuan Hou Zong Lun* 诸病源候论 ("Treatise on Causes and Symptoms of Various Diseases", 610), the first Chinese medical encyclopaedia compiled by Chao Yuan-Fang (550?–630?) and collaborators, unseasonable or excessive weather is still seen as the cause of epidemic febrile diseases:

> Epidemic diseases belong to the same category as diseases due to an influence contrary to the season, and as diseases due to a hot influence or a warm influence, for they all originate from the fact that, in the course of one year, the influences of the solar periods have not been in harmony, that cold and hot are out of order, that violent wind and heavy rain suddenly occur, or that fog and dew take too long to dissipate. Most of the time this causes epidemic diseases among the people, the manifestations of which are the same for the young and for adults alike and evoke the ferocity of demons. That is why they are also called pestilential diseases (*yi li bing* 疫疠病). (fascicle 10; translated in Despeux 2001)

2.4 First Critics to the Cold Damage Theory

It was during the Song-Jin-Yuan Dynasties (960–1368) that the approach developed by Zhang Ji for the diagnosis and treatment of exogenous febrile diseases began to be challenged. During the Northern Song Dynasty (960–1279), a wave of deadly epidemic diseases, "mostly southern in origin" (Goldschmidt 2009), swept out Chinese provinces. They were possibly favoured by the ongoing movements of migration from the north to the south, the growth of the volume of trade, the expansion of trade routes and the growing urbanization (Goldschmidt 2009). Anxious to find a cure for them, the imperial government distributed remedies to the people and, in 1057, instituted a "Bureau for Revising and Printing Medical Treatises" which was charged to collect, revise, edit and publish old and contemporary

---

[13] Such as *ma huang* (*Herba ephedrae*) ou *gui zhi* (*Ramulus cinnamon cassiae*). Acrid substances have the property to "clear the surface [of the body]". In warm diseases, however, they may damage body fluids and favour the progression of the disease within the organism (Liu 2001).

treatises of medicine. Consequently, earlier medical treatises (including the *Shang Han Lun* of Zhang Ji) enjoyed a greater divulgation among scholarly physicians and became the objects of annotated and critical editions. It was during these periods of recurring epidemic diseases that physicians began to point out the inadequacy of the conventional theory on epidemic diseases and the inefficiency of traditional remedies in the context of contemporary diseases. In the early twelfth century, the invasion of northern China by Jurchen people coming from Manchuria which culminated with the foundation of the Jin Dynasty (1115–1271) led the Song Imperial Court to flee to the Yangzi Delta and to set up the Southern Song Dynasty (1127–1279) in Hangzhou, Zhejiang province. The boundaries of China now extended to the Lingnan ("south of the Ling ranges") region (modern-day Guangdong and Guangxi provinces). This shift of the Han civilization towards the south

> fostered regional awareness among physicians […] who began to identify differences in climates, environments, bodily constitutions and medical conditions between northern and southern regions and populations of China. (Hanson 2011)[14]

That is why some scholarly physicians from Northern and Southern China began to condemn their contemporaries for their exaggerated observance of old canons of medicine, for their indiscriminate use of ancient therapeutic approaches that were not tailored to the nature of contemporary diseases and/or to the different climates and regions of China and also for paying little attention to the symptoms of warm diseases which, according to them, lead them to confuse cold damage disorders with warm diseases. It is also during the Jin-Yuan Period that the term *wen bing* began to take the meaning of "epidemic febrile diseases". These, however, were still linked to abnormal climatic conditions (Obringer 2010).

Pang An-Shi (1042–1099) emphasized the need to adapt traditional medicinal formulas to the different climates and bodily constitutions of China. He alluded, for example, to the fact that *gui zhi tang*, the warm acrid Cinnamon Twig Decoction prescribed in the Treatise on Cold Damage Disorders, should be adjusted to suit the climate and location of the patient: e.g. it could be administered in any season to patients living in the north or west of China but only in winter or spring to those living in South Central China where the weather was warmer (Warm Disease Theory – Wēn Bìng Xué 2000; Liu 2001). In the *Shang Han Zong Bing Lun* 伤寒总病论 ("General Treatise on Cold Damage Disorders," 1093), he advanced another aetiology for seasonal febrile diseases. These are not the result of abnormal climatic conditions but are caused by an extremely virulent *qi* (*yi qi* 异气) (Obringer 2010). The concept of "pestilential *qi*" (*li qi*) advanced by Wu You-Xing during the late Ming Dynasty shows some relationship with this notion of an abnormally "virulent *qi*" (Obringer 2010).

Liu Wansu (Liu Shou-Zhen, 1110–1200), the founder of the "Cold and Cooling School of Medicine" (*Han Liang Xue Pai* 寒凉学派), recommended the use of

---

[14] Differences in climates, environments, bodily constitutions and nature of diseases, foods and therapies were first alluded to in *Su Wen* 12 which divided China into five directions (*wu fang* 五方, e.g. east, west, north, south and centre). On the theory of *wu fang* and the resulting regionalist perspective in medicine, see Hanson (2011).

bitter, acrid and cold herbs in the treatment of exogenous febrile diseases. He also stressed that exogenous pathogenic factors may transform into fire within the organism and that emotional disturbances (e.g. the internal causes of diseases) also lead to the formation of fire/heat within the body (Liu 2001).

Zhang Yuan-Su (Zhang Jie-Gu), a physician of the twelfth century, advanced the view that, given the changing conditions between ancient and modern times, physicians should discard traditional medicinal formulas in the treatment of the new diseases and also devise a system of their own:

> In the ordinary course of events, when one is treating [a new] disease, one does not use the old remedies… The movements of the internal ethers are not the same. The past and the present follow different tracks, and to use the old remedies for the new illnesses is ineffective. (Cited by Elvin 1973)

A further example of the scepticism towards the *Shang Han Lun* is illustrated by Wang Lu (Wang An-Dao, 1332–1391) who denounced the confusion made by his contemporaries between cold damage disorders and warm diseases to which he credited the therapeutic inefficiency of cold damage formulas and he proposed specific therapeutic formulas for these two categories of diseases. Contending that old remedies were ineffective for present-day diseases, he also advocated the need to go against the tide of the classics of medicine (Hoizey 1988; Liu 2001).

2.5 From Cold Damage Disorders to Warm Diseases

The late Ming Dynasty (1368–1644) and early Qing Dynasty (1644–1911) mark a decisive turning point into the conceptual and medical approach of exogenous febrile diseases. These periods were marked by a series of natural disasters, famines and widespread deadly epidemic diseases (*da yi* 大疫 “great epidemic disease”). For example, about 19 major epidemic outbreaks with countless deaths have been registered between 1408 and 1643, in especial during the years 1639–1643 (Wang et al. 1999). In 1641, the worst year of the period, 79 localities from ten provinces were affected. There were epidemic diseases at all seasons of that year, the worst being in spring and summer (Elvin 1973; Dunstan 1975). Mortality rates varied between 20 % and 90 % according to the localities (Elvin 1973). The nature of these epidemic diseases is uncertain. Various aetiologies have been proposed: pneumonic and septicaemic plague, haemorrhagic influenza, anthrax, cerebrospinal fever and bubonic plague.[15]

---

[15] According to Dunstan (1975) and Benedict (1986), the aetiology of bubonic plague is improbable given the absence in contemporary local gazetteers and medical works of any clear mention of buboes (the most characteristic symptom of the disease) and of widespread death of rats prior to the outbreak of the disease in humans. Actually, rat epizootics and buboes or enlarged lymph glands are the criteria used by medical historians to establish a retrospective diagnosis of bubonic plague through historical sources.

In 1641, the physician Wu You-Ke (Wu You-Xing, 1580–1660), a native of Suzhou (present-day Jiangsu province, Jiangnan region, South China), observed the rapid progression of the epidemic diseases in each village and family. He also noted the therapeutic inefficiency of cold damage formulas which he explained by the wrong appraisal, by his contemporaries, of the aetio-pathogeny and clinical manifestations of the epidemic diseases. After an extensive research, he concluded on the distinct nature of epidemic febrile diseases and cold damage disorders. In the *Wen Yi Lun* 温疫论 ("Treatise on Warm Epidemic Diseases") written in 1642, e.g. one year after the 1641 deadly epidemics, he proposed a new aetiology and natural history for epidemic febrile diseases which can be summarized as follows[16]:

1. Epidemic febrile diseases are not directly caused by climatic factors acting out of their proper time or when in excess (e.g. the six excesses). They are instead caused by a great variety (*za* 杂 "miscellaneous")[17] of "pestilential *qi*" (*li qi* 疠气) which reside in the nature (lit. between "Heaven and Earth", *tian di* 天地). Therefore, the nature of epidemic diseases varies according to the specific nature of the pestilential *qi* ("One [epidemic] disease, one [pestilential] *qi*").
2. Pestilential *qi* are shapeless and invisible to the naked eye, and they are only perceived through their effects within the body.
3. They have a warm or hot nature and attack people at their will (e.g. at any season).
4. They may be contracted from the contaminated atmosphere (*tian shou* 天受, lit. "received from heaven") or via personal contact (*chuan ran* 传染). In both cases, the disease is the same.
5. Pestilential *qi* enter the body through the nose and mouth rather than through the skin and body hair as it was postulated before.
6. Once in the organism, pestilential *qi* lodge into the "membrane source" (*mo yuan* 膜原)[18] located in the chest where conventional therapies could not get at them.
7. Human beings and animals are afflicted by specific pestilential *qi*; moreover, pestilential *qi* differ according to animal species (e.g. diseases in oxen, sheep, chickens or ducks are caused by specific pestilential *qi*).
8. Pestilential *qi* manifest in the body with the same signs and symptoms of the six excesses. They differ however from them by their greater virulence and contagious power. They pass from one person to another and diffuse widely and quickly between people. They may invade the healthiest organisms and afflict everyone in the same way regardless of the age and physical constitution of the person.

---

[16] On the *Wen Yi Lun*, see Dunstan (1975), Hoizey (1988), Liu (2001), Obringer (2010), and Hanson (2011).

[17] The term *za* ("miscellaneous") alludes to the existence of various types of pestilential *qi* which produce different kinds of epidemic diseases of varying virulence (Obringer 2010; Hanson 2011).

[18] The "membrane source" (*mo yuan* 膜原) is located between the stomach and the muscle layer at mid-distance from the inner and outer parts of the body. Wu You-Xing elaborated a special formula (the decoction *da yuan yin*) to reach this area, diminish the heat, dry the dampness and favour the circulation of the *qi* within the organism in order to expel the pestilential *qi* (Liu 2001; Hanson 2011).

Pestilential *qi* are, therefore, not directly brought on by abnormal seasonal conditions. Their emergence is also unpredictable. The views expressed in the *Wen Yi Lun* in response to the great epidemics of the period 1639–1644 (as the *Shang Han Lun* was written in reaction to the epidemics of the late Eastern Han Dynasty) were radically different from the conventional seasonal explanation of epidemic diseases derived from the conception of the harmony between the body microcosm and the universe macrocosm. The *Wen Yi Lun* inspired studies on diseases caused by warm and heat factors which led to the foundation of the "School of Warm Diseases" (*Wen Bing Xue Pai* 温病学派) during the Qing Dynasty.

During the Qing Dynasty, a wave of severe epidemic diseases swept out again various regions and provinces, in especial the Jiangnan region. The four main theoreticians of the School of Warm Diseases are native of this region. They differentiated warm diseases from cold damage disorders and proposed new systems of diagnosis and treatment.

In *Wen Re Lun* 温热论 ("Treatise on Warm-Heat Diseases"), the Suzhou physician Ye Tian-Shi (Ye Gui, 1667–1746) distinguished four levels (*si fen* 四分) in the progression of a warm disease within the body, each one presenting with specific syndromes: "defensive level" (*wei fen* 卫分), "*qi* level" (*qi fen* 气分), "constructive/nutritive level" (*ying fen* 营分) and "blood level" (*xue fen* 血分). Usually, warm-heat pathogens attack first the body surface (e.g. the defensive level), impairing the body defence functions which are linked to the lung system, skin and body hair. The most important symptoms at this level are fever, slight aversion to cold and small increased thirst. Other potential signs and symptoms are sneezing, nasal congestion, sore throat and cough, headache, red-tipped tongue, floating and rapid pulse, etc. At this level, the disease is considered as mild. In cases it is left untreated or improperly treated, the warm-heat pathogen will progress to the *qi* level or directly to the other levels, causing different syndromes. When it reaches the last level (e.g. the blood level), it leads to a loss of blood, hence blood vomiting, nosebleed, haemoptysis, bloody stools and urines, purple or black skin eruptions, deep-red tongue, etc. Other potential symptoms are fever, restlessness or delirium, coma, etc. Ye Tian-Shi designed a system of differentiation of syndromes based on the progression of the disease according to the four levels. With this system, the physician may anticipate and follow the progression, transformation and worsening of a warm disease from the beginning to the end, judge its severity and also differentiate the syndromes over the course of the disease.[19]

Ye Tian-Shi also clarified the notion of latent *qi* or lurking pathogen (*fu qi* 伏气 or *fu xie qi* 伏邪气). As seen above, the possibility for a pathogen to lurk for a while within the organism was first alluded to in the *Nei Jing – Su Wen*. However, the concept of latent or lurking pathogen was only developed by the School of Warm Diseases. A lurking pathogen is a pathogen which invades the body at a specific season and incubates within the organism where it changes its nature and emerges later either by itself or stimulated by the attack of another pathogen. Ye Tian-Shi

---

[19] On differentiation of syndromes in warm diseases according to the four levels, see Warm Disease Theory – Wēn Bìng Xué (2000) and Liu (2001).

distinguished two kinds of diseases caused by a lurking pathogen: *chun wen* 春温 (“spring warmth”) and *fu shu* 伏暑 (“lurking summer heat”). The first results from the invasion in winter of the body by pathogenic cold which transforms into heat within the organism before emerging as a warm disease with the warmth of spring; the second results from the aggression in summer of the body by pathogenic summer heat which lurks within the organism and then combines with dampness in autumn or winter before emerging at this or that season. Diseases due to a lurking pathogen present with symptoms of internal heat (e.g. fever, dry mouth, thirst, dark urines) are more serious and have a longer evolution than diseases manifesting immediately after the attack of the body by a warm-heat climatic pathogen.[20]

In *Shi Re Tiao Bian* 湿热条辩 (“Differentiation of Damp-Heat Diseases”), Xue Xue (Xue Sheng-Bai, 1681–1770) discussed on the aetio-pathogeny, differentiation and treatment of damp-heat diseases. He showed that heat was somehow trapped into dampness (hence, the high fever but without any sensation of hot body) resulting in a blockage of the *qi* which cannot circulate anymore within the organism. It is thus necessary to disperse dampness, refresh heat and favour the circulation of *qi* in the body (Warm Disease Theory – Wēn Bìng Xué 2000; Liu 2001).

In *Wen Bing Tiao Bian* 温病条辨 (“Systematic Differentiation of Warm Diseases”, 1798), Wu Tang (Wu Ju-Tong, 1758–1836) expanded the theory developed by Ye Tian-Shi and set up a complementary system of differentiation of syndromes based on the pathological changes in the triple burner or upper, middle and lower body cavities where warm or hot pathogens may stagnate.[21] In this way, warm diseases are differentiated into three categories according to their location in the three burners. Usually, a warm disease initiates in the upper burner. If left untreated, it will successively invade the middle and lower burners. With this diagnosis system, it is possible to locate the disease and follow its progression within the body. Wu Tang distinguished six types of *wen bing*, namely, *feng wen* 风温 (“wind warmth”), *wen re* 温热 (“warm heat”), *wen du* 温毒 (“warm toxin”),[22] *wen nue* 温疟 (“warm malaria”),[23] *shi wen* 湿温 (“damp warmth”) and *shu wen* 暑温 (“summer heat warmth”). Wu Tang also differentiated warm diseases in two categories

---

[20] On lurking pathogens and associated diseases, see Warm Disease Theory – Wēn Bìng Xué (2000) and Liu (2001).

[21] See note 5 above.

[22] The concept of “toxin” (*du* 毒) in Chinese medicine differs from that of western medicine where it is related to a toxic protein released by some bacteria. In Chinese medicine, “toxin” refers to three different realities: toxic nature of herbs, particular patterns in dermatology (e.g. herpes zoster) and toxic warm heat which may manifest within the body with localized symptoms (e.g. local redness, swelling and pain, sometimes also local eruptions or open ulcerations). Three main diseases in Chinese medicine are understood in reference to the concept of warm toxin: “big head fever” (*da tou wen* 大头温), “putrefying throat eruption” (*lan hou sha* 烂喉沙) and “throat-entwining wind” (*chan hou feng* 缠喉风). These diseases somehow overlap certain diseases of western medicine, respectively erysipelas or mumps, scarlet fever and diphtheria (Dunstan 1975; Hoizey 1988; Warm Disease Theory – Wēn Bìng Xué 2000; Liu 2001).

[23] In Chinese medicine, the term *nue* 疟 refers to diseases which manifest with regular alternation of chills and fevers and sweating (Liu 2001). Of course, it is impossible to assert with any degree of certainty that diseases described in the past with these symptoms are really malaria.

according to the presence or absence of dampness, and he proposed specific therapeutic principles for each stage and syndrome. Finally, he described the aetiology and pathogeny of the disease known under the name of "big head fever" (*da tou wen* 大头温) which is due to an attack of the head and face by pathogenic warmth or heat, hence the swollen and redness of this body part. Medical and historical records show that this disease was responsible of severe epidemic outbreaks during the 1580s (Dunstan 1975; Hoizey 1988; Liu 2001).

In *Wen Re Jing Wei* 温热经纬 ("Warp and Woof of Warm-Heat Diseases", 1852), Wang Meng-Ming (Wang Shi-Xiong, 1808–1867) showed the close dependence of summer heat and dampness. He also proposed different treatments for warm lurking diseases and diseases following an initial attack by a warm climatic pathogen. Finally, he warned against the use of too cold remedies in the early stage of a warm disease due to their potentiality to "congeal" the warm-heat pathogen (Liu 2001).

Other physicians elaborated on the differences between cold damage disorders and warm diseases, devoted books to specific epidemic diseases (e.g. smallpox, measles, scarlet fever, cholera, bubonic plague, etc.), further studied the pathomechanism of warm toxins or attempted to reconcile the theory of warm diseases with that of cold damage disorders (Hoizey 1988; Liu 2001; Hanson 2011). Wang Meng-Ming, for example, who observed the incursion of cholera in Hangzhou in 1837, dedicated a book on seasonal and unseasonal forms of choleric affections.[24]

Nowadays, Chinese medicine distinguishes various categories of warm diseases according to their season of emergence, the nature of the climatic pathogen involved and the fact that they occur after the initial attack or after a phase of latency: *feng wen* 风温 ("wind warmth") and *chun wen* 春温 ("spring warmth") in spring, *shu wen* 署温 ("summer heat warmth") in summer, *shi wen* 湿温 ("damp warmth") in the late summer, *qiu zao* 秋燥 ("autumn dryness") and *fu shu* 伏暑 ("latent or lurking summer heat") in autumn or winter and, finally, *dong wen* 冬温 ("winter warmth") in winter when temperature is abnormally high. Each of these diseases is characterized by specific syndromes according to the body level affected and its location in the triple burner.

2.6 Conclusion

The School of Warm Diseases introduced important changes into the medical perceptions and apprehension of the natural history, aetio-pathogeny and evolution of exogenous febrile diseases and epidemic diseases. Although the concept of warm

---

[24] The modern term for cholera is *huo luan* 霍乱. In the past, in China as in Europe, the term "cholera" was used to refer to the seasonal or sporadic diarrhoea. In 1841, e.g. during the third pandemic of cholera, John Snow first demonstrated the aquatic nature of the disease. However, its causal agent was only discovered in 1883 in Calcutta and Alexandria by the German bacteriologist Robert Koch. Since that time, the term "cholera" refers only to this affection. On Wang Meng-Ming's perception of cholera, see Hanson (2011).

diseases was present in the early treatises of medicine which ascribed them to the transformation into heat of pathogenic cold contracted in winter, this concept took another meaning with the development of this school of thought. It shows that warm diseases and cold damage disorders have a different nature and that warm diseases are brought on by warm-heat pathogens. Depending on the nature of the climatic pathogen, they may appear at any season. They are characterized by a rapid onset and evolution, with predominance of heat symptoms, and they readily injure body fluids. They may also occur under an endemic or an epidemic form. For example, damp-heat diseases are more common in humid and warm coastal regions of Southeast China than in dry and cold regions of the Northeast (Liu 2001).

The School of Warm Diseases also introduced new aetio-pathogenic concepts for epidemic febrile diseases: heterogeneous pestilential *qi* and epidemic toxins; invasion of the body by the nose and mouth; warm nature of pestilential *qi* or of epidemic toxin; specificity of pestilential *qi* according to the nature of the epidemic disease and to the species (e.g. humans, animals and between animal species); and favouring role of extreme climatic, social or environmental conditions (e.g. droughts, floods, famines, wars and other social turbulences, etc.) in their outbreak.

Two schools of thought on exogenous febrile diseases exist today in China: the School of Cold Damage Disorders and the School of Warm Diseases. Both have developed specific diagnosis and therapeutic approaches. The identification of patterns according to the six stages is used in the diagnosis and treatment of diseases caused by pathogenic wind and cold. The four layers and triple burner approaches are used in the diagnosis and treatment of warm diseases. Nowadays, both serve as a conceptual and diagnosis tool for the differentiation of the underlying syndromes of a wide range of infectious (e.g. eruptive fevers, Japanese encephalitis, typhoid and paratyphoid fevers, dengue fever, HIV/AIDS, scarlet fever, mumps, etc.) and not infectious (e.g. burns, allergies) diseases of western medicine, including some emerging diseases such as the H5N1 influenza or the severe acute respiratory syndrome (SARS).[25]

The theory on warm diseases arises from a thousand years of clinical observations and therapeutic experiences during the various epidemic diseases which plagued China over the time in different environments and regions. It results from the failure of other schools of thought to successfully treat warm diseases and epidemic febrile diseases. As some scholars have put it,[26] this shift in the medical perceptions on infectious and epidemic diseases may be related to the changing nature of epidemic diseases over the time and also to the physicians' growing awareness of local and regional environments with their climatic, epidemiological and medical specificities.

---

[25] On the apprehension of viral influenza and SARS within the framework of *wen bing*, see Tiquia (2010) and Hanson (2011).

[26] On the impact of the regional perspective in medicine on the formation of the School of Warm Diseases, see Hanson (2011).

References

Benedict C (1986) Bubonic plague in the nineteenth-century China. Stanford University Press, Stanford

Buchillet D (2010) La conception des maladies de tiédeur dans la médecine chinoise. Revue d'Anthropologie des Connaissances 4(1):195–241. http://www.cairn.info/revue-anthropologie-des-connaissances-2010-1.htm. Accessed 25 Jan 2011

Despeux C (2001) The system of the five circulatory phases and the six seasonal influences (*wuyun liuqi*), a source of innovation in medicine under the Song (960–1279). In: Hsu E (ed) Innovation in Chinese medicine. Cambridge University Press, Cambridge, pp 121–165

Dunstan H (1975) The late Ming epidemics: a preliminary report. Ch'ing-shih wen t'i 3(3):1–59

Elvin M (1973) The pattern of the Chinese past. A social and economic interpretation. Stanford University Press, Stanford

Goldschmidt A (2009) The evolution of Chinese medicine: Song dynasty, 960–1200. Routledge/Taylor & Francis Group, London/New York

Hanson ME (2011) Speaking of epidemics in Chinese medicine. Disease and the geographic imagination in late imperial China. Routledge/Taylor & Francis Group, London/New York

Hoizey D (avec la collaboration de Hoizey J-M) (1988) Histoire de la Médecine Chinoise. Editions Payot, Paris

Kaptchuk TJ (2000) Chinese medicine. The web that has no weaver. Understanding Chinese medicine. Rider, London

Kong YC (2010) Huangdi Neijing. A synopsis with commentaries. The Chinese University Press, Hong Kong

Liu Y (1988) The essential book on traditional Chinese medicine. Vol. 1: Theory. Columbia University Press, New York

Liu G (2001) Warm diseases. A clinical guide. Eastland Press, Seattle

Maciocia G (1989) Les principes fondamentaux dans la médecine chinoise. Elsevier Masson SAS, Issy les Moulineaux

Marié E (1997) Précis de médecine chinoise. Fondements historiques, théorie et pratique. Éditions Dangles, Saint-Jean de Braye

Obringer F (2010) Wu Youxing 吴有性 et les épidémies pestilentielles. Une figure d'expert à la fin des Ming. Revue de Synthèse 131(3):342–372

Qu Q, Jinchang L, Baozhong J (1994) Population and the environment in China (trans: Gu Ran, Boardman RB). Lynne Rienner Publishers/Paul Chapman Publishing Ltd., Boulder/London

Shāng Hán Lùn (1999) On cold damage. Translation & Commentaries by Craig Mitchell, Féng Yè and Nigel Wiseman. Paradigm Publications, Brookline

Tiquia R (2010) A cultural and linguistic translation of warm factor epidemics *wenbing* as seasonal viral influenza epidemics in Australia. Eä J Med Humanit Soc Stud Sci Technol 2(1). http://www.ea-journal.com/art2.1/A-Cultural-and-Linguistic-Translation.pdf. Accessed 10 Jun 2011

Unschuld PU (1986) Nan-Ching. The classic of difficult issues. With commentaries by Chinese and Japanese authors from the third through the twentieth century. University of California Press, Berkeley/Los Angeles/London

Unschuld PU (2003) Huang Di Nei Jing Su Wen: nature, knowledge, imagery in an ancient Chinese medical text. University of California Press, Berkeley/Los Angeles/London

Van Nghi N (1973/1991) Hoang Ti Nei King So Ouenn. Imprimerie SOCEDIM (tomes I-II, 1973–1975)/Editions N.V.N. (tomes III–IV, 1988-1991), Marseille

Wang Z, Ping C, Peiping X (1999) History and development of traditional Chinese medicine. Science Press/IOS Press/Ohmsha, Beijing/Amsterdam/Tokyo

Wēn Bìng Xué (2000) Warm disease theory. Translated by Jian Min Wen and Garry Seifert. Paradigm Publications, Brookline

Zhen Z (1995) Advanced textbook on traditional Chinese medicine and pharmacology. Vol. 1 History, basic theory, diagnosis. New World Press, Beijing

Chapter 3
Long Life of People Living with HIV/AIDS and the Practice of Medical Power

Malee Sitthikriengkrai and Chayan Vaddhanaphuti

Abstract As the AIDS virus was brought into the public consciousness toward the end of the twentieth century, the initial response around the world including Thailand contributed to AIDS becoming one of the most feared and controversial diseases in modern medical history. The Thai government initial response was to launch a campaign "AIDS is death" and to portray people living with the disease in a negative light. This led to the stigmatization and discrimination of people living with HIV/AIDS (PLHIV). This chapter describes the history and responses to HIV/AIDS from a sociocultural perspective by showing how PLHIV in Thailand had a way to interpret the meaning of their problem and how they took power into their own hands through the formation of self-help groups and through redefining the way they lived with the disease. The chapter analyzes how PLHIV, through the platform of self-help groups, have organized themselves using antiretroviral drugs as an organizing tool and how these actions not only transformed the lives of PLHIV but changed the power relations within Thai society. An attempt is made to understand how the practice of medical power, realized through antiretroviral drugs, controlled and managed PLHIV and how they, through negotiation, assumed hegemonic medical control.

3.1 Introduction

Toward the end of the twentieth century, the disease known as "acquired immune deficiency syndrome" (AIDS) sent shockwaves all over the world including Thailand. Since then there has been an unprecedented global response to the disease, and the implementation of national, strategic, and institutional partnership approaches has been instrumental in making responses more effective and scaling up treatment. However, in the early years, the initial global response was to embark on scare tactics. In Thailand there was the constant bombardment of people with the

M. Sitthikriengkrai (✉) • C. Vaddhanaphuti
Center for Ethnic Studies and Development, Faculty of Social Sciences,
Chiang Mai University, Chiang Mai, Thailand
e-mail: maleetow2@hotmail.com

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_3

message "Contacting AIDS leads to death" while, at the same time, portraying people living with HIV/AIDS[1] (PLHIV) as helpless with thin emaciated bodies, dark complexions, and inflicted wounds. It was hoped that such a campaign would have made people fearful of the disease preventing its spread to the larger population. This approach had negative effects and, instead, led to stigmatization and discrimination of PLHIV as evidenced in Northern Thailand during the period 1992–1995, where many families and communities had fear of contagion, made value-based assumptions, and had negative attitudes directed at PLHIV. This prejudices manifested in discriminatory practices such as maltreatment and abuses, the consequence of which resulted in people being ostracized by their family, peers, and community making it difficult to live a normal life and being forced into hiding. Though HIV/AIDS-related stigma and discrimination was still pervasive in the lives of PLHIV, in Northern Thailand, people slowly started to come to terms with their HIV status and disclosed themselves to the public. Many traveled to the city of Chiang Mai to connect with their peers and organized themselves into self-help groups where they could provide each other with psychosocial support and share experiences about common issues. The response to HIV/AIDS in Northern Thailand later became recognized nationally and internationally as best practice in dealing with this fatal disease.

It is important to note that the success of these self-help groups was not in the discovery of a cure for HIV/AIDS but, rather, that, through its approach, became its own proponent of the rights of its constituency and created a new source of power through the flow of ideas, information, alliances, and strategies (Reich 2002). In addition, the participation in these groups enhanced their quality of life, decreased isolation and feelings of shame, improved self-care behaviors, and created mutually empathetic relationships among members (Madiba and Canti-Sigaqa 2012). Their knowledge on self-care was accumulated from their own experiences and shared among peers with each of them applying this shared knowledge to their own situation. These self-help groups became a social space that created a sense of belonging for PLHIV, allowing them to meet, consult, support, and share their suffering and loss with each other and neutralize stigma (Tanabe 2008a). In 1996–1997, the first antiretroviral drug, zidovudine (AZT), was introduced on an experimental basis by the Thai government in order to contain the transmission of HIV/AIDS from mother to newborn baby (Shaffer et al. 1999). At that time, the cost of AZT was extremely high, making the drug inaccessible to PLHIV, and it was only until 2002 that the Thai government passed the National Health Insurance Act enabling all PLHIV to have access to antiretroviral drugs (ARTs). Mortality rates among PLHIV have sharply decreased from an average of 3,979 per annum during 1983–1993 to 2,164 per annum during 1995–2011. This downward trend is evident with only 307 cases reported on 15 November 2011 (Bureau of Epidemiology 2011). It was observed

---

[1] The term HIV/AIDS is used throughout this chapter when referring to either HIV or AIDS. It is noted, as per the UNAIDS Guidelines, that the term AIDS refer to the advanced state of the HIV infection.

that one of the major reasons for the increase in life expectancy of PLHIV was due to the fact that they had access to antiretroviral drugs (Im-em n.d.).

This article aims to explain the development of HIV/AIDS from a sociocultural perspective. It seeks to delineate how PLHIV in Northern Thailand explained their own problems and how they established their groups and networks and constructed a new meaning of the disease in such a way that it was something they could manage and live with. More importantly, the paper will examine how ARTs had altered social relations among the PLHIV. It will also seek to analyze how medical power, realized through ARTs, controlled and managed PLHIV and lastly how they responded to such control.

3.2 Medical Power, the Definition of Risk Group, and the Exclusion of Alternatives

The outbreak of HIV/AIDS in Thailand began in 1984. Through the Ministry of Public Health, Thailand's response was to adopt an epidemiological approach to control and prevent the spread of the disease by separating PLHIV from what they thought were "normal" and healthy people. In identifying those infected by the disease, high prevalence of HIV/AIDS was found among who they considered to be "high risk." These "high-risk" groups[2] included men who have sex with men (MSM), sex workers, those who have "high-risk" sexual behavior, transgendered men and women, and injecting drug users. This finding led to unprecedented discrimination and prejudice directed at those involved in what were considered socially unacceptable activities such as sex work and drug use.

The discourse that HIV/AIDS is linked to groups such as gay men and people who are "promiscuous" and, as a consequence, creates social problems has led to double stigmatization of key high-risk populations as defined from a medical point of view. The effects of this stigmatization were worse for those in Thai society who were already marginalized because of their gender, sexuality, ethnicity, or substance abuse. The discourse on who spreads the disease, who is "dangerous," and who is "polluted" comes from the knowledge constructed through epidemiological premise aimed at identifying what they called "high-risk" groups so as to manage, control, and contain the spread of HIV/AIDS. This is similar to the case of ethnic Haitians who were listed by the Centers for Disease Control (CDC) as one of the four "high-risk" groups in the United States (USA) for HIV/AIDS. This labeling subsequently sparked off a new wave of discrimination of Haitian people with many losing their jobs and finding difficulties obtaining accommodation, accessing health-care services, and finding schools for their children (Farmer 1992).

The state's policy of control and prevention of HIV/AIDS during this period was largely based upon the epidemiological logic, which aims at defining the "agent" of

---

[2] More recently the term "key populations" is preferred to the term "high-risk" groups. The term "high-risk" group is thought to increase stigma and discrimination.

epidemiology. As a result, policies to build asylums for PLHIV; voluntary blood testing among employment seekers, immigrants, and emigrants; and so forth were quickly adopted and implemented. These policies were based on the idea of screening PLHIV in order to set them apart from the rest of Thai society. While these policies and practices might be able to reduce the spread of the disease to some extent, they stigmatized PLHIV as evil and dangerous "others" who spread fatal diseases to other people. As a consequence, PLHIV were not the only ones affected by stigma and discrimination but so too were their family and relatives. Although the Thai state was able to construct discourses on key populations and the spread of HIV/AIDS to convince Thai people to refrain from risk behavior, it could not contain the epidemic. Research indicates that the 1990s was the most severe era of the HIV/AIDS epidemic in Thailand, and since 2002, a drop in new infections has led to a decrease in HIV/AIDS incidence as has HIV/AIDS-related deaths (Punyacharoensin and Viwatwongkasem 2009).

Apart from being discriminated against by their family and community, PLHIV in Northern Thailand were largely excluded from alternative healing systems. In 1994, news spread about a herbalist who had discovered a "herbal tonic" which could "cure" HIV/AIDS and improve health conditions attracted the attention of many PLHIV (Bangkok Post, 25 Feb 1994). This herbalist was hailed as the "Divine Doctor" who could transform the life of those who were "hopeless and suffering" of incurable diseases. The Ministry of Public Health adopted an oppositional stance and ordered the Chiang Mai Provincial Office to arrest the herbalist who was subsequently charged for deceiving the public on the basis that he did not have professional credentials and that he falsely claimed that his herbal tonic could cure HIV/AIDS.

From defining the key populations at higher risk of HIV/AIDS exposure to excluding alternative healing practices, medical institutions had largely assumed the sole power of defining truth. As Ivan Illich (1976) observes, medical institutions are no different from industrial institutions; it emphasizes specialization, standardization, and centralization through having the hospital as the core production unit, staffed with specialists, such as medical doctors, and equipped with modern technology ready to define who is a "patient" (Lupton 1997). The medical institution is a professional institution, which uses professional certification as a means to give legitimacy to those in the medical profession in order to diagnose and treat diseases, whereas those without such certification have no legitimacy (Illich 1976). It should be noted that those in the medical profession define their practice as an act of "consumer protection." Moreover, medical institutions assume the role of assisting society to screen which medical practice is, indeed, worthy of professional standard, is scientifically sound, and is supported by research or proven efficacious. They constitute de facto governance, and any medical practice with a different norm will be disallowed, prohibited, and even charged with violating medical profession law. The arrest of the herbalist is a case in point. The practice of herbal medicine, whose theory and definition of illness is different to that of the Western science-based medical model, is viewed with distrust and is seen as illegitimate in treating HIV/AIDS. As a result, PLHIV were excluded from the benefits of alternative medical practice.

3.3 Group and Network of People with HIV: Governmentality from Below

The response undertaken by the government in controlling and segregating PLHIV and their exclusion from alternative medical practice as described above did little to effectively prevent the spread of HIV/AIDS in Thailand. Their campaigns failed to create an understanding and awareness about HIV/AIDS, and moreover, it created and perpetuated stigma and discrimination of PLHIV resulting in ostracization from their community or living in seclusion at the back of their village. Community members stopped socializing with the families of PLHIV, avoided trading, and reduced regular contact with them. In several communities, community members refrained from sending their children to the same school that children of PLHIV attended or did not attend their funeral ceremony.

Stigma and discrimination faced by the PLHIV undermines their personal identity and capacity to cope with the disease and disrupts functioning in personal and social spaces. Despite this, many people constructed their own narratives, telling the public about their own suffering as a result of HIV/AIDS and of discrimination and challenged judgmental attitudes and assumptions about their sexual lives. Chayan Vaddhanaphuti (1999) observes that the self-transformation of PLHIV can be seen as a process of "self-disclosure and self-reconstitution." It is a social movement in which the PLHIV engaged so as to live their life with dignity. Self-disclosure and self-reconstitution is a process to "redefine" the meaning of PLHIV as people who are still socially valuable and useful and who uphold moral standard. Self-reconstitution is seen as a formation of a network of learning and problem sharing and of self-help for PLHIV who negate the "disease-killing" approach and choose, instead, the alternative self-caring approach which emphasizes a "living with HIV" practice. The change from individual struggle to cope with HIV/AIDS to collective action through the process of self-disclosure and self-reconstitution is essentially a spatial contestation; it is a social movement of PLHIV from both rural and urban areas in Northern Thailand. Not all PLHIV groups and networks are successful; however, their experiences and lessons learned are worthy to be shared.

The self-disclosure and self-reconstitution movement became quite successful, on the one hand, in giving new lease of life to PLHIV who previously felt hopeless and, on the other hand, educating broader society about the epidemic, reducing social discrimination and enhancing knowledge and understanding among PLHIV themselves. Pimjai,[3] one of the key members of a group of PLHIV in Chiang Mai, said: "Thanks for being infected by AIDS." During 1993–1994, some PLHIV in rural Northern Thailand who gathered in Chiang Mai to demand that the authorities

---

[3] Pimjai is from Mae Rim District, Chiang Mai; she finished primary education and is now 48 years old. She knew that she contacted HIV+ when she got pregnant and decided to have an abortion. She suffered a great deal from social discrimination, but she was able to overcome it and turned her suffering into positive action by sharing her experiences with other PHAs. She became advisor cum counselor to those who had similar experience like her. She was selected as representative of PHA in national and international conferences. In 1997, she was awarded as Kon Dee Sri Sangkom (Distinguished Citizen of the Society) (see Suthisakorn 2007; Chaiprasitti 1994).

release their "Divine Doctor" decided to organize themselves as a self-help group. This group was initially called "Living with Nature" but later changed to "Friends of Life Center." This center played an important role in connecting the self-help group with provincial authorities and medical doctors as well as assisting other groups and networks of PLHIV in rural areas. Several government or semigovernment agencies, such as Red Cross Thailand, encourage the movement of self-help groups for PLHIV. As a result, the number of self-help groups in Chiang Mai increased rapidly from just a single group established in 1993 and later expanding to 63 groups. This phenomenon took off and, by 1998, grew to 196 groups in Northern Thailand (Network of NGOs against AIDS in Northern Thailand 1999). During this period, the major issues that these groups organized around were about giving emotional support to each other, improving their health care and getting support from government and nongovernment agencies. The issue of access to ARVs was not yet on the agenda.

The intriguing aspect of these self-help groups is that it was a new space created by those who share similar problems, that is, they were stigmatized and discriminated against by their family and their community. In this supportive climate of a group, they could engage with others and talk openly about the challenges of living with HIV, learn from each other's experiences of health care, and provide psychosocial support to each other. These are the crucial threads which bound them together. Shigeharu Tanabe sees this movement of self-help groups for PLHIV as governmentality from below, meaning governmentality by the PLHIV which is drastically different from the control and provision of health care by modern medicine (Tanabe 2008b). Through these self-help groups, PLHIV became empowered. They could find their own solutions, choose alternative health-care systems including the usage of herbal medicine, adopt certain dietary preference, and pursue moral conduct according to a certain religious faith.[4] It can be argued that governmentality from below by PLHIV is a response to the hegemony of modern medical power or the governmentality from above which excludes their alternatives to health care.

3.4 People with HIV+ and Their Access to Antivirus Medication

Thailand began to provide ARTs to low-income people in 1992 under the policy adopted by the National AIDS Committee (NAC). In 1995, ARTs were given to pregnant women with HIV in order to reduce the transmission from mother to child.

---

[4] In Upper Northern Thailand, several Buddhist monks had played an important role in caring for PHAs. For example, monks from Doi Keung Monastery applied "spinning meditation" method to PHAs. The PHAs practiced mediation under the supervision of the monks. During the mediation, some PHAs vomited and threw up some foul liquid, which was believed to have AIDS virus from their body (see Chiralak Jongsathitman 1995). Another monk, Phra Pongthep, set up a hospice in Chiang Mai to care for the PHAs, most of whom had no place to go, had no income, and almost reached the last stage of their life.

Zidovudine (AZT) was used, but there was no clear policy to prescribe this drug for all patients. In 1996, Red Cross Thailand launched the Project to Reduce the Transmission of HIV from Mother to Child, a project implemented under the royal patronage of Her Royal Highness Princess Soamsawali which provides funds to procure medicine for pregnant women. At the same time, the Ministry of Public Health implemented a 2-year pilot project in two regions of Thailand, starting from the North in 1997 and the Northeast in 1998. This project provided pregnant women with medication for a short-term period before delivery. The result shows that the risk of transmitting HIV/AIDS from mother to child was reduced to one out of two among mothers who did not practice breastfeeding, but no result was available among mothers who breastfed their child.

As a consequence, in 2000, the project was adopted nationwide to prevent the transmission of HIV/AIDS from mother to child by the use of AZT by 2007. The rate of infection, 25–30 %, was brought down to lower than 10 %. Other types of ARTs, such as nevirapine (NVP) and zidovudine (AZT), were also used in order to reduce the rate of infection (Office of AIDS, Tuberculosis and Sexually Transmitted Diseases 2003: 2). With a satisfactory result, the Ministry of Public Health proceeded to set up a national Project for Prevention of Transmission of HIV from Mother to Child in Thailand aimed at HIV-infected pregnant women and women with newborn babies. The project provided these women with access to counseling and voluntary blood testing services as well as the provision of powdered milk for their child. Unfortunately, the rest of the population of PLHIV had little access to ARTs, given that the price was quite high. HIV/AIDS practitioners, nongovernmental organizations, and government officials have all shared the same conclusion that the main obstacle which limited access to ARTs came from the exceedingly high price of the medicine.

It was during this time that the movement of self-health care, group support, and home visits undertaken by groups and networks of PLHIV was gradually reoriented toward access to antiretroviral therapy. People demanded the government to announce an official policy and to ensure compulsory licensing in order to lower the price of AZT. In 1999, people gathered in front of the Office of the Ministry of Public Health to demand the implementation of compulsory licensing. However, this demand was not met because the then Minister of Public Health opted to request the Government Pharmaceutical Organization to produce didanosine (ddl) in powder form instead. In 2006, many years later, there was a protest against the licensing of AZT+3TC leading to the withdrawal of its license from Thailand by GlaxoSmithKline Company. As a result, the price of antiretroviral drugs dropped substantially, and other pharmaceutical companies began to produce more antiretroviral drugs for the market. This enabled greater access to lifesaving medication.

Under the “30 Baht Scheme for Every Disease” policy, PLHIV were able to pay for medical expenses incurred from opportunistic infectious diseases as well as for drugs that prevented the transmission of HIV/AIDS from mother to unborn child. However, the policy did not cover the expenses of antiretroviral drugs. As a result, institutions and HIV/AIDS activists and practitioners, again, demanded that the government increased the benefits and privileges to include access to antiretroviral drugs. In addition, a buyers' cooperative called the "Buyers' Club" was formed to buy antiretroviral drugs from India where there was no compulsory licensing. HIV/AIDS advocate community also coordinated with *Médecins Sans Frontières* (Belgium) and AIDS Access Foundation for information on sources of low-price drugs and how to negotiate with them. The Buyers' Club operated at two levels: local and national. Groups at a local level provided information on treatment and care of opportunistic infections, side effects of antiretroviral drugs, and health monitoring systems. At a national level, they were responsible for the provision of information regarding the care of those who had side effects from antiretroviral drugs as well as employing tactics to find cheaper drugs to sell to PLHIV who had no health insurance. The Buyers' Club worked side by side with lobbyists at the policy level in order to keep the price of the antiretroviral drugs low. Later on, even though there was an attempt to include the cost of antiretroviral drugs in the National Health Insurance Scheme, several limitations on the part of the PLHIV made them non-eligible to the health insurance. For example, some groups did not trust the anonymity of the system and were reluctant to use the services. As a result, the Buyers' Club had to work closely together to find cheap antiretroviral drugs through various channels for its members who could not access the state-supported health-care services or for those who did not want to disclose their HIV status, as well as those PLHIV who could not afford to pay for their drug by themselves.[5]

At the same time, the Government Pharmaceutical Organization of Thailand produced a combination of anti-HIV medications consisting of three types of drugs in one tablet called GPO-VIR at a cost of 1,200–1,300 baht (Network of PWHIV/AIDS, Thailand 2008). This obviously led to an increase in the number of people seeking antiretroviral therapy from Project ATC (Access to Care) resulting in the number of people on treatment increasing from 3,000 to 10,000 per year. In 2003, Thailand began to receive financial support from the Global Fund to Fight AIDS, Tuberculosis and Malaria (GFATM) which rapidly augmented the number of people who could have access to antiretroviral drug up to 50,000 per year. This project, which is still in operation, is known as the National Access to Antiretroviral Programs for PLHIV (NAPHA).

In 2006, the "Baht 30 Scheme for Every Disease" was suspended; the government came up with a more attractive scheme, which aimed to provide antiretroviral drugs to PLHIV under the Health for All policy. This meant that all PLHIV living in Thailand who were Thai nationals had full access to health care and antiretroviral drugs; however, non-Thai nationals were unable to access services and treatments. In 2007, a project known as NAPHA Extension was launched in order to provide such access for all PLHIV who were socially disadvantaged. It was an extension of the former NAPHA Project targeting those who had no privilege and had less opportunity to have access to health services, including transnational migrant workers, ethnic minorities, displaced Thais, and so forth. The project, financed by GFATM covering the period of 6 years (2008–2014), aimed to reach 2,000 PLHIV in the whole country (NAPHA Extension (n.d.); Chitvarakorn 2010).

---

[5] This information was obtained from the interview conducted with Sister Aauw. See Sect. 3.5.2.

The success of antiretroviral drug provision, which covered PLHIV nationwide, came about from the close collaboration between the networks of PLHIV and NGOs. The demand for PLHIV to have access to antiretroviral drugs began in 1995 when representatives of groups and networks of PLHIV met in order to find ways to negotiate for their rights. They agreed to work together as a network asserting their rights to have access to better health-care services. Their move corresponded with the political situation at the time when the government wanted to expand its political base using a free health-care policy provided by the medical profession with the standardization of medical institutions. In Thai society, however, only Western scientific-based medicine is seen as the credible model. As a result, PLHIV and their networks had to seek health-care services under the National Health Insurance Scheme. In the absence of such schemes, most PLHIV who were from rural areas or working as laborers would never have been able to afford treatment.

On the one hand, it should be noted that the changing concept of self-care toward the adoption of antiretroviral therapy made PLHIV gain more confidence in the health-care system and believe that antiretroviral drugs would enable them to live a longer life, that they would not die from an opportunistic infection, and that they would be able to live a normal life. On the other hand, it is observed that the state's policy supporting ARTs also greatly altered the social relations among PLHIV, and, more importantly, it excluded them from other health-care practices. Formerly, PLHIV relied upon their self-help groups for information on self-care; they sought diverse means to treat their illness, and they involved traditional healers to work with them in searching for means to deal with their health problems as well as getting psychological support from them. After the change, access to antiretroviral therapy reduced the "collective" self-health care to "individual" health care, making PLHIV more dependent on Western medicine (Lyttleton et al. 2007). In other words, modern medical practice expanded its power over to control PLHIV with their consent. It did not force PLHIV to take antiretroviral drugs, but the PLHIV themselves were the ones who demanded for their right to have access to the drugs. We can, then, see that the governmentality from below was no longer a resistance, but collusion with medical practice in expanding its power to care for PLHIV.

3.5 ARV: The Practice of Power/Knowledge and the Body of the PLHIV

The body is a unit of analysis which postmodern sociologists have been interested in. As we can see from the 1970s, French philosopher Michel Foucault analyzed the way in which medical power acts upon the body or "anatomical atlas" as he called it (Foucault 1975). According to Foucault, our body is constructed through the surveillance of medical science. He contends that since the end of the eighteenth century, the invention of treatment tools, such as stethoscope and microscope, medical examination, postmortem autopsy, physiological knowledge, psychology, surgery, X-ray, etc., largely empower those specialists who act upon the body. However, our body is not controlled only by medical power and knowledge, but it is also regulated and controlled by surveillance from other institutions, such as educational facilities (schools), correctional facilities (prisons), mental health facilities (asylums) and the army, and so forth. For Foucault, modern medicine is an institution which surveys bodies more than any other institution since it examines, investigates, and touches the flesh and blood of the patients' body with (or without) their consent. The patients often have minimal knowledge about medical practice. Undergoing surgical procedures, the patient's body yields to medical power as if it is an object waiting for medical doctor's tools to cut open, slice, examine, and alter it (Lupton 1994).

The life of PLHIV is under the surveillance of medical practice. The following case demonstrates how PLHIV become "docile bodies" for Western medicine, although, to some extent, they are able to negotiate and search for new knowledge.

3.5.1 Damrong

Damrong, a 52-year-old man, is from Chiang Dao District, Chiang Mai. Coming from a lower middle-class family, his father worked as a government official in this small town where he grew up. Damrong is good at dancing and flower arrangement and is a talented tailor. He became aware of his positive HIV status in 1993. He was one of those who demanded for the release of the "Divine Doctor." Later on, he became a core member of an HIV/AIDS group known as "Living with Nature." He became a resource person sharing his own experiences with other people so that they could gain better understanding about the problems faced by PLHIV. Sharing the suffering of stigma and social discrimination of other's and providing counseling and psychological support to many PLHIV transformed Damrong from a hopeless and stigmatized person into someone with a new and meaningful life.

Damrong often shared his experiences with other PLHIV as well as with diverse groups of people, such as government officials, NGO workers, academics, and students. From each meeting with PLHIV, Damrong realized that he had learned many lessons, and he was able to cultivate friendships and expand his network. For instance, he was nominated to be a representative of PLHIV attending the First Asia-Pacific AIDS Conference in 1995. During this time he was ill, but, fortunately, he received advice from one of his international friends on how ARTs worked. As a result, he was among the first group of PLHIV who tried ARTs although it cost him 1,800 baht per day. Later, he participated in a research project which studied the side effects of the antiretroviral drug which meant that he did not have to pay for the drug anymore. However, he suffered from its side effects and had to change drugs every 2–3 years. Sometimes, he took a certain kind of drug only 6 months and had to switch to another one.

> I felt dizzy and I had diarrhea; my heart bounced and jittered. After I took the medicine for half of an hour, I felt dizzy. I could not do anything and then I got a fever, too. When I asked my doctor, he said that it was the side effect of the medicine, so I had to bear with it for six months more. It had not been improved and I wondered how long I had to bear with it.

Damrong regularly exchanged information with international PLHIV making him exceptionally well informed about the developments of antiretroviral drugs. He also received information from *Médecins Sans Frontières* and Access. He was quite competent to look after his own health. For example, he had monthly CD4 blood tests and viral load tests every 2 months, while more common practice was to have a CD4 test done every 2 months or when an opportunistic infection was detected. His special attention to his health meant that he had to pay for his own medical expenses. However, he tried to have his viral load tested when there was a discounted rate or when there was a special occasion, such as on World AIDS Day or national holidays.

Later on, Damrong faced a new challenge when *Médecins Sans Frontières*, who provided him with support so that he could have access to antiretroviral drugs, had to end its support. He then had to depend upon his Social Security and Health Insurance for All schemes. He learned how to use different kinds of antiretroviral drugs cleverly so that he could maximize his access to health insurance. In his view,

> Social security system in Thailand does not include Group 3. When I want to take Group 3 totally, I cannot do it. Therefore I had to choose from the first two groups which include AZT and ddl. This is mixed with the one which was developed by Government Pharmaceutical Organization, and together with one tablet of PI 1 and a Calitha which is the main drug. Calitha contains tenofovir mixed with AZT and ddl. All of this is the first solution. Those who have the Gold Card (Health Insurance) can get it free.

Damrong gained knowledge on antiretroviral drugs and could analyze the processes of how the drugs worked with his body. He had to be able to identify the drug he took and be aware of the time of the day he was supposed to take specific medication. He observed the changes which occurred in his body after the drug was taken and how the drug produced different effects analyzing which drug was suitable for his body at any given time. He prepared himself before he went to see his doctor, not as a passive player being informed of his diagnosis, but rather he turned himself into a key informant for his doctor who accommodated Damrong's self-defined situation. He was very cautious not to let his life fall into the hands of an inexperienced doctor. For this reason, he paid careful attention to his health, and when he found any health issues, he would be even more vigilant in taking care of himself. If, despite his efforts, the situation was not improved, he would change the drugs he took, even though drug resistance had not yet occurred. Damrong believes that PLHIV must prepare themselves by knowing themselves, their experiences in taking drugs, their lifestyle, and any previous and current illnesses. Most importantly, PLHIV must know about the various drugs and their side effects.

As of today, Damrong is a core member of the Purple Group and remains an active mentor who gives advice on antiretroviral drug to PLHIV.

3.5.2 Sister Aauw

Sister Aauw, a core member of a group of PLHIV, was infected in 1992; she joined other PLHIV in demanding the herbal tonic. Later, she became a core member of, and played an important role in, the Friends of Life Center. Aauw was different from Damrong in that she began to take antiretroviral drugs in 2000 after she had been infected for 8 years. Before that, she took care of herself by taking herbal medicines. As a core member of PLHIV, she had an opportunity to gain information about antiretroviral therapy. She stated that when she was first diagnosed, she read the Red Ribbon Magazine, published by the Red Cross Thailand, which gave information about some registered drugs and their side effects. She learned that the side effects of efavirenz included strange dreams, motion sickness, and dizziness. She could not imagine what having strange dreams would be like.

Aauw decided to take antiretroviral drugs due to her CD4 count which dropped to a very low level, between 140 and 160, as well as her experiencing extreme weight loss. She was advised by a medical doctor to take antiretroviral drugs; she then sought for more information about these drugs by asking several doctors whom she knew. The first treatment regimen she took was AZT together with ddl. She took the drugs for more than 1 year before she switched to efavirenz, 3TC, and AZT. During the period between 2002 and 2007, when she took efavirenz, she experienced several strange dreams.

> The dreams I often have are about something weird, strange, thrilling and challenging. Sometimes, I feel like someone was trying to attack me, I dreamed of seeing ugly earthworms; the dream was so clear and ugly that I wanted to vomit. The side effect always occurs after I take the drug for 40 minutes. It makes me feel motion sickness; my saliva turns sticky. I have to lie down and after that I feel I was in a swinging cradle. Sometimes, I feel my body spins on by itself. It occurs every day whenever I take the medicine. It puts me to sleep, but my body seems to struggle endlessly as if I do sleep. I feel very exhausted indeed.

In 2003, Aauw discovered that she had diabetes; she thought that it came from her use of antiretroviral drug for 3 years. At the end of 2007, Aauw's weight dropped severely and she felt very exhausted. Her blood test showed that her CD4 count had decreased while her viral load had increased. Fortunately, she had no opportunistic infection. Her medical doctor prescribed two kinds of drugs from Group PI and 3TC for her. However, since the two kinds of drugs from Group PI were not included in the list of drugs under the Social Security Scheme, she decided not to change the drugs. More than that, she was afraid to readjust herself to the newly prescribed medication. She continued to take the drugs for 6 months to which she had developed drug resistance before she switched to Calitha, tenofovir, and 3TC, all of which were covered by her Social Security Scheme.

Both Damrong and Aauw were core members of the network of people living with HIV/AIDS. They had extensive experience in giving advice to other PLHIV. At the beginning, they provided a model of alternative health care for PLHIV, and later they decided to switch to antiretroviral therapy. Both of them had their unique ways to control and negotiate the use of ARTs. Damrong used networks of PLHIV, at home and abroad, as well as NGOs for information exchanges, and learned how to deal with the problems of drug side effects. He did not have confidence in medical doctors, especially those who just graduated, since they did not have any experience. Damrong had a "direct" experience taking several kinds of antiretroviral drugs and understood its side effects. He also had "indirect experience" because he belonged to a network of PLHIV which provided him with information, while he, in turn, reciprocated in sharing his experiences and giving advice to its members. In Aauw's case, she was very fearful of the side effects, but she also tried to find out more information by researching problems related to HIV, reading from books, and consulting with other PLHIV. She had learned to choose ARTs that suited her biophysical conditions. Even though she had to suffer a great deal from the side effects, she had never stopped taking the drugs with the reasoning that it was her last choice.

The social practice of these two cases can be seen from Anthony Giddens' view as "reflexive project" (Giddens 1991). That is, an individual can articulate with a structure and negotiate with it, in order to make it serve his or her goals, an individual who is not idle but is always ready to change. With this attribute, when the technology of medical power extends over and penetrates the body of the individual infected with HIV, they are bound to adapt themselves to the dynamics of treatment issues associated with antiretroviral therapy. However, at the same time, they always search for knowledge which enables them to be ready to respond and negotiate this dynamism to the extent that they are able to control themselves and develop self-responsibility in taking antiretroviral drugs. The experiences of Damrong and Aauw demonstrate that the body has become a space where medical science demonstrates that if they neither strictly take medicine on time nor undertake medical checkup according to the doctors' order, some changes will definitely occur clearly in the body, for example, relocation of fat, strange dreams, dizziness, diarrhea, and so forth. Therefore, if they wish to get rid of these undesirable strange syndromes, they must take medicine as prescribed by medical doctor on time. Such a practice of medical power makes it necessary for PLHIV to strictly discipline themselves, and, at the same time, they have to search for more knowledge and learn from experiences of other PLHIV. Medical science merely establishes a certain criteria for PLHIV to monitor their own syndromes, for example, CD4 testing and viral load tests. The surveillance by standardized medical science like this will reinforce the need among PLHIV to take greater control of their body and thus their health, without orders from, or close supervision of, a medical doctor.

3.6 Comprehensive Continuum of Care Center and the Integration of Technology of Power: A Conclusion

In modern medicine, a criterion for a continuing follow-up of medication PLHIV is known as "good adherence" which aims to contain the virus to the lowest amount at the longest period and, equally important, to prevent it from becoming drug resistance. Previous studies show that ARTs require an adherence of more than 95 % if it is going to be effective in containing the breakup of the virus. On the other hand, medical doctors would be concerned with the side effects which come from irregular drug intake or "poor adherence," leading to drug resistance and the under-development of immunity, conditions which easily lead to and invite opportunistic infections. Most importantly, PLHIV under this situation would have to change their antiretroviral drugs, which can result in greater expense.

As of 30 September 2010, there were 143,064 PLHIV who had been on antiretroviral drug (National Health Security Office). In order to establish "good adherence" among antiretroviral drug users, it is necessary to develop a good monitoring and follow-up system. As a result, the Comprehensive Continuum of Care Center was established in order to provide knowledge on drug use and monitor and study drug-use behavior and side effects. It was realized that to run the center effectively, one could not only rely on medical doctors and other medical personnel as they had limited knowledge and experience. PLHIV, with their extensive experience of antiretroviral drug usage, liaised between the new drug users and the medical doctors and personnel, using their vast and personal experiences to assist other PLHIV. They also negotiated with health-care providers so as to help them gain a better understanding of PLHIV. At times, they worked as medical aides, demonstrating the changes in the provision of health care. It can be seen that the network of PLHIV working with the Comprehensive Continuum of Care Center differed a great deal from the former one as observed by Tanabe (2008b). In analyzing the dynamics of this network during 1994–1997, he contends that a network of PLHIV becomes a space where technology of governmentality plays itself out yet is also a public space where resistance and negotiations occur. In this "network of governmentality" which coexists with the "network of resistance," the self-help group holds public power and is a "becoming" community.

The so-described network of PLHIV is essentially different from the one which worked with the Comprehensive Continuum of Care Center and forms part of the formal medical network. The new network was not meant for resistance, but merely a network of monitor and control ensuring that PLHIV would follow the regulations of drug use and undertake regular physical checkups. As a result, the practice largely integrated the governmentality from below by the network of PLHIV with the one from above. As earlier argued, governmentality from below is an attempt to incorporate traditional medical knowledge, herbal medicine, and experiences gained from living together among PLHIV while using them in resisting the dominant Western medicine which once produced the discourses "Contacting AIDS leads to death" and "AIDS is a contagious disease." In this regard, it is no doubt that the technology of medical power has turned to be even more powerful because PLHIV themselves also take part in the use of power to control themselves, their health, and their bodies. PLHIV therefore fall under the technology of medical power completely, using their potential in taking care of their own health and becoming docile followers of the technology of medical power.

References

Bangkok Post (1994, February 25) Aids victims stage rally in North. Bangkok Post, p 3

Bureau of Epidemiology (2011) A patient situation. http://www.boe.moph.go.th/files/report/20111206_93584707.pdf. Accessed 22 Jun 2014

Chaiprasitti S (1994) Decision making process in maintaining pregnancy of HIV-infected women. Dissertation, Mahidol University

Chitvarakorn A (2010) An evaluation of the impacts of AIDS prevention and care project under the support of Global Fund, First Round. http://www.thaiprddc.org/download/article/article_20090630160548.pdf. Accessed 7 Jun 2014

Jongsathitman C (1995) Kan raksa phu ti cuea HIV duay kan patibat dham: koranee seuksa Wat Doi Keung, Amphoe mueang, Changwat Mae Hongson (Caring of people with HIV through Buddhist teaching: a case study of Wat Doi Keung, Muang District, Mae Hongson Province). Women's Studies Center, Chiang Mai University, Chiang Mai

Farmer P (1992) AIDS and accusation: Haiti and geography of blame. University of California Press, Oakland

Foucault M (1975) The birth of the clinic: an archaeology of medical perception. Vintage Books, New York

Giddens A (1991) Modernity and self-identity: self and society in the late modern age. Polity Press, Cambridge

Illich I (1976) Limits to medicine: medical nemesis: the expropriation of health. M. Boyars, London

Im-em W (n.d.) Than khauw mun kan sia chiwit duay AIDS-kan chai prayote lae naew nom sathanakan thi plian pai (Database on Mortality from AIDS-the usage and trend). http://www.mahidol.ac.th/IPSR/AnnualConference/Conference II/Article/Article11.htm. Accessed 7 Jun 2014

Lupton D (1994) Medicine as culture: disease and the body in Western societies. Sage, London

Lupton D (1997) The imperative of health: public health and the regulated body. Sage, London

Lyttleton C, Beesey A, Sitthikriengkrai M (2007) Expanding community through ARV provision in Thailand. AIDS Care 19(Supplement 1):S44–S53

Madiba S, Canti-Sigaqa V (2012) Barriers to participate in support groups for people living with HIV: a qualitative study with men receiving antiretroviral treatment in a HIV clinic in Mthatha, South Africa. J Health Sci 4(2):119–128

NAPHA Extension (n.d.) Extension available. http://dpc9.ddc.moph.go.th/aids/napa_ex.html. Accessed 7 Jun 2014

Network of NGOs against AIDS in Northern Thailand (1999) Krabuankan kaw keut klum phutitcueu lae patisumpun kap chumchon (The process of HIV+ group formation and its interaction with community). A report presented in a workshop on lesson learned Arun on 25 Jan 1999 at Suriwongse Hotel, Chiang Mai

Office of AIDS, Tuberculosis and Sexual Transmission Disease (2003) Naew thang kan du lae phutitcueu HIV+/AIDS yang pen rabob lae taw nueng, 2003 (A comprehensive and continuing approach to the care of people with HIV+/AIDS). Department of Disease Control, Ministry of Public Health, Nonthburi

People with HIV/AIDS Network Thailand (2008) Jak Khon Mai Lek 0 Su Naew Na Kong Pak Prachachon (From people number 0 to the front line of people movement: the lessons and the struggle of people with HIV/AIDS network). People with HIV/AIDS Thailand, Bangkok

Petersen A, Lupton D (1996) The new public health: health and self in age of risk. Sage, London

Punyacharoensin N, Viwatwongkasem C (2009) Trends in three decades of HIV/AIDS epidemic in Thailand by nonparametric backcalculation method. AIDS 23(9):1143–1152. doi:10.1097/QAD.0b013e32832baa1c

Reich MR (2002) Reshaping the state from above, from within, from below: implications for public health. Soc Sci Med AIDS Care 54(Supplement 1):1669–1675

Shaffer N et al (1999) Short-course zidovudine for perinatal HIV-1 transmission in Bangkok, Thailand: a randomised controlled trial. Bangkok Collaborative Perinatal HIV Transmission Study Group. Lancet 352(9155):773–780

Suthisakorn O (2007) Rung Kong Wan Mai…Nai Ngao Meud (The dawn of a new day…in the shadow: Pim Jai Inthamul). Praew Publishing House, Bangkok

Tanabe S (2008a) Suffering, community, and self-government: HIV/AIDS self-help groups in Northern Thailand. In: Tanabe S (ed) Imagining communities in Thailand: ethnographic approaches. Silkworm Books, Chiang Mai, pp 161–181

Tanabe S (2008b) Chumchon kap kan pokkhrong chiwayan: klum phu titcuea HIV nai phak nuea khong thai (Community and government: HIV self-help groups in Northern Thailand). Sirindhorn Anthropology Centre, Bangkok

Vaddhanaphuti C (1999) Pheay rang sang tua ton: Kan keung wai tang sangkom kong kum phu titcuea AIDS (HIV/AIDS self disclosure: social movement of people living with HIV/AIDs). Paper presented at annual conference of social sciences faculty, Chiang Mai University

Chapter 4
Socio-environmental Global Changes and Infectious Diseases: Interdisciplinary Approach Applied to Tourism Studies

Bernard Moizo

Abstract I am dealing with the issue of infectious diseases in relation to social and environmental global changes. I suggest few ideas to develop interdisciplinary approaches despite long-time obstacles. I use the example of growing tourist activities as one possible agent of disease spreading. Infectious diseases, some really new but others known for centuries, are spreading widely outside previous limited areas because of ecologic and economic transformations. A growing interest of research in social sciences in fields such as health and environment has emerged simultaneously since social uses, access and practices on the environment are crucial to understand how epidemics can spread or not. Exchange and dispersion of diseases are one of the many global consequences of tourism. Movement of infectious organisms by tourists is an important aspect of international travel. Tourism can contribute in different ways to exchange and dispersion of both pathogens and diseases. More than ever, there is an urgent need to build capacity in the environmental community and the interdisciplinary approach. Tourists are at risk to acquire new infections, and they aid as vectors in the global dispersal of microbes. Infectious diseases are responsible for about 35 % or the mortality throughout the world and during past 30 years more than 30 new disease-causing organisms have been identified.

4.1 Introduction

In this chapter, I am addressing several issues related to the emergence and re-emergence of infectious diseases in the light of social and environmental global changes. I am stressing the need for further development of multi- and interdisciplinary approaches since they look promising to get a better understanding on how

---

B. Moizo (✉)
UMR 220 GRED (Gouvernance, Risque, Environnement, Développement),
Institute of Research for Development, French Institute for Research
and Development & UPVM, Université Paul Valéry Montpellier,
BP 64501, 34394 Montpellier Cedex 5, France
e-mail: bernard.moizo@ird.fr

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_4

and why disease outbreaks happened in the past and propose a scenario on how they may occur in the future.

I am then turning to look at links between spreading and emergence of disease and tourism in the context of growing touristic activities worldwide suggesting future paths and new topics for research in that field.

This chapter is not based on first-hand data nor on extensive field research; it is rather a reflexion based on personal experience as a social scientist involved in multidisciplinary programmes for more than a decade combined with a compilation of papers, from various scientific backgrounds, highlighting new research paths to answer growing concerns in health and tourism studies regarding the infectious disease issue.

My aim is not to come with ready-made solutions or answers but to draw the attention of colleagues, scholars and research centres from a large ray of disciplines to opportunities that will exist in that field of studies in the very near future and need to be urgently addressed for the benefit of all.

4.2 Infectious Diseases, Ecological and Social Changes and Globalisation

It is now fully admitted that the past two decades have been the most eventful in the long history of infectious diseases (Morse 1995). Looking at emerging and spreading of infectious diseases, most studies make a clear distinction between some infectious diseases which are really new, while others have been known previously, sometime for centuries, but are now spreading widely outside the previous limited areas because of many ecologic and economic transformations worldwide (Wilson 1995b).

Many factors could indeed be at the origins of new or re-emerging diseases, but global environmental changes and increased movements of populations worldwide are amongst the two most influential and most cited in publications (Weiss and McMichael 2004):

> Most emerging infections are caused by pathogens already present in the environment, brought out of obscurity or given a selective advantage by changing conditions and afforded an opportunity to infect new host populations. These changes include ecological changes, such as those due to human activities or to anomalies in climate; demographic changes and behavior; travel and commerce; technology and industry; microbial adaptation and change; and breakdown of public health measures. (Morse 1995: 8–9)

For over two decades or even more in some parts of the world, scientists have expressed strong concern regarding global health issues in the light of this potential threat. Several studies were conducted in regions of the world mostly at threat (South East Asia and Africa) in order to get a better understanding of the overall phenomenon. Facing emerging diseases, we are not all equal and the poorest are probably most vulnerable (McMichael and Confalonieri 2012), together with war refugees and displaced populations. Indeed, the importance of social inequalities in emerging disease is a strong factor and has to be taken into account very seriously, but such approach is not meant simply to see the poor as ‘sentinel’ but to ask what are the mechanisms by which these diseases come to have their effects in some bodies but not in others (GECHH 2012).

As early as the mid-1990s, efforts were made to increase health worldwide watch on emerging and re-emerging infectious diseases; they start to have good results, but there is still a long way to go since changes, both social and ecological, occur at a faster pace, thus making it difficult for scientists to keep an edge ahead from coming public health threats. Despite this worldwide watch, poor countries which are more vulnerable to epidemics and spread of diseases seem to interfere with international watch and actions. For example, at a regional level, permeable borders, refugees, wars, droughts, food crisis, tsunamis and floods may have direct consequences on the spreading of diseases. There are indeed strong border issues, and one can ask what turbulence is introduced when the border in question is between a rich and a poor nation.

Worldwide health and sanitary risks are nowadays major social issues that are raising great concerns in both developed and Third World countries. As already mentioned, globalisation and combination of human and natural factors are largely responsible for setting favourable conditions for the emergence of new diseases in many parts of the world. They play a crucial role as well in disease outbreaks and/or regional spreading of diseases. Thus, it is with no doubt a global issue which has already been addressed at international level but so far proved difficult to handle. It is not at all clear and experts disagree widely to identify if there is more emerging diseases now than before (Parks et al. 2005). They acknowledge that human actions upon environment and global warming are creating more opportunities for new microbes and diseases to develop, even in areas that seemed to be preserved so far.

Many factors do contribute to the emergence or re-emergence of infectious diseases; amongst the most commonly cited in most studies on the topics, the following ones are coming on the top of the list: microbial adaptation and change, human demographics and behaviour and environmental changes (Wilcox and Colwell 2005).

It is not indeed a new phenomenon since, already in the mid-1990s, a WHO report stated that ‘during the past 20 years, at least 30 new diseases have emerged to threaten the health of hundreds of millions of people’ (McMichael and Confalonieri 2012). The socioecological conditions for this appear propitious: Human mobility and long-distance trade have increased; ever-larger cities, often girded with slums, have become highways for microbial traffic; poverty perpetuates vulnerability to infectious diseases; and sexual practices, drug injecting, intensified food production and much modern medical technology all create new opportunities for microbial opportunism.

4.3 Infectious Diseases and Interdisciplinary Approach

Growing interest of research in social sciences in fields such as health and environment has emerged in the late 1990s. Many scientific objects and items that were previously under the scope of biological and physical sciences, such as deforestation, water uses, natural risks, HIV mother-to-child transmission and cholera or chikungunya outbreaks, are now studied by social scientists with full legitimacy. The evolution in scientific discipline scopes and topics did not emerge suddenly but is rather a combination of international research and funding opportunities usually under multisites and multidisciplinary research programmes. Since emerging and new diseases are direct consequences of both social and environmental changes, some topics such as social uses, access and practices on environment and natural resources are crucial to understand how epidemics can spread or not (Brito et al. 2012). Similarly, new social dynamics, population growth and movements as well as disease identification and perceptions by various societies need also to be well identified and understood in order to come up with the most appropriate answers in the case of epidemics or disease outbreaks. These issues are clearly in the scope of social science studies. But if we want to go further to get a better understanding of emergence, re-emergence and transmission of infectious diseases, it is fundamental to integrate data from environmental and wildlife fields in human health studies. These fields of studies are thus to be dealt with through interdisciplinary research programmes combining social and health sciences with biological and physical approaches.

> The coupled human–natural systems perspective embodied in these ideas is fundamental to the development of a science of sustainability…No issue could be a more fundamental measure of sustainability than public health, and the increasing emergence and reemergence of infectious diseases globally is possibly the world's most challenging public health problem today. (Wilcox and Colwell 2005: 254)

Clearly, many factors, often interacting, can influence the emergence and re-emergence of infectious diseases. Thus, what is the relative importance of 'environmental' and 'social' factors? It may not be necessary to clearly state which ones are more important, since according to each situation, it obviously may differ greatly. What is crucial to bear in mind is that factors belong to two main categories, each one interfering and combining with the other; thus, both need to be studied, even if methods, scale of observation and length of study do not necessarily match between social sciences and environmental sciences, for example.

We live in a strange world where infections pass easily across borders (social and geographic), while resources, including cumulative scientific knowledge, seem to be blocked at 'customs'. Therefore, there is a need to build up cumulative regional knowledge and to exchange research experiences within the region particularly sensitive to disease outbreaks such as South East Asia. When subregions within a given part of the world do share similar social and environmental contexts, research projects should not be limited at the country level, but collaboration between researchers across borders should be encouraged both financially and scientifically, if we want to be able to come up with appropriate answers and tools to address emerging diseases or epidemic outbreaks. Uncontrolled movements of populations, increased civil wars and crises leading to more refugees and flora and fauna illegal trades are some of the factors that facilitate regional spreading of microbes. Data collected in these fields should be shared and exchanged by regional organisations dedicated to health studies and health watch programmes. Despite the fact that sometimes neighbouring countries are barely inclined to share scientific knowledge or to engage in joint research programmes due to political or historical reasons, they should be encouraged at the regional level to collaborate actively for the benefit of all and to gain a better efficiency in the case of threats to public health.

4.4 Interdisciplinary Approach

Data collected in the past ten years and figures from previous studies on similar topics tend to show that chikungunya and dengue fever represent a major risk of a worldwide epidemic starting from small islands or less developed countries and spreading in Europe and the USA and could create havoc in health systems in world leading countries. Such threats do exist worldwide and could lead to a global catastrophic scenario if nothing is done to prevent or to forecast such events. Medical and health studies alone can no longer address emerging diseases or outbreak phenomenon without the help of other scientific disciplines which are familiar with one or more interacting factors that influence epidemics or disease outbreaks (Colwell and Patz 1998).

The need is urgent to build capacity in the environmental community, social science fields and medical studies and to promote above all an interdisciplinary approach. Unfortunately, there are strong barriers to interdisciplinary programmes in academia: they are to be found in the cultural, historical and institutional context of disciplinary scholarship. For example, very few research institutes or universities have an appropriate committee in charge of evaluation of research conducted within the discipline as part of an interdisciplinary programme or project. As pointed out by the EAESS (see below), ‘interdisciplinarians’ are often confronted by a hostile context: they must fight for identity, recognition, roles, legitimacy and standing not only with their peers but sometimes with other scholars engaged with them in multidisciplinary studies. On top of this, like all scholars, they must compete for funding for which multidisciplinary projects are not always eligible, and most of the time, evaluation criteria for publishing, teaching, research and service are no longer in tune with the new dynamics in many fields of studies (environment, health, governance, risks, global changes) that are calling for a bridge between disciplines and encourage multidisciplinary. This move is fully acknowledged by the fact that there is growing recognition of the limits of disciplinary, in social, medical and environmental sciences alike; Health issues and especially emerging diseases, because of the multiple causing factors, need multidisciplinary and institutional approaches to address these problems, and they tend to indicate, on the basis of available results, a recognition of the promises of integrated, genuinely interdisciplinary approaches (Parks et al. 2005).

Past experiences have shown that although there are promising many scientific fields and topics, multidisciplinary projects are confronted by many difficulties that need to be addressed and overcome well upstream in order to clarify methodology- and concept-related inconsistencies that do exist between disciplines. For example, the scale level at which an anthropologist and an epidemiologist do collect data does not necessarily match. Similarly, notions of ‘resilience’ and/or ‘emergence’ do not have the same meaning for environmentalist specialists and health scientists. To go even further, the notion of disease itself will be understood differently not only by scientists and scholars from various backgrounds but also from different populations and/or ethnic groups in various parts of the world, according to the local context as well as the relationships between local communities and the State, for example. To sum up, problems, problem solving and interdisciplinarity are complex subjects, to be sure, but understanding them is essential if we are to effectively address environmental problems and health-related issues at the global level (Colwell 2010). One last point has to do with results in journals that are specialised and therefore reluctant to publish papers or important research breakthrough only because they do not fit within the journal’s main discipline, whereas a more flexible approach and different publication policy will help greatly as pointed out in a survey conducted by the American Academy of Microbiology (AAM 1997):

> Since research into questions of relationships between climate and infectious disease is interdisciplinary in scope, journals should be encouraged to publish the result of studies that fall outside of or straddle traditional disciplinary boundaries. (AAM 1997: 22)

The emergence of the Association for Environmental Studies and Sciences which provides a professional community to take on these issues through focused discussion and action has gained a lot of support throughout the scientist community and is making new positive grounds in promoting interdisciplinary approach despite setbacks and reluctance from many ‘traditional’ scientists.

4.5 Diseases and Tourism

Globalisation has prompted a growing interest for the international movements of persons, goods and information, but more than commercial exchanges and travels amplification it printed out the speed and scale of infectious diseases: in the last 30 years, more than 40 new diseases appeared, and many have or will spread rapidly internationally (Wilcox and Colwell 2005).

Human migration has been the main source of epidemics throughout human history; it favoured the emergence of infectious diseases through many mechanisms not all yet identified (Gushulak et al. 2004). Thus, human beings do travel and move, both within and between countries as do diseases. Disease is travelling as well, both ways, but when in the past European diseases were brought to the New World and spread during the discovery and first phase of the colonial era with deadly impacts on indigenous and autochthonous populations, nowadays infectious tropical diseases are becoming more and more frequent amongst travellers in the USA or northern Europe. Microbes are building resistances to many antibiotics, and vaccines against new forms of flu, for example, have to be combined with several formulas based on the previous year influenza epidemic with no full warranty of a total immune success.

Similarly, the transmission of malaria in Europe is closely linked to two main phenomenon travellers and migrants, both combined and risks of a major epidemic is pending especially in the context of global climate changes that is adding another cumulative element.

According to WTO, tourism is nowadays the world's fourth exportation commodity behind oil, chemical and cars (WTO 2009/2010). This is confirmed by the World Travel and Tourism Council (WTTC), which stated that in 2010, tourism (including transportation) represents nearly 5 % of world economic exchanges and provides 3 % of world total job opportunities. If all activities related to tourism are taken into account, figures jump to 10 % and 9 %. For many developing countries, tourism is one of the main sources of foreign currencies, employment and development (WTO 2010). Unfortunately, some touristic development programmes are generating social and environmental issues in developing countries mainly in terms of sustainability, education and health. In the last two decades, new forms of tourism have emerged and have gradually been implemented in developing countries, prompting new risks for travellers, tourists, host populations and wildlife.

Travel medicine is getting more and more complex and has to face new challenges brought by multiplications of new diseases, traveller's risky behaviour and growing importance of touristic-related activities (Houston 2000). Some diseases were underemphasized in the past and are now considered a major risk for tourists in an ever changing and more complex situation, leading to difficulties for practitioners to be able to deliver the right advises and practices.

> In the past, some risks, such as cholera, have been overemphasized while others, such as hepatitis, tuberculosis, motor vehicle accidents, and sexually transmitted diseases, have been underemphasized. (Houston 2000: 127)

Ecotourism and other nature-related forms of tourism bring tourists to remote and isolated areas in some parts of the world from which visitors can bring diseases back home (Wilson 1995a). They can also bring with them microbes that are already resistant which locally can mix or adapt to produce new unknown pathogens. Contacts with wildlife and tourism in wildlife reserves put tourists in close and direct contact with wild fauna which can be a vector as some zoonotic pathogens pass from animals to human.

"Wildlife plays a key role in their emergence by providing a "zoonotic pool" from which previously unknown pathogens may emerge" (Daszak et al. 2000: 446). This element is causing great concern amongst medical scientists and health authority since we know little about the transmission process as well as speed of mutation.

Similarly, food-borne diseases seem to spread more rapidly and more extensively than before and have direct consequences on touristic activities and tourism development in remote areas as well as population movements across continents.

> The factors contributing to the emergence of food-borne diseases are changes in human demographics and behavior, technology and industry, and international travel and commerce; microbial adaptation; economic development and land use; and the breakdown of public health measures. (Altekruse et al. 2007)

Once again, we see that the main factors causing the emergence of disease combine with social and environmental elements which are also central in most current forms of tourism activities; thus, there is an urgent need for research that will be able to embrace an interdisciplinary approach to both phenomena.

4.6 Tourism: Social and Environmental Issues

Tourism studies, especially in social and conservation sciences, although not new, are recent. Most journals, nowadays published worldwide, dedicated to tourism and related topics, are flourishing, but the older are only a few and appeared in the 1980s. Tourism was for a long time restricted to economic and managing research; it is now a booming topic in many scientific programmes in both western and developing countries that is particularly appropriate to interdisciplinary approaches. Many curriculums in universities worldwide are now available, and most of them combined social and environmental training. Amongst new interdisciplinary approaches dedicated to tourism, health and disease related to tourism are gaining a lot of attention from World Health Organisation, World Tourism Organisation, scientists and researchers and many world leading tourism companies as well as government bodies from many countries.

Maybe because tourism is above all linked to travel which bears a potential force in disease emergence and spread, especially since the current volume speed and reach of travel are unprecedented compared to 20 or 30 years ago (Wilson 1995a). Indeed, the exchange and dispersion of diseases are one of the many global consequences of tourism. Movement of infectious organisms by tourists is an important aspect of international travel. Tourists are at risk to acquire new infections, and they also act as vectors in the global dispersal of microbes; then, tourism can contribute in many and different ways to exchange and dispersion of both pathogens and diseases. This exchange and dispersion concern primarily human beings, but they do also expend flora and fauna and can contribute in some cases to bridge pathogen adaptation process between animals and men, as noted above (Maller et al. 2009).

In 2010, more than 800 million international tourist arrivals were counted worldwide. Even though a global activity of this scale can be assumed to have substantial impact on the environment, its consequences have never been fully assessed and quantified, nor were its devastating and perverted blows from a social perspective.

In order to simplify the overall process, we have selected a list of six major aspect alteration of the environment, following an international survey; some are interrelated, and others do combine to deteriorate further resources available:

- Land use and land cover change
- Energy use
- Biotic exchange and extinction of wild species
- Exchange and dispersion of diseases
- Changes in human-environment relations
- Water

For the purpose of this chapter, I will develop some ideas related to the exchange and dispersion of disease. In northern Europe, medical researchers have pointed out an increase of leptospirosis cases in several developed countries after journeys in tropical countries. Swimming and freshwater-related activities, associated with new forms of tourism such as ecotourism, green tourism and adventure tourism including rafting, canoeing and canyoning in tropical countries, represent a significant risk for tourists to develop leptospirosis. In that instance, it is clear that international tourism and new forms of tourism are responsible for the re-emerging of that disease. But one has to bear in mind that this case study is far from being isolated and strong attention should be given for further research in that field.

Tourists may be at risk of contracting diseases while travelling in remote tropical countries, but they also represent a threat for animals and plants, as pointed out by Homsy (1999), who severely criticised the management of parks and protected areas in wild mountain gorilla tourism since this activity, if maintained as it was running at the time of study, could bring gorillas to extinction. He proposed strong measures to reduce human risk and enhance gorillas' protection. Other case studies in botanic and environmental studies are stressing the role of tourism in bringing to new areas invasive and alien plants which are competing with native flora as well as diseases that can spread rapidly to local species and impact them deadly.

I will not go into details as far as social impacts of tourism are concerned but can pick out only the major ones, and it will be easy to understand that they are as important as those linked to environment degradation. For some time, tourism was limited to costal zones, and huge hotel complex were built as sea resort in many countries relying on mass tourism to generate foreign currency revenues. Many communities whose activities were closely dependant on sea access found themselves in distressed situations. Job opportunities occurred, but they benefited usually skilled or trained people, mainly from other regions and sometimes form overseas, who were often underpaid and socially marginalised. This era is partly over, and new forms of tourism such as rural tourism, ecotourism, discovery or adventure tourism or again green or solidarity tourism became more popular as an alternative to mass tourism. They attracted attention both in host countries and amongst tourists worldwide, but if these alternative tourisms sound more sustainable, both socially and environmentally, and less benefit oriented, they nonetheless impacted greatly areas in which they were implemented and caused social disorder alike. Many local communities in Morocco had no alternatives but to accept rural tourism development programmes initiated by the government and abandon many economic activities expecting great financial return from tourism, no need to say that most of them were extremely disappointed and many communities had to face social and economic crises as a direct result of projects failures (Berriane and Moizo 2014). In South East Asia, the so-called ethnic tourism can be blamed for a higher HIV infection rate in areas so far preserved from it and is directly linked to drug addiction in villages established on most tourist-frequented paths in the mountainous areas of northern Thailand and Laos. These villagers are now confronted by the outbreak of pneumonia and tuberculosis resulting directly from their impoverishment, marginalisation and social distress caused by many changes in their livelihoods (Cohen 1996; Moizo 2008). Many more examples could be given, and even though fortunately successful experiences and projects do exist, they remain a minority.

This leads to call for more interdisciplinary research dedicated to tourism with a peculiar concern for social and environmental impacts in order to get a better understanding of the main pitfalls of touristic activities and then to come up with alternative ways of developing tourism that will benefit both tourists and host population within a more sustainable approach (Froger 2010).

4.7 Conclusion

In this chapter, I have attempted to call on researchers' attention for sharing concerns and expertise to address two issues that seem nowadays to share a lot in common, that is, emerging disease and tourism. Both recently became important research topics in social sciences and have equally important connection with environmental issues and global change. This does reinforce the need for interdisciplinary research combining social and environmental approaches to address diseases and emerging diseases in the light of tourism and tourism-related activities.

Global travel and the evolution of microbes will continue. New infections will continue to emerge, and known infections will change in distribution, severity and frequency. Global environmental and social changes will maintain favourable conditions to facilitate emerging diseases to spread particularly if associated with climate changes. Similarly, travels, development of touristic activities and tourism in remote areas will continue to be a potent factor in disease emergence.

Globalisation and the current world juxtapose people, parasites, plants, animals and chemicals in a way that precludes timely adaptation; we need to be fully prepared to face this new challenge threatening countries and regions' health public systems. The current situation regarding emerging diseases calls for a need for integration of knowledge and skills from many disciplines: social, biological and physical sciences. Unfortunately, scholars and academics are sometimes reluctant to get engage in multidisciplinary approach.

There are definitely new grounds for interdisciplinary research that could be explored to better understand the microbial world, to better utilise existing data from both social and environmental sciences and most importantly to work towards a unified international agenda as suggested by McMichael and Confalonieri (2012) who conclude a stimulating study by adding that the "Increasing recognition of the interplay between demographic, social and environmental factors in infectious disease occurrence is leading to a more integrative, ecological, approach to studying, understanding, preventing and responding to infectious disease risks and outbreaks" (McMichael and Confalonieri 2012: 61). We would need to integrate knowledge and expertise from various disciplines—the social, biological and environmental and physical sciences—to address such a holistic dynamic than emergence and spread of diseases; but the core of the research should be centred on system analysis and the ecosystem rather than a disease or host (Wilson 1995b).

References

AAM (1997) Climate, Infectious diseases and health. A report based on the colloquium held by the American Academy of Microbiology, Montego Bay, 20–22 June 1997. AAM, Washington, DC, 23p

Altekruse SF, Cohen ML and Swerdlow DL (2007). Emerging foodborne diseases. http://www.nc.cdc.gov/eid/article/3/3/97-0304.htm. Accessed 19 Aug 2012

Berriane M, Moizo B (2014) Local initiatives, public policies and the development of tourism in the rural Morocco: a 15 year perspective on development initiatives in rural tourism. Front Sci Eng (FSE) 1(1):23–40, An international journal edited by Hassan II Academy of Science and Technology

Brito L et al (2012) Science for sustainable development. Science 336:1396–1398

Cohen E (1996) Thai tourism: hill tribes, islands and open-ended prostitution, collected papers. White Lotus, Bangkok

Colwell RR (2010) Towards an interdisciplinary ecological approach to infectious disease. Water challenges and solutions: opinion, posted July 25. http://water.jhu.edu/magazine/towards-an-interdisciplinary-ecological-approach-to-infectious-disease

Colwell RR, Patz JA (1998) Climate, infectious disease and health: an Interdisciplinary Perspective. A report from The American Academy of Microbiology, 25 p (unpublished)

Daszak P et al (2000) Emerging infectious diseases of wildlife– threats to biodiversity and human health. Science 287:443–449

Froger G (ed) (2010) Tourisme durable dans les Suds? Peter Lang, Bruxelles

Gushulak BD, Douglas W, MacPherson DW (2004) Globalization of infectious diseases: the impact of migration. Clin Infect Dis 38(12):1742–1748

Homsy J (1999) Ape tourism and human diseases: How close should we get? Report of a Consultancy for the International Gorilla Conservation Programme, 86p. www.primate.org/best_practice_disease

Houston S (2000) From Livingstone to ecotourism: what's new in travel medicine? Can Fam Phys – Le Médecin de famille canadien 46:121–128

Maller C et al (2009) Healthy parks, healthy people: the health benefits of contact with nature in a park context. G W Forum 26(2):51–83

McMichael AJ, Confalonieri U (2012) Environment, climate change, social factors and the implications for controlling infectious disease of poverty. In: Harris M, Reza JM (eds) Global report for research on infectious diseases of poverty. WHO, New York, pp 45–65

Moizo B (2008) Land allocation and titling in Laos: origins, problems and local impacts on minority groups. In: Leeprecha P, McCaskill D, Buadaeng K (eds) Impact of globalisation, regionalism and nationalism on minority peoples in Southeast Asia. Silk Worm, Chiang Mai, pp 97–115

Morse S (1995) Factors in the emergence of infectious diseases. Emerg Infect Dis 1:7–15

Parks MW et al (2005) All hands on deck: transdisciplinary approaches to emerging infectious disease. Ecohealth 2:258–272

The Global Environmental Change and Human Health (GECHH) (2012) RIO+20 POLICY BRIEF #9 Global health for a planet under pressure, transition to sustainability: interconnected challenges and solutions, Joint project report, 8 p

Weiss RA, McMichael AJ (2004) Social and environmental risk factors in the emergence of infectious diseases. Nat Med 10:570–576

Wilcox BA, Colwell RR (2005) Emerging and reemerging infectious diseases: biocomplexity as an interdisciplinary paradigm. Ecohealth 2:244–257

Wilson ME (1995a) Travel and the emergence of infectious diseases. Emerg Infect Dis 1:39–46

Wilson ME (1995b) Infectious diseases: an ecological perspective. Br Med J 311:1681

WTO (2009/2010) Faits saillants du tourisme. http://unwto.org/facts/eng/highlights.htm. Accessed 12 Jul 2012

WTO (2010) Tourism and least developed countries – a sustainable opportunity to reduce poverty. http://unwto.org/sustainable/doc/tourism-and-ldc.pdf. Accessed 21 Aug 2012

Part II

Socio-ecosystems and Health

Chapter 5
Heavy Metals Contamination in the Ecosystem of Mae Thang Reservoir in Northern Thailand

Séraphine Grellier, Patrick Seyler, Clément Petitjean, Marie-Paule Bonnet, Warinya Thothong, and Jean-Louis Janeau

Abstract One critical concern for Thailand reservoirs which are used for irrigated agriculture (mainly paddy rice) and aquaculture is the lack of information on contamination from trace metal element (TME) in waters and biological compartments of the reservoirs. TME are both from natural and anthropogenic origins and may affect the quality of lake waters and food chain. The goal of this study was to evaluate the contamination in TME and study their transfer between the different compartments in and downstream of the reservoir. Fourteen TME have been measured in water column (dissolved phase), fishes, and sediments of the Mae Thang Reservoir (northern Thailand) as well as soil and rice grains of irrigated area. Analyses were performed by inductively coupled plasma-mass spectrometer (ICP-MS). This 2-year study showed that TME concentrations in water were lower than standards for irrigation and aquatic life. However, localized values of Fe and Mn were higher than the standard in the bottom of the reservoir in dry season. TME in sediments were relatively high compared to pristine lakes. Two species of fish were contaminated in As and Ni. Soils exceeded standard values for Cr, Ni, and Cu, while rice grains showed contamination in Ni that indicated a transfer between soil and rice grain. The accumulation of TME in sediments showed that upstream cultivated areas may have contributed to bring TME in the reservoir. TME concentrations in

---

S. Grellier (✉)
University of Sciences and Technology of Hanoi (USTH),
H2 building, 18 Hoang Quoc Viet, Hanoi, Vietnam
e-mail: grellier_seraphine@yahoo.fr

P. Seyler
Laboratoire HydroSciences Montpellier, UMR CNRS 5569 – IRD 050,
CC 0057 – MSE – Place Eugène Bataillon, 34095 Montpellier, Cedex 5, France

C. Petitjean • M.-P. Bonnet
Géosciences Environnement Toulouse, OMP, Université Toulouse-IRD-CNRS-,
14 Av. Edouard Belin, 31400 Toulouse, France

W. Thothong
IRD-BIOEMCO, Ecole Nationale Supérieure 46 Rue d'Ulm, 75230 Paris Cedex 05, France

J.-L. Janeau
IRD - iEES-Paris (UMR 242) c/o Soils and Fertilisers Research Institute (SFRI),
Hanoi, Vietnam

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_5

fishes were thus affected and should be controlled. Accumulation of TME in soils of paddy field due to the use of pesticides and fertilizer may increase contamination of rice in the long term.

5.1 Introduction

Among the numerous pollutants that are discharged by human in the environment, trace metal elements (TME) are a potential threat for ecosystems and human health (Förstner and Wittmann 1979). TME can accumulate and persist in ecological systems such as lakes or reservoirs (Biney et al. 1994; Bronmark and Hansson 2002; Liu et al. 2011). After being transported to aquatic ecosystems by atmospheric deposition, direct input, or erosion due to rain (Veena et al. 1997; Islam et al. 2000), TME can be found in sediments, water column, and living aquatic organisms (Avila-Péreza et al. 1999; Yang et al. 2002; Chale 2002; Altindag and Yigit 2005; Rai 2009) with a possibility of transfer between these compartments. Due to a biological amplification for some TME concentrations through the food chain (Dallinger et al. 1987; Unlu and Gumgum 1993; Croteau et al. 2005; Mazej et al. 2010), the consumption of aquatic food products such as fish may be a source of health problem for human (Mok et al. 2012; Smuc et al. 2012). Moreover, when water stored in reservoir is used for irrigation, there is as well a possible contamination of irrigated areas (soil and plants) by contaminated water (Kien Chu et al. 2009). All the compartments of the ecosystems linked to a lake or a reservoir can thus be affected by TME contamination from upstream to downstream areas (water, sediments, aquatic biological organisms, irrigated soils, and irrigated cultures). Transfer of TME between these compartments is still a debated scientific question (Croteau et al. 2005; Yu et al. 2012a) that is complex due to the numerous processes involved and the different physicochemical properties of each TME.

In dry-tropical climate, such as in northern Thailand and other southeastern Asian countries, many reservoirs have been built to remediate water scarcity. These reservoirs are often located in rural areas and are mainly used for irrigation and flood control of downstream areas. Recreation and fisheries have also been developed within these reservoirs. If TME contamination is often reported in mining or industrial areas (Rai 2009; Mariani and Pompêo 2008; Siyue et al. 2008; Avila-Péreza et al. 1999), TME measured in rural ecosystem can also be at a high level (Pertsemli and Voutsa 2007). Scientists (Stumm and Morgan 1996; Bonnet and Wessen 2001) recognized that these reservoirs deeply modify the ecosystem and generate hydrological alterations and impaired water quality. Soil degradation inducing huge runoff in northern Thailand (Janeau et al. 2003) and the use of chemical pesticides and fertilizers can bring TME in the reservoir (Calamari and Naeve 1994). One critical concern for Thailand reservoirs which are used for irrigated agriculture (mainly rice) and aquaculture is the lack of information on trace metal element (TME) concentrations in water and the food chain, in particular those considered as unlikely (Hg, Cd, Pb, Cu, Zn, etc.) for living organisms and food products consumed by human (Grellier et al. 2013).

The main goal of this article that synthesize several studies realized between 2004 and 2006 is to evaluate the TME contamination in different compartments linked to the ecosystem of the Mae Thang Reservoir (northern Thailand). Water (dissolved phase) and sediments of the reservoir have been studied as well as some fish species from the reservoir (wild and farmed fishes) together with rice and soil from irrigated areas of the reservoir. The study focuses on the following TME: Fe, Mn, Cd, Al, Pb, V, Cr, Co, Ni, Cu, Zn, As, Mo, and U and their transfer between the different compartments mentioned above.

5.2 Study Site and Methods

5.2.1 Study Site

The study was conducted in northern Thailand, in Phrae province (Fig. 5.1). The watershed of the Mae Thang River with 120 km^2 is a sedimentary basin with calcite alternating with shales and black limestones. A reservoir of water has been built in

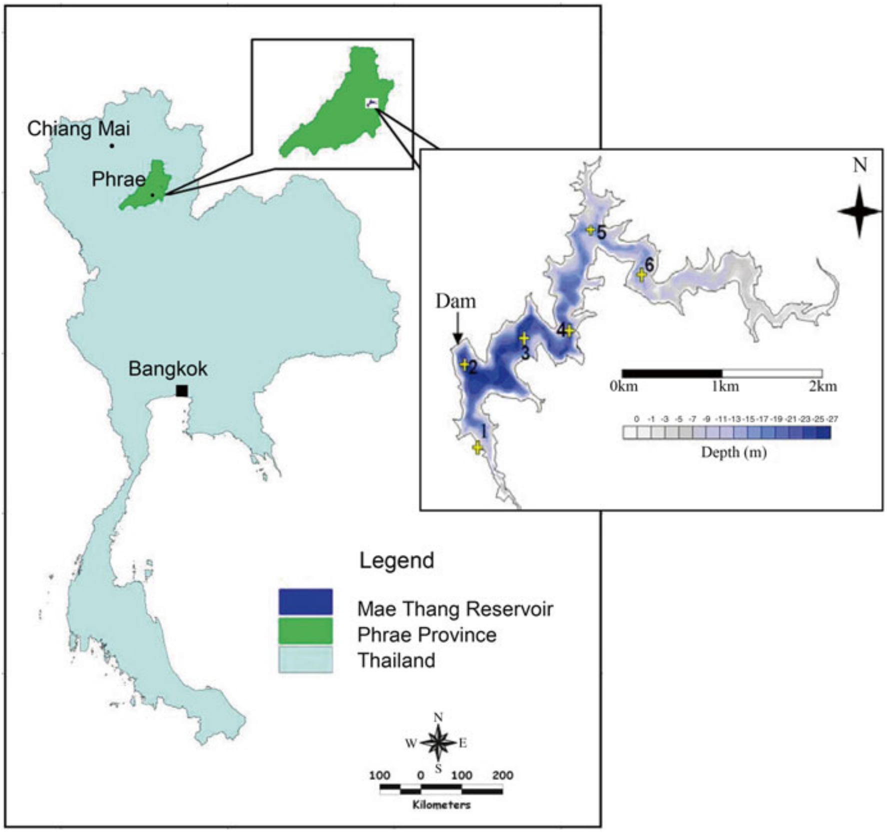


Fig. 5.1 Location of the study site in northern Thailand, Phrae province, and sample location of water and sediments in the reservoir

this watershed in 1995 (18° 13′ 08″N and 100° 19′ 22″E) to avoid water scarcity and to develop irrigated agriculture in the area. This reservoir is used to irrigate an area of 3,520 ha of rice, corn, and mung bean. Other uses such as household consumption, aquaculture, flood protection, and tourism are also developed thanks to this reservoir. Its size of 2.2 km^2 at the maximum water storage and 37 m deep allow it to store 35 million cubic meter of water. It is in the average of the numerous medium-sized reservoirs in northern Thailand. Sedimentation of the reservoir has been observed since its construction, and the reservoir has lost 6.7 % of its storage capacity due to sediment deposition (Thothong 2009). Annual water residence time was estimated at 4.2 months (Thothong 2009).

Climate of the area is tropical with two contrasted seasons: the wet southern monsoon from April to October and the dry northern monsoon from November to April. Temperature ranges from 18 to 33 °C, with an annual mean of 25.5 °C, and the mean annual rainfall was 1,265 mm from 2004 to 2006.

5.2.2 Experimental Design

Water samples were collected at different depths in the water column during two surveys (dry and humid seasons) at six stations along the longer axis of the lake (Fig. 5.1). The samples were collected with Niskin X™ bottle at different depths along the water column depending on the thermocline and chemocline depth locations, given by a multiparameter probe CTD90. Samples were filtered immediately on-site through 0.22 µm Millipore® membranes, under a clean air bench. Filtered solutions were acidified to pH 2 with 10 N double-distilled HNO3 and stored in high-density polyethylene (HDPE) bottles, previously washed with 1 N double-distilled HCl and rinsed with Milli-Q deionized water and stored at 4 °C until analysis (Seyler and Elbaz-Poulichet 1996).

Sediments at 10–20 cm depth were sampled in 2004 using a KC Kajak sediment core sampler at the same six sites than water samples (Fig. 5.1). After clean collection with plastic devices, sediments were stored in plastic bags until analyses.

Two types of fish were analyzed for TME: wild fishes that were bought directly from fishermen on-site and farmed fishes from fisheries established on the reservoir. Five small wild fishes (between 8 and 10 cm length) of the same species *Mystacoleucus marginatus* were used, and we collected one "standard-length fish" for each of the four following species from fish farms: *Ictalurus melas*, *Oreochromis niloticus* (Nile tilapia), *Probarbus jullieni* (Jullien's golden price carp), and *Barbonymus altus*. The four fishes from fisheries were between 8 and 11 months old and weighted between 0.7 and 1.5 kg. All fishes were caught or bought alive and were stored in freezer at −18 °C until analyses.

Soil and rice grain samples were collected downstream of the reservoir in the irrigated paddy fields at three points according to the distance of the reservoir (point 1 being the closest of the reservoir). Soil surface, between 0 and 10 cm depth, was sampled and oven dried before analyses. Rice grains were taken from the plants just before harvest on the same location than soil samples and were stored until further analyses.

5.2.3 *Analyses*

Before analyses, sample preparation was done in the laboratory for sediment, fish, soil, and rice samples. Soil, sediment, and rice samples were all finely crushed (<40 μm) with an electrical agate grinder. Quadrate method was used to select a homogeneous fraction of the samples for TME analyses (Flower et al. 1995).

Fishes were analyzed differently according to their origin (wild or farmed). The whole fish was used for TME analyses of wild fishes while only muscle parts were used for farmed fishes. This method was used to follow consumption habits of the Mae Thang people. They usually eat small wild fishes as whitebait, while they only eat the filet of bigger fish from fisheries. Frozen wild fishes were first roughly crushed in a plastic bag and then further frozen with liquid nitrogen. After being dried in the oven at 50 °C for 48 h, wild fishes samples and muscle samples from fisheries were finely crushed (<40 μm) in agate grinder. All crushed samples obtain for soil, rice, and sediments were finely digested in sealed Teflon beakers with HNO_3-HF-$HClO_4$ ultrapure acids before analyses.

Trace metal concentrations (Fe, Co, Cd, Pb, Mn, Ni, As, Cu, Mo, Zn, Cr, Al, V, U) of all the samples as well as water samples were measured by ICP-MS at the Geosciences Environnement Toulouse laboratory in France. Indium (In) and Rhenium (Re) were used as internal standards in order to correct for instrumental drift. The international geostandard SLRS-4 (riverine water reference material for trace metals, certified by the National Research Council of Canada), LKSD-1 (soil and sediment reference, Canmet, Canada), and SRM-1515 (rice and fish reference, National Institute of Standards and Technology (NIST), USA) were used to check the validity and reproducibility of the analysis by ICP-MS (Seyler and Elbaz-Poulichet 1996).

5.3 Results and Discussion

5.3.1 *Water*

The spatial variation of dissolved TME concentrations at the different sampling location on the reservoir was low, while there was clear spatial vertical variation according to the depth. Almost all dissolved TME concentrations either increased or decreased at 4 m depth at the thermocline in the dry season (Fig. 5.2). Al ranged from 8.3 ppb at the surface to 1.2 ppb at the bottom and V ranges from 4.5 to 0.75 ppb. Both had higher concentrations in the epilimnion. Zn ranged from 5.9 to 6.9 ppb with a decrease in the epilimnion, while As ranged from 1.1 ppb at the surface to 1.56 ppb at the bottom with a regular increase. Cr, Ni, and Mo presented lower values in the epilimnion and increased at the thermocline. On the contrary, Cu had a peak concentration in the epilimnion and ranged from 0.7 ppb at the surface to 0.24 ppb at the bottom. Co and Pb increased from the surface to the bottom, but with a strong decline

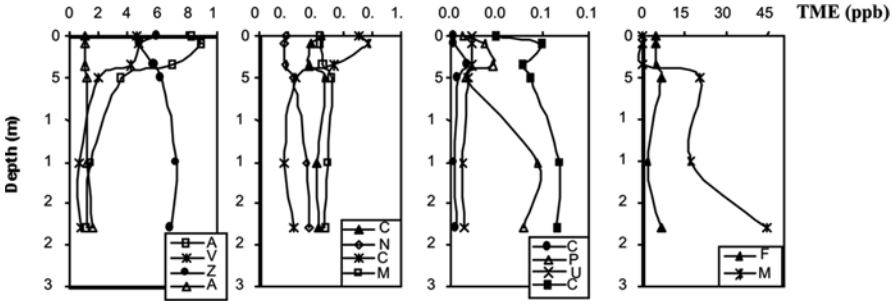


Fig. 5.2 Dissolved TME (ppb) in water column, March 2006 (dry season) location 2 (Fig. 5.1)

at the thermocline. Co ranged from 0.05 ppb at the surface to 0.12 ppb at the bottom and Pb ranged from 0.013 to 0.08 ppb. Cd had a slight increase at the thermocline at 0.017 ppb. U ranged from 0.022 ppb at the surface to 0.015 ppb at the bottom and decreased regularly. Fe ranged from 46.2 to 68.7 ppb, while Mn ranged from 0.96 to 446 ppb with a strong increase at the thermocline and below from 15 m depth to the bottom. Dissolved TME in the water column of the reservoir were distributed according to the depth with a strong influence of the thermocline and chemocline especially in the dry season (Fig. 5.2). These results in comparison with the wet season are discussed in detailed in Grellier et al. (2013). These authors showed that TME were strongly related to physicochemical parameters of the water column.

Mean TME concentrations of the wet and the dry season were not higher than standard limits of Thailand and World Health Organization (WHO 2004) for irrigation and aquatic life (Table 5.1). Our results (except for Fe and Mn) were lower than TME concentrations measured in the Danjiangkou Reservoir of industrial area in China (Siyue et al. 2008) and were similar to the concentration of Constance Lake used for drinking water (Petri 2006). However, localized values of Fe and Mn were higher than the WHO standard limits (WHO 2004) in the bottom of the reservoir in dry season and were much higher than in water of Danjiangkou Reservoir and Constance Lake. These high concentrations at the bottom of the reservoir are associated with anoxic conditions that may occur in dry season when weak mixing of the water column occurs (Grellier et al. 2013). Fe and Mn may be a source of pollution when the water is used for irrigation, especially if the output gate is located at the bottom of the dam, which is the case in Mae Thang Reservoir.

5.3.2 *Sediments*

TME in surface sediments presented spatial variations in the reservoir. Sampling points 1 and 2 were localized in the south part of the reservoir where small river inputs are found. Sampling point 4 was localized in the middle of the reservoir.

Table 5.1 Mean dissolved TME concentrations (ppb ± SD) in the water column of Mae Thang Reservoir compared with standards and other studies

TME	Mean water		Max	Standard limit for irrigation, Thailand*	Standard limit for irrigation (WHO)	Standard limit for aquatic life (WHO)	TME in reservoir of industrial area in China (Siyue et al. 2008)	TME in reservoir for drinking water (Petri 2006)
Al	4.94	±2.33	11.13	–	–	–	203.69	4.5
V	1.81	±1.16	4.75	–	–	–	71.33	–
Mn	80.64	±148.55	657.51	5,000	–	–	5.69	–
Fe	50.72	±38.79	249.80	–	200	100	19.14	6
Co	0.15	±0.24	1.88	–	–	–	1.08	0.08
Ni	0.30	±0.11	0.82	200	–	–	1.73	–
Cu	0.46	±0.71	5.84	1,000	200	500–6,000	13.32	1.1
Zn	2.92	±3.16	24.22	5,000	–	–	2.02	–
As	0.97	±0.29	2.08	250	100	10	11.08	1.2
Cd	0.01	±0.01	0.10	30	10	0.15	1.17	<0.025
Pb	0.03	±0.03	0.14	100	200	0.2	10.59	–

*Pollution Control Department of Thailand, 1995

Sampling points 5 and 6 were localized in the North part of the reservoir where the Mae Thang River serves as main water input.

The normalized values were calculated to take out the influence of the grain size and compare our results of the different locations on the reservoir (Horowitz 1991; Forstner 1989, 2004). Our results showed that initial concentrations of TME measured in points 5 and 6 were often maximal (except for Mn, As, Pb, and U). On the contrary, their normalized concentrations hide these differences. This comparison indicates that all these elements (V, Cr, Fe, Co, Ni, Zn, Mo, Cd) come from the watershed sediments and that a separation according to granulometry may have occurred in the reservoir (Horowitz 1991; Yu et al. 2012b). However, the normalization with Zr does not clearly show it. The maximal concentrations of Mn and As in the deepest zone (location 2), where anoxic conditions were measured, indicate that the redox conditions may play an important role in their distribution. Pb and U also showed maximum concentrations in location 2. They could have been adsorbed and scavenged in the water column (Table 5.2).

The mean average TME in sediments showed that Fe, Mn, Cr, Ni, Cu, Zn, and Pb were higher than those in other studies concerning polluted and nonpolluted areas (Table 5.3) indicating a contamination of the sediments. Geology plays an important role in the Fe and Mn concentrations in the area as rocks of the area can be a source of Fe and Mn. The high presence of Fe and Mn in the sediments can explain the extreme values in the bottom of the reservoir in dry season for these two elements due to dissolution processes at the sediment-water interface. Geology is certainly not the only factor affecting TME concentration in the sediments. An input of TME through eroded soil particles (high sedimentation of the reservoir has been measured by Thothong (2009)) is probably also at the origin of the concentration of TME in sediments.

5.3.3 Fishes

TME and major cations in wild and farmed fishes showed some differences (Table 5.4). Calcium was 20 times higher in wild fishes. This was due to the analytical methods. We analyzed the whole wild fishes which contain the bones where Ca concentrates, while we only analyzed muscles (filet) of farmed fishes. Al, V, Mn, Zn, Cd, and Pb were higher, while Fe and As were lower in wild fishes than in farmed fishes. This result is linked to the accumulation of heavy metals in specific part of the fish, such as the liver (Saad and Ezzat 1981; Karadede et al. 2004; Mhadhbi et al. 2012). Taking into account that local people eat the whole small wild fishes and specifically only filets of farmed fishes, our results indicate that exposition to trace metal elements will be higher with small wild fishes. The higher values of Fe and As in farmed fishes indicate either a higher exposition for these two elements or a different storage mechanisms of muscles and other parts of the fish body. A possible explanation is a contamination either through metal structure used in fisheries or food for fish that can be a source of TME (Russell et al. 2011). It has

Table 5.2 TME concentrations in sediments of Mae Thang Reservoir. Initial concentrations and normalized values (X/Zr) are presented

Sample location		V	Cr	Mn	Fe	Co	Ni	Cu	Zn	As	Mo	Cd	Pb	U
1	Initial concentrations (ppm)	109.7	55.98	662	36.355	11.56	33.78	35.57	99.22	15.19	0.15	0.05	9.11	1.44
2		130.33	65.03	973	40.129	19.35	36.8	44.33	110.95	25.79	0.22	0.07	15.7	1.88
4		116.05	52.45	768	35.850	16.53	32.16	38.14	107.89	23.31	0.2	0.07	14.38	1.85
5		207.53	174.66	731	58.122	27.4	95.25	64.48	138.81	19.89	0.45	0.09	9.91	1.54
6		200.44	157.2	676	53.758	27.4	91.87	64.91	136.36	17.73	0.31	0.17	11.64	1.65
1	Normalized values X/Zr	0.7	0.36	4.22	231	0.07	0.22	0.23	0.63	0.1	0.001	0	0.06	0.009
2		0.74	0.37	5.5	226	0.11	0.21	0.25	0.63	0.15	0.001	0	0.09	0.011
4		0.5	0.23	3.31	154	0.07	0.14	0.16	0.46	0.1	0.001	0	0.06	0.008
5		0.75	0.64	2.66	211	0.1	0.35	0.23	0.5	0.07	0.002	0	0.04	0.006
6		0.81	0.63	2.72	216	0.11	0.37	0.26	0.55	0.07	0.001	0.001	0.05	0.007

Table 5.3 Mean TME concentrations in sediments (ppm ± SD) of Mae Thang Reservoir compared with other studies

TME	Mean sediments		Nonpolluted area India (Rai 2009)	Polluted area India (Rai 2009)	Turkey lake (Karadede and Unlu 2000)
V	152.81	±47.38	–	–	–
Cr	101.06	±59.71	0.5	8.5	–
Mn	762.00	±125.41	2.1	133	514
Fe	44842.80	±10379.68	1.9	85	19,265
Co	20.45	±6.93	–	–	–
Ni	57.97	±32.55	0.3	27	139.69
Cu	49.49	±14.25	0.6	28	22.7
Zn	118.65	±17.84	1.7	57	59.14
As	20.38	±4.24	–	–	–
Mo	0.27	±0.12	–	–	–
Cd	0.09	±0.05	0.2	4.6	–
Pb	12.15	±2.83	0.2	7.5	–
U	1.67	±0.19	–	–	–

been shown that fish muscles concentrate As and Cr and thus decrease the concentration of these metals in the liver (Mok et al. 2012; Ciardullo et al. 2008). In our study, the increase of As in farmed fishes (only muscles were analyzed) could also be due to this mechanism of concentration of As in muscles.

The comparison with other studies shows that TME concentrations of fishes in Mae Thang Reservoir are still relatively low (Table 5.4). Almost all concentrations are lower than the values for fishes from Zambezi River (FFEM/AFD 2005), Kariba Lake (FFEM/AFD 2005), and Tanganyika Lake (Chale 2002). V and Zn values that exceeded other study values are related to the entire small wild fishes. These two values can only be compared with the results from the last column of the Table 5.4 where the whole fishes from Tanganyika Lake have been analyzed. In the latter case, our results do not exceed the values measured by Chale (2002). However, the four studied farmed species of fish presented different values especially for As and Ni (Fig. 5.3). Arsenic values for *O. niloticus* and *B. altus* were higher than for the two other species (Table 5.5). *O. niloticus* also concentrated Ni which was higher for this species (Fig. 5.3). Even if the mean of TME for farmed fishes was lower than Australian and European standards (Table 5.4), *O. niloticus* and *B. altus* showed extreme values for As and Ni that were over the Australian limits (Fig. 5.3). The contamination in As and Ni for two species of farmed fishes was not linked to dissolved TME concentrations in water as there was no contamination for these two elements. Two hypotheses can be proposed: (1) the source of contamination is related to food and metal structure of fisheries (Russell et al. 2011), (2) or the source of contamination is linked to suspended matter (particulate phase) that is eroded from the upstream part of the watershed (Janeau et al. 2003) and that is contami-

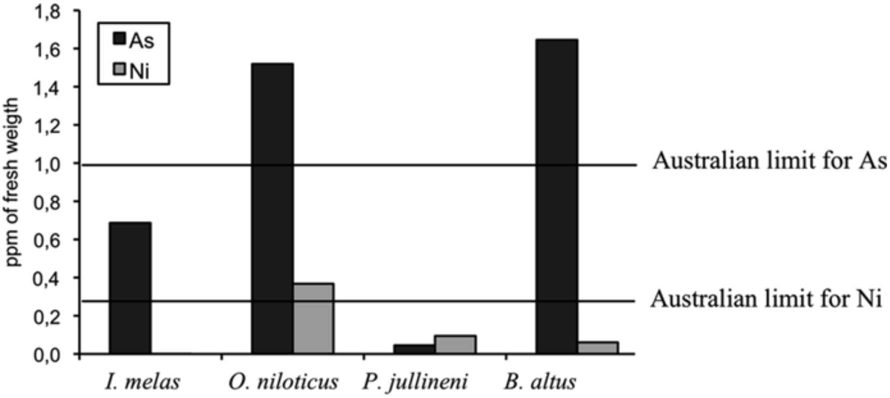


Fig. 5.3 Arsenic and nickel concentrations in the four farmed species of fish from the Mae Thang Reservoir compared with Australian standards. Concentrations are given in ppm of fresh weight of fish

nated in TME through agricultural practices, especially pesticides (Calamari and Naeve 1994). This second hypothesis relates to the one we proposed for contamination of sediments. The measure of TME concentrations in particulate phases in the water column will be an interesting aspect to study to understand better the transfer of TME between soil, water, and fish.

5.3.4 Paddy Soil and Rice

TME concentrations in paddy soils of Mae Thang presented high values compared to other agricultural soils (Table 5.6). V, Cr, Co, Ni, Cu, As, and Pb were all higher than agricultural soils in Canada (Haluschak et al. 1998). Cr, Ni, and Cu were higher or very close to the CE standard limits. This pollution could be due to two sources: (1) contaminated irrigation water from the reservoir and (2) fertilizers and pesticides used in the paddy field. The first hypothesis cannot be confirmed in our case. If the dissolved phase was not contaminated in Cr, Ni, and Cu, we do not have data about particulate phase transported by water that could also carry such elements (Ruiz Canovas et al. 2012). However, we showed that these elements are not brought in abnormal quantity under dissolved phase in the paddy fields. The second hypothesis is the one we support most due to extensive use of fertilizers and pesticides (personal observation) that can be a source of TME (Calamari and Naeve 1994).

TME concentrations in the three studied soils showed an increase with the distance to the reservoir. Soil sample 1 (upstream) was the closest to the dam, while soil sample 3 (downstream) was the furthest (Fig. 5.4). This result indicates that TME accumulation in the downstream part may be linked to concentration by runoff at the lower slopes (De Siervi et al. 2005; Kien Chu et al. 2009; Singh et al. 2000).

Table 5.4 Mean TME and major ion concentrations for wild and farmed fishes in Mae Thang Reservoir compared to international standard and data from other studies. Concentrations are given in ppm (±SD) of fresh weight of fish

TME and major elements	Mean wild fishes (±SD)		Mean farmed fishes (±SD)		CE standard limit (Directive 2001/22/CE)	Australian standard Maximal Residue Limit (NFA 1992)	Zambezi River (FFEM 2005)	Kariba Lake (FFEM 2005)	Tanganyika Lake, muscle (Chale 2002)	Tanganyika Lake, whole fish (Chale 2002)
Na	471.67	±177.28	420.63	±59.01	–	–	–	–	–	–
Mg	274.49	±69.55	267.90	±51.24	–	–	–	–	–	–
K	2425.90	±343.42	4322.88	±578.06	–	–	–	–	–	–
Ca	7265.74	±4813.30	359.63	±470.08	–	–	–	–	–	–
Al	0.61	±0.14	0.10	±0.03	–	–	–	–	–	–
V	0.31	±0.26	0.01	±0.02	–	–	0.24	0.17	–	–
Mn	0.91	±0.73	0.61	±0.01	–	–	–	–	1.15	11.8
Fe	0.25	±0.42	3.41	±1.02	–	–	–	–	–	–
Co	0.01	± <0.00	0.02	±0.01	–	–	0.36	0.47	–	–
Ni	0.11	±0.08	0.13	±0.16	–	0.27	5.83	8.53	–	–
Cu	0.29	±0.12	0.21	±0.06	–	10	8.88	8.93	4.05	5.90
Zn	28.64	±17.45	8.10	±1.83	–	150	–	–	16	133
As	0.04	±0.02	0.97	±0.75	–	1.0	1.06	1.39	–	–
Cd	0.02	±0.01	0.01	± <0.00	0.05	0.2	0.01	0.28	0.25	0.39
Pb	0.01	±0.01	<0.00	±0.01	0.2	1.5	1.15	1.41	4.95	4.95

Table 5.5 TME and major ion concentrations (± error) in four farmed fish species of the Mae Thang Reservoir. Concentrations are given in ppm of dry weight of fish

TME and major elements	*I. melas*		*O. niloticus*		*P. jullieni*		*B. altus*	
Na	1818.71	±57.45	1801.02	±59.80	1329.21	±44.65	1781.19	±61.19
Mg	793.42	±18.17	1190.70	±29.80	1255.62	±32.71	1046.72	±26.10
K	14305.37	±367.60	19531.81	±503.28	18619.74	±470.78	16709.08	±405.57
Ca	316.91	±24.74	549.50	±17.96	4251.76	±88.92	635.87	±20.63
Al	–	–	0.40	±0.14	–	–	–	–
V	0.01	±0.01	0.03	±0.01	0.18	±0.01	0.01	± <0.00
Mn	–	–	–	–	2.42	±0.06	–	–
Fe	16.51	±0.88	17.77	±0.71	9.93	±0.32	10.39	±0.82
Co	–	–	0.04	± <0.00	0.11	±0.01	–	–
Ni	<0.00	±0.07	1.47	±0.13	0.38	±0.08	0.24	±0.08
Cu	1.23	±0.06	0.78	±0.05	0.69	±0.05	0.72	±0.04
Zn	38.86	±1.08	36.00	±0.91	32.68	±0.83	22.08	±0.68
As	2.75	±0.11	6.08	±0.17	0.18	±0.02	6.58	±0.19
Cd	0.05	±0.01	0.03	±0.01	0.03	±0.01	0.02	±0.01
Pb	–	–	–	–	0.03	± <0.00	<0.00	± <0.00

Table 5.6 Mean TME concentrations in soils (ppm ± SD) of paddy fields located downstream of the Mae Thang Reservoir compared with standards and other studies

TME	Mean soils		Agricultural soils (Haluschak et al. 1998)	CE standard limit for agricultural soils
V	338.46	±175.25	76	–
Cr	325.07	±136.64	46	150
Co	45.42	±24.00	12	–
Ni	237.53	±122.58	21	50
Cu	98.87	±49.30	18	100
As	19.48	±10.03	5.8	–
Mo	1.65	±0.61	3	–
Pb	15.90	±8.46	15	100

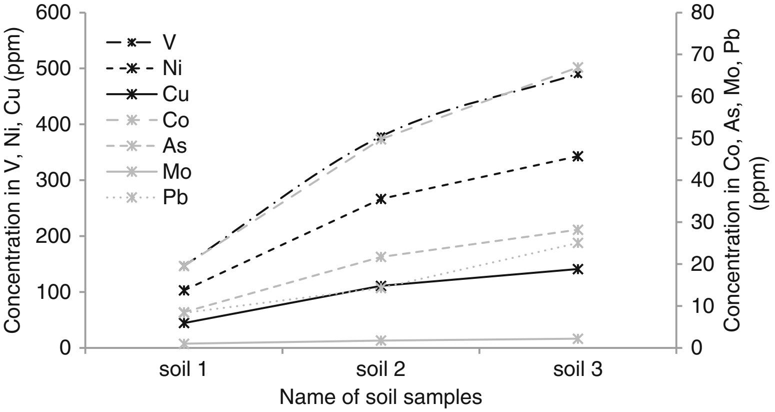


Fig. 5.4 Concentrations of TME (ppm) in soils of three paddy fields located downstream of the Mae Thang Reservoir

If soils exceeded limits for Cr and Ni and was very close for Cu, rice showed contamination in Ni which was much higher than the Australian standard limit and results of two other studies in Nigeria and China (Table 5.7). There is a transfer of TME from the soil to the plant that accumulates TME in different parts (Singh et al. 2011). This transfer can be calculated by a ratio of TME in the rice grain and in soil. We calculated this ratio for Ni, Cu, Co, and As and obtained, respectively, in average for the three soils 0.08, 0.023, 0.005, and 0.007. According to Bliefert and Perraud (2001), these ratios are considered to be low (0.001–0.1) to moderate (0.1–1). The ratio for Ni was the highest which is linked to its high concentration in rice. TME

Table 5.7 Mean TME and major ions concentrations (ppm ± SD) in rice of paddy fields located downstream of Mae Thang Reservoir, compared with European standard and other studies

TME and major elements	Mean rice		CE standard limit (Directive 2001/22/CE)	Australian standard Maximal Residue Limit (NFA 1992)	Rice grains of Nigeria (Chukwuma 1995)	Rice grain of Guangxi, China (Liu et al. 2011)
Na	–		–	–	–	–
Mg	228.61	±40.56	–	–	–	–
K	981.83	±68.22	–	–	–	–
Ca	74.70	±15.23	–	–	–	–
Al	6.72	±6.47	–	–	–	–
V	0.03	±0.02	–	–	–	–
Mn	9.86	±2.23	–	–	278 ± 108.8	–
Fe	12.66	±2.84	–	–	–	–
Co	0.17	±0.03	–	–	–	–
Ni	13.39	±1.48	–	0.27	1.45 ± 1.2	1.91 ± 0.87
Cu	1.79	±0.16	–	10	3.9 ± 1.8	4.88 ± 1.70
Zn	25.36	±3.66	–	150	33.4 ± 14.8	–
As	0.12	±0.04	–	1.0	–	–
Cd	0.14	±0.03	0.2	0.2	–	0.03 ± 0.02
Pb	0.07	±0.01	0.2	1.5	–	0.22 ± 0.05

accumulation in soils of paddy fields may have a long-term impact on the TME concentrations in rice.

5.4 Conclusion

The Mae Thang Reservoir and associated irrigated areas have been studied to assess TME contamination in water, sediments, fishes, soils, and rice. This ecosystem presented a contamination by TME. The accumulation of TME in sediments of the reservoir indicated that upstream cultivated areas (through eroded soil particles) and fisheries may have contributed to bring TME in the reservoir. TME concentrations in fishes were thus affected as Ni and As exceeded standard limits and should be controlled. Accumulation of TME in soils of paddy field mainly due to the use of pesticides and fertilizers may induce higher contamination of rice in the long term. As Ni concentrations in rice exceeded standard limit, there is a need of limiting soil TME pollution in the area by reducing fertilizers and pesticides use. For irrigation use, we advise local authorities and farmers to pump out the water at the surface where Fe and Mn concentrations are acceptable. There was no clear transfer from dissolved TME in the water column of the reservoir to the irrigated areas. However, particulate phase in the water column could be studied to further investigate transfer processes of TME in such ecosystem.

Acknowledgments The authors thank the National Park, Wildlife and Plant Conservation Department of Thailand, the Irrigation Department of Phrae province for the logistical support, the people of the Mae Thang catchment, and reviewers for comments on the manuscript. This study was supported by the Institute for Research and Development (IRD) and has been achieved thanks to ATI U2SIS budget (IRD 2003–2006) managed by JL Guyot.

References

Altindag A, Yigit S (2005) Assessment of heavy metal concentrations in the food web of lake Beysehir, Turkey. Chemosphere 60:552–556

Avila-Péreza P, Balcázar M, Zarazúa-Ortega G, Barceló-Quinta I, Díaz-Delgado C (1999) Heavy metal concentrations in water and bottom sediments of a Mexican reservoir. Sci Total Environ 234:185–196

Biney C, Amuzu AT, Calamari D, Kaba N, Mbome IL, Naeve H et al (1994) Review of heavy metals in the African aquatic environment. Ecotoxicol Environ Saf 28:134–159

Bliefert C, Perraud R (2001) Chimie de l'environnement. Air, eau, sols et déchets. De Boeck, Bruxelles, Belgium

Bonnet MP, Wessen K (2001) ELMO, a 3-D water quality model for nutrients and chlorophyll: first application on a lacustrine ecosystem. Ecol Model 141:19–33

Bronmark C, Hansson LA (2002) Environmental issues in lakes and ponds: current state and perspectives. Environ Conserv 29:290–307

Calamari D, Naeve H (1994) Revue de la pollution dans l'environnement aquatique africain. FAO, Rome, 129

Chale FMM (2002) Trace metal concentrations in water, sediments and fish tissue from Lake Tanganyika. Sci Total Environ 299:115–121

Chukwuma C (1995) Evaluating baseline data for copper, manganese, nickel and zinc in rice, yam, cassava and guinea grass from cultivated soils in Nigeria (vol 53, p 47, 1995). Agr Ecosyst Environ 56:71–74

Ciardullo S, Aureli F, Coni E, Guandalini E, Lost F, Raggi A et al (2008) Bioaccumulation potential of dietary arsenic, cadmium, lead, mercury, and selenium in organs and tissues of rainbow trout (*Oncorhyncus mykiss*) as a function of fish growth. J Agric Food Chem 56:2442–2451

Croteau MN, Luoma SN, Stewart AR (2005) Trophic transfer of metals along freshwater food webs: evidence of cadmium biomagnification in nature. Limnol Oceanogr 50:1511–1519

Dallinger R, Prosi F, Segner H, Back H (1987) Contaminated food and uptake of heavy metals by fish. A review and a proposal for further research. Oecologia 73:91–98

De Siervi M, de Iorio AF, Chagas CI (2005) Heavy metals in sediments and runoff waters in soils of the Matanza river basin, Argentina. Commun Soil Sci Plant Anal 36:2303–2314

Directive/Euro (2001) Directive Européenne n°2001–22 du 8 mars 2001 2001/22/CE DE LA COMMISSION du 8 mars 2001 portant fixation des modes de prélèvement d'échantillons et de méthodes d'analyse pour le contrôle officiel des teneurs en plomb, cadmium, mercure et 3-MCPD dans les denrées alimentaires

FFEM/AFD (2005) Trace metals and other contaminants in fish from the Zambezi basin. Pollution monitoring and management on the Zambesi River. Technical report. Fonds Français pour l'Environnement Mondial/Agence Française de Développement

Flower RJ, Monteith DT, Mackay AW, Chambers JM, Appleby PG (1995) The design and performance of a new box corer for collecting undisturbed samples of soft subaquatic sediments. J Paleolimnol 14:101–111

Forstner U (1989) Contaminated sediments. Lectures on environmental aspects of particle-associated chemicals in aquatic systems. Lecture notes in earth sciences 21

Forstner U (2004) Traceability of sediment analysis. Trac-Trend Anal Chem 23:217–236

Förstner U, Wittmann GTW (1979) Metal pollution in the aquatic environment. Springer Verlag, Berlin

Grellier S, Janeau JL, Thothong W, Boonsaner A, Bonnet MP, Lagane C et al (2013) Seasonal effect on trace metal elements behaviour in a reservoir of northern Thailand. Environ Monit Assess 185:5523–5536

Haluschak PW, Mills GF, Eilers RG, Grift S (1998) Status of selected trace elements in agricultural soils of southern Manitoba. Technical bulletin 1998-6E. Land resource unit. Brandon Research Centre, Research Branch, Agriculture and Agri-Food, Brandon

Horowitz A (1991) A primer on sediment. Trace element chemistry, 2nd edn. USA Lewis Publishers, Chelsea

Islam MR, Lahermo P, Salminen R, Rojstaczer S, Peuraniemi V (2000) Lake and reservoir water quality affected by metals leaching from tropical soils, Bangladesh. Environ Geol 39:1083–1089

Janeau JL, Bricquet JP, Planchon O, Valentin C (2003) Soil crusting and infiltration on steep slopes in northern Thailand. Eur J Soil Sci 54:543–553

Karadede H, Unlu E (2000) Concentrations of some heavy metals in water, sediment and fish species from the Ataturk dam lake (Euphrates), Turkey. Chemosphere 41:1371–1376

Karadede H, Oymak SA, Unlu E (2004) Heavy metals in mullet, Liza abu, and catfish, *Silurus triostegus*, from the Ataturk dam lake (Euphrates), Turkey. Environ Int 30(2):183–188

Kien Chu N, Van Noi N, Bang Nguyen D, Le Son T, Tanaka S, Kang Y et al (2009) Arsenic and heavy metal concentrations in agricultural soils around Tin and Tungsten mines in the Dai Tu district, N. Vietnam. Water Air Soil Pollut 197:75–89

Liu J, Zhang X-H, Tran H, Wang D-Q, Zhu Y-N (2011) Heavy metal contamination and risk assessment in water, paddy soil, and rice around an electroplating plant. Environ Sci Pollut Res 18:1623–1632

Mariani CF, Pompêo MLM (2008) Potentially bioavailable metals in sediment from a tropical polymictic environment–Rio Grande reservoir, Brazil. J Soil Sediment 8:284–288

Mazej Z, Al Sayegh-Petkovsek S, Pokorny B (2010) Heavy metal concentrations in food chain of Lake Velenjsko Jezero, Slovenia: an artificial lake from mining. Arch Environ Contam Toxicol 58:998–1007

Mhadhbi L, Palanca A, Gharred T, Boumaiza M (2012) Bioaccumulation of metals in tissues of Solea vulgaris from the outer coast and Ria de Vigo, NE Atlantic (Spain). Int J Environ Res 6:19–24

Mok WJ, Senoo S, Itoh T, Tsukamasa Y, Kawasaki K -i, Ando M (2012) Assessment of concentrations of toxic elements in aquaculture food products in Malaysia. Food Chem 133:1326–1332

NFA (1992) National Food Authority 1992, the 1992 Australian market basket survey: a total diet survey of pesticides and contaminants. NFA, Canberra

Pertsemli E, Voutsa D (2007) Distribution of heavy metals in Lakes Doirani and Kerkini, Northern Greece. J Hazard Mater 148:529–537

Petri M (2006) Water quality of lake constance. In: Knepper TP (ed) The rhine, vol 5L, The handbook of environmental chemistry. Springer, Berlin/Heidelberg, pp 127–138, http://link.springer.com/book/10.1007/b11739

Rai PK (2009) Heavy metals in water, sediments and wetland plants in an aquatic ecosystem of tropical industrial region, India. Environ Monit Assess 158:433–457

Ruiz Canovas C, Olias M, Miguel Sarmiento A, Miguel Nieto J, Galvan L (2012) Pollutant transport processes in the Odiel river (SW Spain) during rain events. Water Resour Res 48

Russell M, Robinson CD, Walsham P, Webster L, Moffat CF (2011) Persistent organic pollutants and trace metals in sediments close to Scottish marine fish farms. Aquaculture 319:262–271

Saad MAH, Ezzat AA (1981) Occurrence and distribution of chemical pollutants in lake Mariut, Egypt. 2. Heavy metals. Water Air Soil Pollut 16:401–407

Seyler P, Elbaz-Poulichet F (1996) Biogeochemical control on the temporal variability of trace element concentrations in the Oubangui river (Central African Republic). J Hydrol 180:319–332

Singh SP, Tack FMG, Gabriels D, Verloo MG (2000) Heavy metal transport from dredged sediment derived surface soils in a laboratory rainfall simulation experiment. Water Air Soil Pollut 118:73–86

Singh J, Upadhyay SK, Pathak RK, Gupta V (2011) Accumulation of heavy metals in soil and paddy crop (Oryza sativa), irrigated with water of Ramgarh lake, Gorakhpur, UP, India. Toxicol Environ Chem 93:462–473

Siyue L, Zhifang X, Xiaoli C, Quanfa Z (2008) Dissolved trace elements and heavy metals in the Danjiangkou reservoir, China. Environ Geol 55:977–983

Smuc NR, Dolenec T, Serafimovski T, Tasev G, Dolenec M, Vrhovnik P (2012) Heavy metal characteristics in Kocani field plant system (Republic of Macedonia). Environ Geochem Health 34:513–526

Stumm W, Morgan JJ (1996) Aquatic chemistry, 3rd edn. Wiley, New York

Thothong W (2009) Source, storage and mineralization of organic matter in a tropical water reservoir (Thailand), relationship with soil erosion on the watershed. University of Pierre et Marie Curry, Paris

Unlu E, Gumgum B (1993) Concentrations of copper and zinc in fish and sediments from the Tigris river in Turkey. Chemosphere 26:2055–2061

Veena KB, Radhakrishnan CK, Chacko J (1997) Heavy metal induced biochemical effects in an estuarine teleost. Indian J Mar Sci 26:74–78

WHO (2004) World Health Organisation 2004. Guidelines for drinking-water quality – volume 1 – Recommendations, 3rd edn. WHO, Geneva

Yang HD, Rose NL, Battarbee RW (2002) Distribution of some trace metals in Lochnagar, a Scottish mountain lake ecosystem and its catchment. Sci Total Environ 285:197–208

Yu T, Zhang Y, Hu X, Meng W (2012a) Distribution and bioaccumulation of heavy metals in aquatic organisms of different trophic levels and potential health risk assessment from Taihu lake, China. Ecotoxicol Environ Saf 81:55–64

Yu T, Zhang Y, Meng W, Hu X (2012b) Characterization of heavy metals in water and sediments in Taihu Lake, China. Environ Monit Assess 184:4367–4382

Chapter 6

Water and Health: What Is the Risk and Visible Burden of the Exposure to Environmental Contaminations? Insights from a Questionnaire-Based Survey in Northern Thailand

Vincent Herbreteau, Kraichat Tantrakarnapa, Wasana Khaungaew, and Jean-Louis Janeau

Abstract Understanding and measuring the consequences of environmental pollution on human health remains a challenge. Several barriers arise, with the difficulty in identifying uncommon pathologies but also with the limited knowledge of the real health status of populations that depends on the supply and use of care. In an effort to assess these barriers, we chose a study area severely affected by agricultural intensification to investigate the potential and visible impact of water pollution on human health. Located in northern Thailand, the study area includes a watershed, its reservoir and the irrigated area downstream. A questionnaire-based survey was conducted to assess the exposure of 297 households to potential water pollutions and understand their behaviour regarding the use of water and recourse to health services. The observations are discussed in the light of the epidemiological records provided by the Ministry of Public Health for the same area. The study shows the heterogeneity of the epidemiological data and the difficulty to assess the sanitary risk. Despite the small size of the study area, inequalities are observed, with remote populations having a poorer access to water with occasional shortage and a limited

---

V. Herbreteau (✉)
Station SEAS-OI, IRD, UMR 228 ESPACE-DEV (IRD/UAG/UM2/UR),
97410 Saint-Pierre, Réunion, France
e-mail: vincent.herbreteau@ird.fr

K. Tantrakarnapa
Department of Social and Environmental Medicine, Faculty of Tropical Medicine,
Mahidol University, Bangkok 10400, Thailand

W. Khaungaew
Phrae Provincial Public Health Office, Ministry of Public Health, Phrae 54000, Thailand

J.-L. Janeau
IRD - iEES-Paris (UMR 242) c/o Soils and Fertilisers Research Institute (SFRI),
Hanoi, Vietnam

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_6

use of health services. In this context, the intensification of agriculture and the massive use of pesticides and fertilizers are likely to have serious consequences on human health. However, the impact of potential environmental pollution is not visible from the epidemiological records, because of a difficult diagnosis, a lack of consultation when symptoms are reversible and the long latency before clinical symptoms are apparent (example of cancers). Prevention and incentive from health authorities should help in reducing this risk.

6.1 Introduction

Access to clean water is a prerequisite for the good health of populations to avoid waterborne infections, to prevent the development of some disease vectors and also to maintain a good hygiene. Water should be safe, reliable, affordable, and easily accessible according to the secretary-general of the United Nations (United Nations 2012).

Difficulties in both direct and indirect effects on health (Hunter et al. 2010). Most importantly, poor-quality water is a major factor of diarrhoea, which is one of the leading causes of morbidity and mortality in less-developed countries (Fewtrell et al. 2005; Pruss et al. 2002). In a more insidious way, water contaminated by organics (including insecticides and herbicides, detergents and chlorinated solvents) or inorganics (including fertilizers, arsenic, copper, fluoride, mercury and lead) chemical agents can have severe effects for health (Hunter et al. 2010; Hunter 1997). These contaminations have been increasing with the conversion of forests to agricultural lands and the intensification of agriculture. Pesticides may cause about 10,000 deaths out of two million poisonings each year according to the United Nations, and three fourth occur in developing countries (Horrigan et al. 2002). Indirect effects of poor water access are various and include difficulties in assuring proper sanitation and hygiene.

Furthermore, several diseases are associated with water, mainly from bacterial origin (leptospirosis; cholera; botulism; dysentery; legionellosis; typhoid fever; cryptosporidiosis; colibacillosis, i.e. infection with *Escherichia coli*; etc.) and parasitic origin (schistosomiasis, dracunculiasis, echinococcosis, enterobiasis, etc.) but also from viral origin (poliomyelitis, hepatitis A and E, gastroenteritis, etc.). While a few of these diseases are caused by water consumption (case of cholera, hepatitis A and E), others require water for the maintenance, development or spread of their pathogens or their associated hosts (such as snails for schistosomiasis and mosquito larvae for malaria or dengue fever).

The quality and availability of ground and surface water are mainly affected by agricultural practices. The development of agriculture has lead to major hydrological changes with the construction of canals, reservoirs or dams. At the end of the twentieth century, there were over 45,000 large dams (impoundments over 15 m high or storing at least three million cubic metres of water) in 140 countries and over 800,00 small dams (Keiser et al. 2005; World Commission on Dams 2000). Several epidemics have followed the construction of large dams: especially schistosomiasis and Rift Valley fever at the Aswan High Dam in Egypt and at the Kariba Dam in Zambia and Mozambique (World Commission on Dams 2000). The impact of small dams on diseases dynamics is underestimated because of the lack of studies even though their total shoreline is greater when compared with large dams (Keiser et al. 2005).

Assessing the consequences of inappropriate water access on the health status is difficult since the effects are various and the symptoms may not be obvious. For instance, diarrhoeal diseases also encompass other causes than consumption of poor-quality water. Diarrhoea is first of all a symptom, and illnesses that are not rightly diagnosed can be classified as diarrhoeal diseases. A high proportion of diarrhoeal diseases among the diversity of pathologies identified in the public health records may also reflect poor diagnosis capabilities. Also populations having difficulties in accessing water are also those having a poor access to health care. Consequently epidemiological records underestimate the real burden of these illnesses.

This study proposes to investigate locally how rural populations deal with their needs for water, how they could be exposed to possible contaminations, and what can be perceived from a public health perspective. A watershed, called Mae Thang, was chosen in Thailand as an example of territory undergoing rapid environmental changes. With a population nearly multiplied by ten in a century (from 8.2 million inhabitants in 1909 to 60.6 million in 2000), the need for agricultural products has lead to clear half of forests and drain swampy areas (Herbreteau 2007). Thailand has promoted the construction of several dams and irrigation canals in lowland areas. The intensification of agricultural production has also resulted in an increasing use of pesticides by a factor of 4 between 2000 and 2010 to reach nearly 120,000 tons of imported active ingredients in 2010 (Panuwet et al. 2012). The study site reflects this problem: a watershed, hosting an increasing population and affected by massive deforestation for agricultural purposes; eroded and polluted soils; and a dam at the outlet with poor-quality water, used for irrigating a large agricultural plain. Aerial pictures taken in 1954 and 1995 by the Royal Thai Survey Department show the marked increase of agricultural lands, the dam and the villages on the left side of the picture (Fig. 6.1).

Thailand has a well-organized public health system with a hierarchy of infrastructures linked together. Since the 80s, hospitals and health centres have been built, respectively, in every district and every sub-district. People have potentially and theoretically an easy access to public health services, with low medical costs. However, those living in remote areas, having low incomes or not having any vehicle may have difficulties to use health services. Furthermore, social inequalities segregate the access to private services (i.e. private hospitals, clinics, pharmacies). Records of patients are kept from the first place of examination (health centre, district or provincial hospitals, either public or private). These records are then reported in a few days to the provincial office of the Ministry of Public Health (MoPH) and later centralized by the Bureau of Epidemiology of the MoPH. Seventy-eight different pathologies are thus reported.

The objective of the study was to study the health status based on these epidemiological records and conduct a survey to observe the behaviour of populations regarding water access and recourse to health care. It focused on populations living in different villages, upstream and downstream the Mae Thang reservoir, and aimed at investigating potential health problems linked to water quality and agricultural practices.

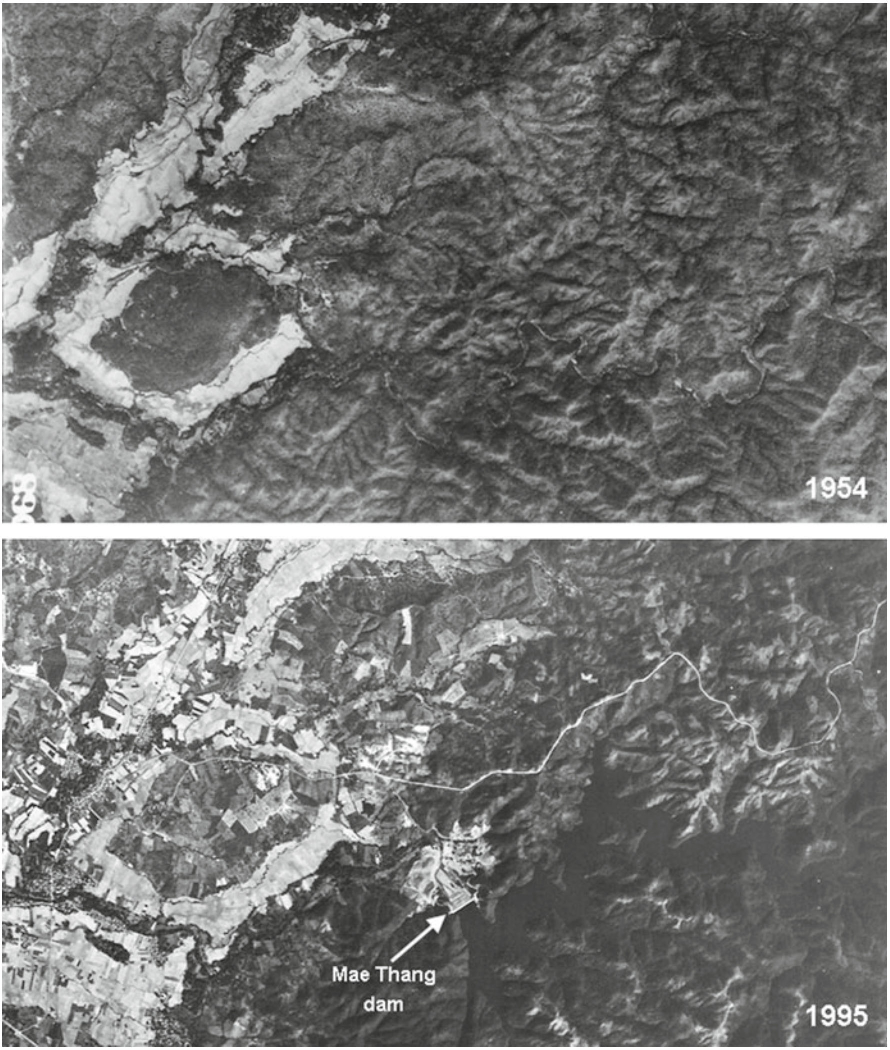


Fig. 6.1 Aerial photographs from the Mae Thang area, in 1954 and in 1995 (Source: Royal Thai Survey Department)

6.2 Survey in Northern Thailand

6.2.1 Study Area

The study area was chosen in Northern Thailand where the landscape has severely been affected by human activities (i.e. deforestation, forest fires, encroachment, agricultural expansion, urbanization) during the second half of the twentieth

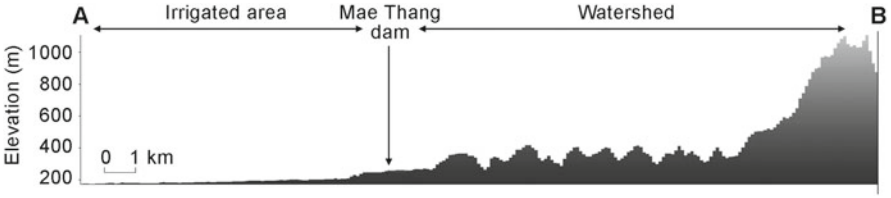


Fig. 6.2 West–east section across the study area (see *A*–*B* location on Fig. 6.3) This section was calculated using the SRTM DEM in SavGIS

century. It is located in Phrae province (17.5°N–18.3°N; 99.5°E–100.2°E), which stretches along the large flood plain of the Mae Yom River, bordered by two mountainous north–south alignments. As in many other Thai provinces, a dam was constructed in 1995 to develop irrigation and increase agricultural production in lowland areas. This dam was chosen as the centre of our study site, which consists of the small watershed (120 km^2) upstream, called Mae Thang, and downstream, the lowland irrigated fields and villages. The study area ranges from 250 to 1,800 m above sea level and encounters forests in the uplands, fields and villages (Fig. 6.2). Two villages are located in the watershed, with scattered houses and a total population of 1,428 inhabitants. The irrigated area has 11 villages with a total of 11,615 inhabitants. Many farmers from these villages commute everyday to the watershed where they have lands and increasingly produce corn.

6.2.2 Epidemiological Data

The provincial office of the MoPH at Phrae provided exhaustive anonymous records of 78 pathologies reported from 1997 to 2004. These records keep track of the code of the patient's village, the place of examination and the date of the onset of the symptoms.

6.2.3 Household Survey

A survey was conducted in the Mae Thang area to learn about the behaviour of populations regarding the use of water, the exposure to potential water-related contamination and the recourse to health services. The Faculty of Public Health at Mahidol University and IRD researchers jointly organized this survey and constructed a questionnaire.

The questionnaire aims at gaining information about the household so that any member of the household could be interviewed. It includes 76 questions divided in 13 themes: (1) general information, (2) health behaviour, (3) activities, (4) housing, (5) domestic animals and livestock, (6) waste management, (7) water usage,

(8) toilet, (9) cooking behaviour, (10) personal hygiene, (11) exposure to arthropod-borne diseases and (12) exposure to rodent-borne diseases.

The interviews were realized from April 4 to 11, 2006, by five groups of two students. One master student from the Faculty of Public Health at Mahidol University in Bangkok and one local bachelor student from Maejo University in Phrae province constituted each pair. Local students helped senior students with their knowledge of the area as well as local languages.

The survey was conducted in three areas, namely, (1) the watershed area (including the villages of Baan Pak Way Oy and Baan Huay Om), (2) the irrigated area (Ban Wang Yen, Ban Huay Hung, Ban Tung Lom, Ban Huay Ma, Ban Srisit, Ban Pong, Ban Pa Kluei Mai, Ban Pa Kluei, Ban Oy, Ban Wiang Nua, Ban Wiang Tai) and (3) the control group (outside the Mae Thang study area: Ban Phai Yoy, Ban Nam Lao Nua, Ban Nam Tai, Ban Huay Khum and Ban Hang Na). These villages group together 15,671 people and 3,859 households according to the 2000 Census (National Statistical Office: http://www.nso.go.th). The objective was to interview about 300 households. Therefore, households were randomly chosen one every other 13. Whereas the questionnaire was anonymous, the location of each household was precisely recorded with a GPS.

6.2.4 Analysis

We integrated data into a geographic information system (GIS), using SavGIS (http://www.savgis.org). This software is available as a freeware and allows complete geoprocessing capabilities while preserving the integrity of the database used.

We used the SRTM (Shuttle Radar Topography Mission programme, http://srtm.usgs.gov/) digital elevation model (DEM) to delineate the extent of the watershed with SavGIS. This DEM provides altitudes at a spatial resolution of 3 arcseconds (approximately 90 m). We went directly in the field to determine the limits of the irrigated area. For this purpose, we used rectified topographical maps (1:50,000), provided by the Royal Thai Survey Department (RTSD), that we integrated into the GIS. Then we could intersect the position of the villages and clearly observe those belonging to each of the three areas.

We recorded the location of each health infrastructure with a Global Positioning System (GPS). We obtained an approximate location of villages from the National Statistic Office (NSO), responsible of the National Census. Codes for villages from MoPH and NSO differ significantly but we could link them together according to their Thai names. As the extent of villages is unknown, we chose to georeference each village with an approximate centre point, which we located using the RTSD topographical maps. Then we could georeference every reported case either at the village of residence or at the place of examination.

We tested the associations between categorical variables (e.g. between the areas and the responses to the survey) with a Fisher's exact tests or a Chi-square ($\chi 2$) test, when appropriate. $P \leq 0.05$ (two-tailed) were considered statistically significant.

6.3 Results

6.3.1 Health Status

Within the Mae Thang study area, the population has access to one health centre in the watershed, two in the irrigated area and two others nearby. Medical doctors are not present in health centres but in hospitals. Therefore, patients with acute illness are sent to hospitals after consultation in any of these health centres. The closest hospital is Rong Kwang Hospital, ten kilometers from the study area. Five doctors and 51 nurses run the hospital, which receives about 5,000 inpatients a year with a capacity of 30 beds (4,915 in 2004).

The overall consultation rate is higher in the study area than in the province with most of the reported infections diagnosed as diarrhoeas from 1997 to 2004 (Herbreteau et al. 2006). Higher incidences of food poisoning are also reported in the study area (reaching twice the incidence of the province in 2002 with 3.5 cases for 1,000 inhabitants). These higher rates remain unexplained but could have an environmental origin. Higher incidences of leptospirosis are also recorded every year (Fig. 6.3). Bacteria that can survive in a wet environment cause this disease. The higher rates observed in the area could reflect an increased exposure of villagers to water-related pollution.

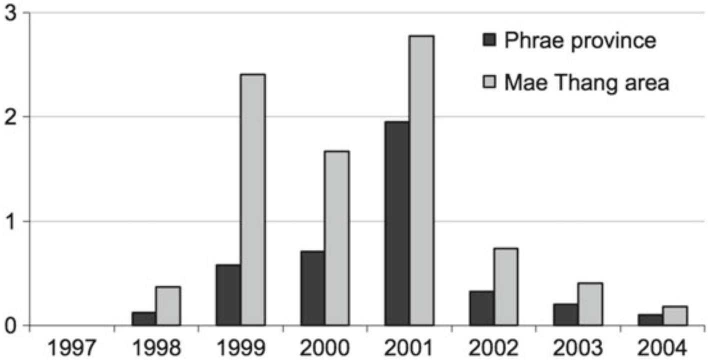


Fig. 6.3 Incidence (for 1,000 inhabitants) of leptospirosis in Mae Thang area and Phrae province, Thailand (Sources: MOPH, NSO)

6.3.2 Housing Conditions

A total of 297 households were interviewed, 20 in the watershed area, 224 in the irrigated area and 53 in the control area (Fig. 6.4). 70.4 % of respondents were female with a lower percentage (60.0 %) in the watershed area without significant difference. 79.1 % of the household interviewed are married families. The structure of villages differs from one area to another: in the watershed, houses are grouped together with 90 % of them having less than 10 m distance with their neighbours. This proportion is lower in the irrigated area (78.1 %) and in the control area (64.2 %). On the contrary, houses are generally at a closer proximity to the fields in the irrigated area (51.3 % are located at less than 100 m to the closest field) and in the control area (54.7 %) than in the watershed area (only 15.0 %). Housing conditions are similar in the three areas with nearly half of the houses being on stilts (54.2 %) and 44.1 % of houses having a garden, which is for a majority (81.0 %) neither clean nor dirty but partially kept.

Nevertheless some differences are observed between the watershed area and areas downstream. The most obvious is the access to water, more difficult in the watershed. 45 % of households declare experiencing a lack of water during the year, while there are only 2.7 % in the irrigated area (watershed vs. irrigated: two-tailed Fisher's exact test, $P = 0.000$) and 1.9 % in the control area. The source of drinking water radically varies between the three areas (Fig. 6.5a). In the watershed, people

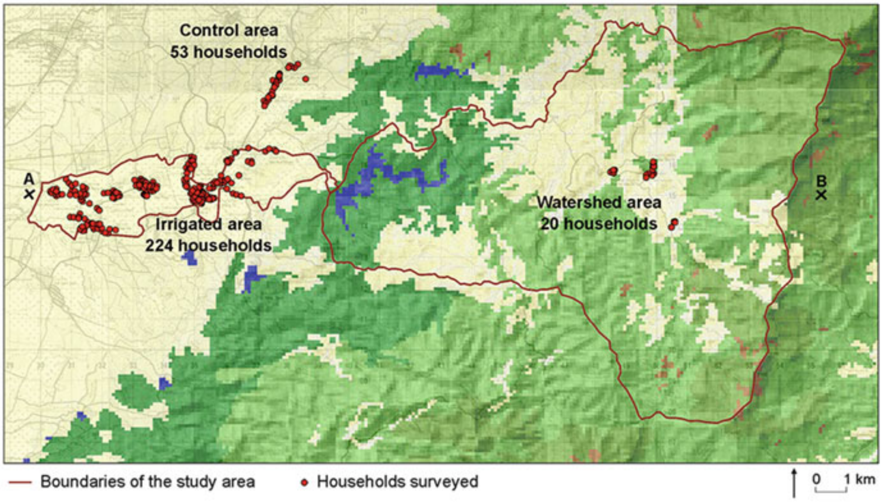


Fig. 6.4 Location of the households surveyed within the watershed and the irrigated areas and outside the Mae Thang study area The background shows: (1) a land use classification made from the analysis of Landsat images (2000) with forested areas in green, agricultural areas in yellow and water areas in blue (including the Mae Thang dam at the output of the watershed) (Source: Royal Forestry Department), and (2) the topographic map (Source: Royal Thai Survey Department), visible through the land use map

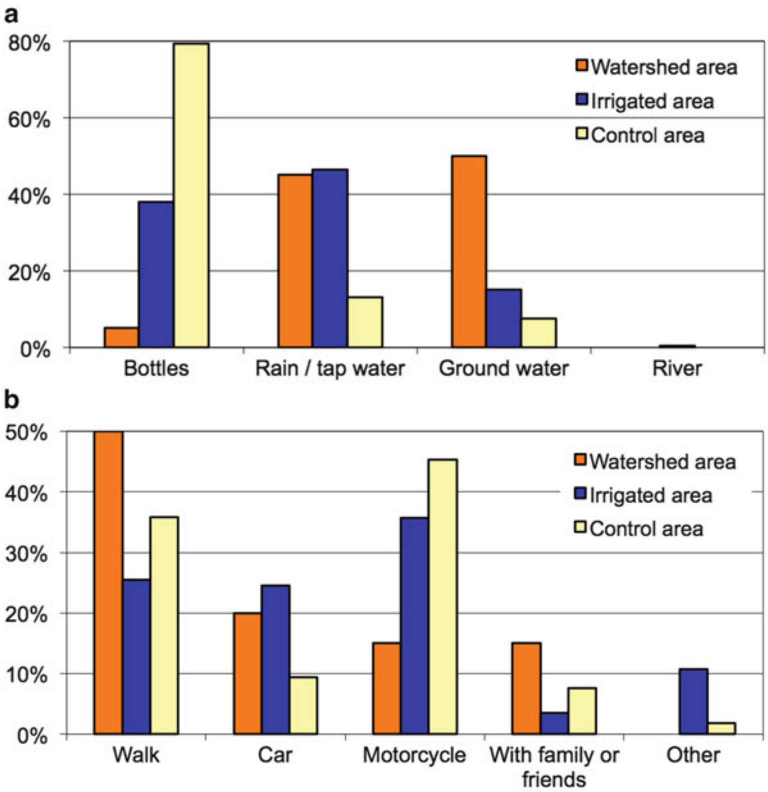


Fig. 6.5 (**a**) Comparison of the source of drinking water. (**b**) Comparison of the mean of transportation to reach health services

drink either groundwater (50.0 %) or tap and rainwater (45.0 %) but rarely bottled water (5.0 %). Bottled water is a main source of drinking water in the control area (79.2 %) and in the irrigated area (37.9 %). People from the irrigated area also mainly drink tap and rainwater (46.4 %). These differences between areas are statistically significant (watershed vs. irrigated, $\chi^2 = 18.1$, $P < 0.05$; irrigated vs. control, $\chi^2 = 29.8$, $P < 0.05$). On the other hand, cooking conditions are very similar, with 58.9 % of the households preparing their food on the ground but 69.7 % keeping food in a dedicated cupboard.

Regarding waste management, the majority of houses have a bin (83.2 % on average) without significant differences between areas (watershed vs. irrigated: two-tailed Fisher's exact test, $P = 0.117$, $P > 0.05$), but houses are less equipped in the watershed area with 30 % of them not having any bin. Indeed, in the watershed, each household incinerates (55.0 %) or buries (25.0 %) its wastes, while the municipalities collect them in both irrigated area (92.4 %) and control area (96.2 %). Also wastewater from houses is generally discharged into the ground in the watershed area (85.0 % of houses), with visible problems in 45 % of the houses (stagnating water, dirty area and/or bad smell). Fewer problems were noticed in the lowlands with 43.3 % of the houses that discharge wastewater into the ground in the irrigated area and 47.2 % in the control area. Almost every house has its own toilet (only one in the watershed area and one in the irrigated area do not have), which is generally a clean place with water.

Most of the households breed farm animals in the watershed area (90.0 %). This proportion is significantly lower (67.0 %) in the irrigated area (watershed vs. irrigated: two-tailed Fisher's exact test, $p = 0.042$) and in the control area (69.8 %). Manure is rarely managed in the watershed area (5.6 % of households use it for compost), while it is more often kept in the irrigated area (32.7 %) and in the control area (37.8 %).

6.3.3 Health Behaviour

In the watershed area, people either go to the local health centre (60.0 %) or directly go to the hospital (40.0 %), while in the irrigated area, people either choose the health centre (47.8 %), the hospital (35.7 %), the clinic (14.3 %) or auto-medication (2.2 %). However, the choices of health services are not significantly different in the two areas ($\chi 2 = 4.0$, $P > 0.05$), also compared to the control area. In the watershed and the irrigated areas, 60.0 % and 59.4 % of the population live at less than 500 m from a health centre, while they are 77.4 % in the control area.

The facility of access to health services regarding the mean of transportation differs significantly between the three areas (watershed vs. irrigated: $\chi 2 = 14.0$, $P < 0.05$). In the watershed, half of the population walks to the local health centre, while they are only a quarter (25.4 %) in the irrigated area and a third in the control area (35,8 %) (Fig. 6.5b). Also the use of car is quite similar in the watershed and the irrigated areas (respectively, 20 % and 24.6 %) and very low in the control area (9.4 %). As a result, people in the watershed generally consult health professionals in case of severe and lasting symptoms. When treated later, consequences are serious.

6.4 Discussion

6.4.1 A Higher Exposure to Environmental Risk for Remote Populations

Remote populations, i.e. those living in the watershed, have quite similar conditions to those living in the valley, when looking at the characteristics of their houses (type of construction, presence of toilets, access to water). Nevertheless, they experience more difficulties with water cutoff, a poor management of wastes and wastewater, and might be consequently more exposed to environmental contaminations. Several studies have highlighted that water shortage can have negative effects on health, undermining the benefit of an improved water system (Hunter et al. 2010; Majuru et al. 2011). Water shortage is frequent in rural Thailand: some villages supply piped water a few hours per day, with villagers having no option but to store water in tanks. These tanks may not properly be covered and not regularly cleaned to maintain water drinkable and to avoid the development of mosquito larvae. In the watershed, the exposure of populations to water contamination is further enhanced by the fact that these people use very rarely bottled water.

Risks coming from domestic animals bred around the houses are also higher since animals were observed around most of the watershed households, without an appropriate manure management.

6.4.2 A Satisfactory Provision of Health Care with Inequalities in Access

The oldest health centre is the one located in the watershed at Ban Pak Way Oy, which was built in 1980. It obviously aimed at providing health care to those populations isolated in the mountain and not been able to go to the hospitals in the lowlands. The four other health centres were built between 1994 and 1999. Three government officials run each of them, while there are only two officials in the watershed. In the three areas, populations give priority to the local health centre. The short distance generally observed between the households surveyed and the closest health centre confirms their role as a convenience service. Nevertheless the mean of transportation differs between areas and reveals that the proximity to the health centre importantly drives this choice: in the watershed (where there is a lack of cars) and in the control area (where more than three quarters of the population are close to the health centre), more people can simply walk to reach the health centre. The watershed area appears clearly isolated from other health resources, having no hospital and private structures, due to its little population. People have no option but to find a car when going to the hospital. When needed, a public ambulance can be requested but populations turn to this service only for severe cases. Although health centres have a fundamental role for the well-being of remote populations, difficulties in access to other public health services can have severe consequences for the recovery from acute illnesses. These observations confirm local inequalities in access to health care.

6.4.3 The Latent Emergence of Cases Associated with Environmental Contaminations

The knowledge of the potential harmfulness of pesticides differs among farmers but remain poor (Panuwet et al. 2012). In Thailand, several studies have related the lack of protective equipment by farmers when spreading pesticides and the necessity to inform about potential health consequences and to recommend a proper use of chemicals (Raksanam et al. 2014; Norkaew et al. 2010). If we consider the magnitude of the nonrational and unprotected use of pesticides, the emergence of a large number of cases associated with exposure to these pesticides seems inevitable.

The real burden of exposure to water pollutants is far to be estimated for several reasons:

(1) Farmers who represent the group of people most exposed to environmental pollution are also the group with the lowest income and made the least use of care.
(2) Short-term symptoms (such as nausea, numbness in hands and feet, tearing caused by exposure to pesticides) are reversible and do not cause disability, so that farmers rarely consult medical doctors in that case (Panuwet et al. 2012).
(3) Technical difficulties and high costs also arise to detect contaminations by pollutants such as heavy metals and imply unknown causes or misdiagnosis.
(4) Also the effects of water contaminations on human health may be revealed several years after exposure with difficulties for doctors and patients to identify the causes. This is the case with pesticides, being recognized as increasing the risk of cancer and disrupting the immune, nervous, reproductive and endocrine systems at the long term (Horrigan et al. 2002). Growth enhancers used in factory farms have been found polluting ground- and surface water and may also cause breast and testicular cancers (Horrigan et al. 2002; Soto et al. 2004). The use of antibiotics for animal growth also may be responsible of an increasing antibiotic resistance in humans and pose a difficulty to find other effective molecules (Horrigan et al. 2002).

Estimating the impact of water pollution on human health is difficult and requires the development of diagnostic methods. Educating people about the dangers of environmental pollution is still a need to avoid certain risky behaviours that persist in a country where, however, the standard of living and health care provision is satisfactory (Fig. 6.6).

Fig. 6.6 Children washing dishes in the irrigation canal, downstream the Mae Thang watershed visible in the background (Photo: Herbreteau et al. 2006)

Acknowledgements This work was funded by the IRD (Institut de Recherche pour le Développement) in the frame of the ATI-U2SIS project (Action Transversale Incitative – Utilisation des Sols et Sédiments: Impacts Sanitaires). It was realized in collaboration with the Ministry of Public Health (MoPH) and the National Park, Wildlife and Plant Conservation Department at Phrae. We thank Narissara Chatwatcharakul (IWMI-SEA, Bangkok), Arthorn Boonsaner (National Park, Wildlife and Plant Conservation Department, Thailand, Bangkok), Primporn Moungthong and her colleagues from the Ministry of Public Health at Phrae provincial office for their precious assistance. We deeply thank the students who realized the interviews, (1) from the Faculty of Public Health at Mahidol University, Prat Intrarasaksit, Wassana Kanawapee, Duangkamon Phihusut, Narut Sahanavin and Sutasinee Ungsoongnern, and (2) from Maejo University, Kwan, Rin, Young, Jo, Green and Mod, and our driver Pee On.

References

Fewtrell L, Kaufmann RB, Kay D, Enanoria W, Haller L, Colford JM (2005) Water, sanitation, and hygiene interventions to reduce diarrhoea in less developed countries: a systematic review and meta-analysis. Lancet Infect Dis 5:42–52

Herbreteau V (2007) Géographie de zoonoses en Thaïlande: de la distribution des rongeurs, vecteurs et hôtes, au risque de transmission. Université de Nanterre – Paris X, Nanterre

Herbreteau V (2010) When geography of heath meets health ecology. In: Morand S, Krasnov B (eds) The biogeography of host-parasite interaction. Oxford University Press, New York, pp 247–265

Herbreteau V, Gonzalez J-P, Khaungaew W, Salem G, Janeau J-L (2006) Agricultural changes, water quality and health: investigating the health status of populations living in an agricultural irrigated area, using spatial analysis, in Phrae province, Thailand. Int J Geoinfo 2:23–28

Horrigan L, Lawrence RS, Walker P (2002) How sustainable agriculture can address the environmental and human health harms of industrial agriculture. Environ Health Perspect 110:445–456

Hunter PR (1997) Waterborne disease: epidemiology and ecology. Wiley, Chichester

Hunter PR, MacDonald AM, Carter RC (2010) Water supply and health. PLoS Med 7:e1000361

Keiser J, De Castro MC, Maltese MF, Bos R, Tanner M, Singer BH, Utzinger J (2005) Effect of irrigation and large dams on the burden of malaria on a global and regional scale. Am J Trop Med Hyg 72:392–406

Majuru B, Mokoena M, Jagals P, Hunter PR (2011) Health impact of small-community water supply reliability. Int J Hyg Environ Health 214:162–166

Norkaew S, Siriwong W, Siripattanakul S, Robson MG (2010) Knowledge, attitude, and practice (KAP) of using personal protective equipment (PPE) for chilli-growing farmers in Huarua subdistrict, Mueang district, Ubonrachathani province, Thailand. J Health Res 24:93–100

Panuwet P, Siriwong W, Prapamontol T, Ryan PB, Fiedler N, Robson MG, Barr DB (2012) Agricultural pesticide management in Thailand: status and population health risk. Environ Sci Pol 17:72–81

Pruss A, Kay D, Fewtrell L, Bartram J (2002) Estimating the burden of disease from water, sanitation, and hygiene at a global level. Environ Health Perspect 110:537–542

Raksanam B, Taneepanichskul S, Robson MG, Siriwong W (2014) Health risk behaviors associated with agrochemical exposure among rice farmers in a rural community, Thailand: a community-based ethnography. Asia Pac J Public Health 6:588–595

Soto AM, Calabro JM, Prechtl NV, Yau AY, Orlando EF, Daxenberger A, Kolok AS, Guillette LJ, le Bizec B, Lange IG, Sonnenschein C (2004) Androgenic and estrogenic activity in water bodies receiving cattle feedlot effluent in eastern Nebraska, USA. Environ Health Perspect 112:346–352

United Nations (2012) The millennium development goals report. United Nations, New York

World Commission on Dams (2000) Dams and development: a new framework for decision-making. Earthscan Publications Ltd, London

Chapter 7
Melioidosis in Laos

Yves Buisson, Sayaphet Rattanavong, Valy Keoluangkhot, Khamsing Vongphayloth, Loungnilanh Manivanh, Rattanaphone Phetsouvanh, Alain Pierret, Jean-Luc Maeght, Vanaporn Wuthiekanun, Paul N. Newton, and David A.B. Dance

Abstract Melioidosis is a serious infectious tropical disease caused by a soil-dwelling bacterium, *Burkholderia pseudomallei*, transmitted from contaminated soil or surface water. Although endemic in Southeast Asia, it is considered an emerging disease in Lao PDR where it has only been recognised for 15 years, becoming one of the leading causes of community-acquired septicaemia. A research programme has been developed by the Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit in collaboration with the Institut de la Francophonie pour la Médecine Tropicale (IFMT) and the Institut de Recherche pour le Développement (IRD) to investigate the environmental reservoir of *B. pseudomallei* in Lao PDR. The first study, conducted in 2009, showed that the geographical distribution of *B. pseudomallei* was very heterogeneous and not limited to the floodplains of the

---

Y. Buisson (✉)
Institut de la Francophonie pour la Médecine Tropicale (IFMT), Vientiane, Laos
e-mail: yvesbuisson@hotmail.com

S. Rattanavong
Institut de la Francophonie pour la Médecine Tropicale (IFMT), Vientiane, Laos

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit, Microbiology Laboratory, Mahosot Hospital, Vientiane, Lao PDR

V. Keoluangkhot
Institut de la Francophonie pour la Médecine Tropicale (IFMT), Vientiane, Laos

Department of Infectious and Tropical Diseases, Mahosot Hospital, Vientiane, Lao PDR

K. Vongphayloth
Institut de la Francophonie pour la Médecine Tropicale (IFMT), Vientiane, Laos

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit, Microbiology Laboratory, Mahosot Hospital, Vientiane, Lao PDR

Institut Pasteur du Laos, Vientiane, Lao PDR

L. Manivanh
Institut de la Francophonie pour la Médecine Tropicale (IFMT), Vientiane, Laos

Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit, Microbiology Laboratory, Mahosot Hospital, Vientiane, Lao PDR

Microbiology Laboratory, Settathirath Hospital, Vientiane, Lao PDR

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_7

Mekong River. The soil samples collected in the province of Saravane (southern Laos) was proved the most heavily contaminated. The second study, conducted in 2010, aimed to detect *B. pseudomallei* in surface water using Moore's swabs. A high proportion of water samples taken from the Sedone River were positive downstream of a heavily contaminated terrestrial site, suggesting contamination by runoff from land reservoirs. Both environmental reservoir studies of *B. pseudomallei* pave the way for future research in order to clarify the areas at risk of melioidosis to facilitate preventive measures amongst populations at risk and better care for those infected.

7.1 Introduction

Melioidosis is a severe tropical bacterial infection that affects man and a range of other animals. It is caused by a Gram-negative bacillus, *Burkholderia pseudomallei*, an environmental saprophyte that is widespread in Southeast Asia and northern Australia. This facultative intracellular bacterium is infectious to man by inoculation or inhalation. The main modes of exposure are occupational (e.g. agricultural work, especially rice farming) or accidental (e.g. near drowning, typhoons, tsunamis). The disease occurs mostly as an opportunistic infection in individuals with underlying predisposition, particularly diabetes mellitus. The infection can be invasive and rapidly fatal, run a subacute or chronic course or even remain latent for long periods. Even with early and appropriate treatment, the mortality rate remains high at 20–50 %.

Melioidosis is a disease that presents a disconcerting number of paradoxes:

- It is considered an ‘emerging disease’ even though it was actually first described more than a century ago in Myanmar (Burma). It is actually unclear whether this reflects true emergence of the disease or increasing recognition, thanks to improvements in diagnostic capacity.
- It is a tropical disease that is usually considered as endemic to Southeast Asia and northern Australia but which is increasingly being identified in other parts of the world.

R. Phetsouvanh • P.N. Newton • D.A.B. Dance
Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit, Microbiology Laboratory,
Mahosot Hospital, Vientiane, Lao PDR

Centre for Tropical Medicine and Global Health, Nuffield Department of Clinical Medicine,
University of Oxford Churchill Hospital, Oxford, UK

A. Pierret • J.-L. Maeght
Institut de Recherche pour le Développement (IRD), Unité mixte de esources 211 –
BIOEMCO (Biogéochimie et Écologie des Milieux Continentaux), Vientiane, Lao PDR

V. Wuthiekanun
Mahidol Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine,
Mahidol University, Bangkok, Thailand

- It is a very serious and often fatal infection in its acute form, highly pleomorphic in its subacute form, which can affect any tissue or organ and escape diagnosis, but it can also remain latent and asymptomatic for many years.
- It is a challenge for researchers to understand how and why this saprophytic environmental bacterium, which is not specifically adapted as a human pathogen, is able to evade the immune defence mechanisms of the host.

In the Lao PDR (Laos), melioidosis was unknown before 1999 even though it had been recognised for several decades in neighbouring countries, most notably Thailand (Leelarasamee 2000). More than 500 cases have been diagnosed in the country over the past 10 years, the majority in Mahosot Hospital in Vientiane (Phetsouvanh et al. 2001), but this apparent emergence really reflects the development of the hospital laboratory to a level that enabled it to grow and identify *B. pseudomallei* (Phetsouvanh et al. 2006). In addition, the rapid advance of diabetes in Laos, as in all the countries of Southeast Asia (Wild et al. 2004), has probably also contributed to the increase in the incidence of melioidosis, which has now become one of the main causes of community-acquired septicaemia.

This situation justified the establishment of a programme of research initiated by the Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit, in collaboration with the Institut de la Francophonie pour la Médecine Tropicale (IFMT) and the Institut de Recherche pour le Développement (IRD).

7.2 Microbiological and Epidemiological Data

7.2.1 Burkholderia pseudomallei*, a Bacteriological Curiosity*

The causative agent of melioidosis is a remarkable pathogen in its capacity for virulence, survival and resistance, at the same time being both an environmental saprophyte and a facultative intracellular parasite. It is experiencing a resurgence of interest since it was classified by the Centers for Disease Control and Prevention as a ‘Category B’ agent of bioterrorism potential (Gilad et al. 2007).

The bacterium was first identified in Rangoon (Burma) in 1912 by Whitmore and Krishnaswami in pus taken from abscesses found at autopsy in morphine addicts. Whitmore’s bacillus was initially named ‘*Bacillus pseudomallei*’ because of its similarity with the glanders bacillus and has subsequently been known as ‘*Pfeifferella whitmori*’, ‘*Malleomyces pseudomallei*’ and ‘*Pseudomonas pseudomallei*’ until it was finally designated as *Burkholderia pseudomallei* by Yabuuchi in 1992.

It is a non-sporing Gram-negative bacillus which often exhibits uneven staining, sometimes staining more intensely at the extremities (likened to a shuttle or safety pin), motile via polar flagella. The latter characteristic distinguishes it from the glanders bacillus, *Burkholderia mallei*, which is nonmotile (Holden et al. 2004). It grows rapidly on most culture media aerobically at 37 °C. After 18 h of incubation, it forms colonies from 1 to 2 mm in diameter, which are usually circular, domed, smooth and grey or whitish in colour. After 48 h, the colonies increase up to 5 mm, become creamy and give off a characteristic smell which has been likened to truffles or wet soil (although since this is a hazard group 3 pathogen, smelling plates should be avoided!). Several different colonial morphotypes have been described and cultures may appear mixed, the commonest forms being smooth and rugose, the latter having a characteristic wrinkled or umbilicated appearance. Some strains are even frankly mucoid. *B. pseudomallei* is an aerobic organism; it is catalase and oxidase positive and able to use glucose and numerous other sugars oxidatively, but it does not assimilate arabinose. Similar avirulent bacteria isolated from the soil in Southeast Asia, which are able to assimilate arabinose, have been assigned to a separate species *Burkholderia thailandensis* (Cheng and Currie 2005).

Burkholderia pseudomallei is intrinsically resistant to several different groups of antibiotics: penicillins G and A, first and second generation cephalosporins, aminoglycosides, macrolides, rifampicin and polymyxins. It is usually susceptible to co-trimoxazole, chloramphenicol, tetracyclines, the combination of amoxicillin and clavulanic acid, ureidopenicillins, third-generation cephalosporins and carbapenems. Fluoroquinolones are relatively inactive, reported susceptibility to ciprofloxacin varying between 8.5 and 50 % (Thibault et al. 2004).

The genome of *B. pseudomallei* has been fully sequenced (Holden et al. 2004). It is large, 7.25 megabase pairs (Mb), and comprises two chromosomes of 4.07 Mb and 3.17 Mb, respectively. The larger chromosome codes for proteins that are essential for growth and survival (e.g. biosynthesis, metabolism, chemotaxis, motility) as well as several virulence determinants. The smaller chromosome codes for accessory functions involved in adaptation to different environmental niches. Phylogenetic analysis shows that *B. mallei* is really a host-adapted clone of *B. pseudomallei* (Inglis and Sagripanti 2006).

7.2.2 Bioecology of **Burkholderia pseudomallei**

Burkholderia pseudomallei and *B. mallei* form a unique species on the basis of their genetic homology; the distinction into two species is based on epidemiological and pathogenic differences. While *B. mallei* is incapable of surviving for long periods outside its mammalian host, *B. pseudomallei* is a saprophytic bacterium adapted to life in soil and surface water. Its remarkable ability to survive has been well studied in vitro: it can accumulate significant energy reserves in the form of polyhydroxybutyrate granules, can persist for several years without nutrients in distilled water and can multiply in soil between 4 and 42 °C, with a pH between 5 and 8 and water content from 10 % to 15 %. These types of conditions are found in rice paddy as well as oil palm and rubber tree plantation soil (Inglis and Sagripanti 2006). Organic matter (e.g. manure) found in cultivated land favours its proliferation (Kaestli et al. 2009). Soil contaminated for 3 years still harbours dormant bacilli that maintain their virulence. The survival of these non-sporing bacteria in the environment can be explained by it entering a ‘viable but non cultivable’ state when it encounters hostile environmental conditions. Its genome can be detected in soil samples that are culture negative (Kaestli et al. 2007). When the pH falls below 5, the concentration of sodium chloride goes above 2.5 %, or after desiccation, it is not cultivable by conventional means but it preserves its pathogenic potential (Inglis and Sagripanti 2006; Shams et al. 2007). It can also tolerate the effect of disinfectants and may not always be inactivated by the concentrations of chlorine used to treat drinking water.

The persistence of *B. pseudomallei* in its natural ecological niches is thought to be related to two properties: (i) the capacity to form biofilms made from capsular polysaccharide in which the bacteria form slowly growing micro-colonies that are protected from disinfectants and antibiotics and (ii) the ability to penetrate into the cytoplasm of free-living amoebae of the genera *Acanthamoeba* and *Hartmannella* by a mechanism of 'coiling phagocytosis' similar to that previously described in *Legionella* and *Listeria* and then to multiply within vacuoles and survive in amoebic cysts (Inglis et al. 2000).

7.2.3 Epidemiology of Melioidosis

The main endemic areas for melioidosis are Southeast Asia (Cambodia, Indonesia, Laos, Malaysia, Myanmar, the Philippines, Singapore, Thailand, Vietnam) and tropical northern Australia. In the rest of the world, the disease is little known (Aldhous 2005). According to phylogenetic studies of isolates of *B. pseudomallei* from Australia, Papua New Guinea and Thailand, the common ancestor of these different strains would have arisen in Australia (Currie 2008). Outside the main endemic areas, animal and human cases have been reported in North America (the USA, Mexico), South America (northeast Brazil, Ecuador) and the Caribbean (Puerto Rico, Aruba, Guadeloupe, Martinique). On the other hand, melioidosis has rarely been documented in Africa, more often from environmental or animal sources (Burkina Faso, Niger, Chad, Côte d'Ivoire) than in man (Madagascar, the Gambia) (Currie 2008; Currie et al. 2008).

The endemic areas are hot and humid regions with a minimum temperature of 11 °C. *B. pseudomallei* is present in various soil types, sediments, stagnant water in ponds and rice fields, but not in estuarine or sea water. Its distribution in the soil is heterogeneous and discontinuous. It can be isolated from 10 % to 50 % of soil samples in northeast Thailand (Vuddhakul et al. 1999). There is a correlation between local rainfall and the incidence of the disease, 50–75 % of cases presenting during the rainy season (Kaestli et al. 2009). Cases are usually sporadic but are sometimes grouped into small outbreaks (Shih et al. 2009), especially during natural disasters such as floods or typhoons (Su et al. 2011), or linked to common sources such as a contaminated water supply.

Human infection can occur by two main routes: cutaneous through contact with soil or water, which is probably the most common and is favoured by walking barefoot or the presence of wounds or superficial abrasions, and inhalation, which was suspected to account for the occurrence of a surplus of cases amongst helicopter crews during the Vietnam War (Aldhous 2005), and also after near drowning in fresh water such as occurred amongst victims of the tsunami of 2004 (Athan et al. 2005). Other routes of infection have been reported less frequently: drinking contaminated water, direct human-human transmission (e.g. mother-infant or sexual transmission), nosocomial infection via inadequately disinfected equipment (e.g. bronchoscopes) and laboratory-acquired infection (Peacock et al. 2008). These remain anecdotal and are not epidemiologically significant. As a general rule, melioidosis is not a contagious disease.

Melioidosis can present at any age, in either sex and in all socio-economic classes. The relative risk is higher in certain subgroups (age >45 years, males, and in Australia, aboriginal ethnicity) which probably partly reflects differences in exposure as opposed to greater susceptibility. Certain occupations involving exposure to soil or surface water also increase the risk of infection: rice farmers, labourers, farmers, potters and other rural activities. Wounds contaminated with soil or water and drowning accidents with aspiration of fresh water are high-risk events. Military activities in natural environments favour different modes of infection (Kronmann et al. 2009). Travellers are less at risk, most cases occurring in people with pre-existing conditions that make them more susceptible to infection. These intrinsic risk factors are underlying conditions that increase both the susceptibility to infection and the severity of the disease. Diabetes is the most significant and increases the risk of infection 5–13-fold: at least half of all patients contracting melioidosis have diabetes. Other predisposing factors include alcoholism; chronic renal disease; chronic lung disease including cystic fibrosis, thalassaemia, malignancy and chronic steroid use. In contrast, HIV infection does not appear to increase susceptibility. In summary, a number of factors appear necessary for the disease to develop: exposure to a sufficient bacterial inoculum, a route of entry and a susceptible host.

Like glanders, melioidosis can cause epizootics in several animal species. The animals most affected are pigs, sheep, goats and horses, but zoonotic infection can also be seen in camelids, kangaroos, large primates, rodents, birds, captive dolphins and killer whales. Strangely, cattle and animals that live in mud, such as water buffaloes and crocodiles, seem to be relatively resistant to infection (Sprague and Neubauer 2004).

In man, the global incidence of melioidosis is low overall, but it is probably under-diagnosed, both in non-endemic countries where it is frequently overlooked and in endemic countries where diagnostic capabilities are often lacking. The reported incidence rates are 12.7/100,000 in northeast Thailand (Limmathurotsakul et al. 2010) and 19.6/100,000 in northern Australia (Currie et al. 2004). In practice, it is difficult to estimate the true incidence of melioidosis in the absence of reliable diagnostic laboratories accessible to rural communities. This explains the delayed rediscovery of the disease in Cambodia (Wuthiekanun et al. 2008) and its oversight for more than 60 years in Burma where it was first described (Wuthiekanun et al. 2006). In the same way, the emergence of the disease in Brazil (Rolim et al. 2009) and in New Caledonia (Le Hello et al. 2005) can be explained by improved microbiological surveillance.

7.3 Melioidosis in Laos

In Laos, the first two patients with melioidosis were confirmed in 1999 (Phetsouvanh et al. 2001). Since then the number of patients reported has continued to increase, mainly affecting the rice farming community in the Mekong flood plain. A preliminary study undertaken in 1998 in rice paddies within a radius of 150 km around Vientiane detected *B. pseudomallei* in 36 % of 110 samples of soil (Wuthiekanun et al. 2005) (Table 7.1). These first data corroborated the conclusions of Thai researchers according to whom there is a correlation between the degree of soil contamination and the incidence of melioidosis in the human population (Vuddhakul et al. 1999). It was decided to try to confirm this through further environmental studies in Laos. The first was undertaken in 2009 to determine the geographic distribution of *B. pseudomallei* in soil, the second in 2010 to detect the bacterium in surface waters (Rattanavong et al. 2011; Vongphayloth et al. 2012). We summarise these findings.

7.3.1 *Research on* B. pseudomallei *in Soil in Laos*

This work, described in Rattanavong et al. (2011), had the objective of answering a double question: is the area of distribution of melioidosis restricted (i) to the province of Vientiane and (ii) to the Mekong valley?

The sampling plan followed two stages: the first geographic, the second probabilistic. In the first stage, six provinces were selected deliberately following three transects: northwest (Vientiane West, Oudomxay and Luangnamtha), northeast (Vientiane East, Xieng Khouang and Huaphanh) and south (Saravane). Vientiane and Saravane Provinces were divided into two (western and eastern) and three (western, central and eastern) areas of equal width, respectively. In the second stage, three sites were selected randomly on each transect, giving a total of nine sampling

Table 7.1 Distribution of *B. pseudomallei* in nine rice growing sites in Laos (study undertaken in 2009)

Sampling sites	Holes positive (%)	Geometric mean (cfu/g)	95 % (cfu/g)	Range (cfu/g)
Vientiane East	0	0	0	0
Vientiane West	0	0	0	0
Xieng Khouang	0	0	0	0
Huaphanh	0	0	0	0
Oudomxay	0	0	0	0
Luangnamtha	1	80	–	–
Saravane East	94	464	372–579	25–10,850
Saravane Central	42	122	65–227	2–4,700
Saravane West	61	82	47–141	2–22,250

Data taken from Wuthiekanun et al. (2005)

areas, using the following criteria: rice fields with an area greater than or equal to 1 ha, ≤100 m from the nearest perennial river, and at least 50 m from a known area of unexploded ordnance and from houses.

The necessary data were obtained from different organisations: *Forest Inventory and Planning Division* (*FIPD*) to localise the rice growing areas from 2008 to 2009, *National Geographic Department* (*NGD*) to clarify their position in relation to the secondary water courses, *Ministry of Communication, Transport and Post* to confirm the absence of buildings near the chosen sites and *Lao National Unexploded Ordnance Programme* (UXO Lao) to be certain of the absence of unexploded ordnance within a radius of 50 m. The coordinates of the sampling sites corresponding to these criteria were determined randomly by computer and identified using a Global Positioning System (GPS). At each site, a grid of 45 × 45 m was defined to dig ten rows of ten holes separated from each other by 5 m.

Samples of soil were collected following a standard methodology adapted from that used previously in Thailand and Laos (Wuthiekanun et al. 2005, 2006). The soil was taken from a depth of 30 cm with a clean shovel which had been washed in fresh water, disinfected with 70 % alcohol and dried between each collection. A sample of 100 g of soil was collected from the bottom of each hole and placed in a numbered plastic bag. Each bag was sealed and placed in a container protected from light at room temperature until its delivery to the laboratory within 48 h. In the laboratory, samples were rehydrated by the addition of 100 ml of sterile distilled water, mixed by agitation and incubated overnight at room temperature. The following day, the supernatant was subcultured onto five plates of Ashdown's agar: two plates with 10 μl, two plates with 100 μl and one plate with 500 μl. A selective enrichment broth containing colistin (SBCT) was also inoculated with 1 ml of supernatant. The cultures were incubated aerobically at 40 °C for 4 days and inspected daily from the second day. The SBCT broth cultures were subcultured after 48 h incubation onto Ashdown's agar. Suspect colonies were preliminarily identified by their cultural characteristics on Ashdown's medium, appearance on Gram stain and oxidase reaction and were counted at the dilution giving the highest countable number of colony-forming units (cfu). The identification was confirmed by a highly specific latex agglutination test which allowed exclusion of *B. thailandensis* (Wuthiekanun et al. 2002) and by confirming susceptibility to amoxicillin-clavulanic acid and resistance to colistin. API 20 NE tests done subsequently on a subset of isolates identified as *B. pseudomallei* by these methods confirmed their identity.

Cultures of *B. pseudomallei* were obtained in four of the nine sites studied (Fig. 7.1): the site in Luangnamtha in the northwest of the country (1 % of samples positive) and the three sites in Saravane in the south (42–94 % of samples positive). The highest geometric mean bacterial concentrations were found in the site in Saravane East (Fig. 7.1). These were the highest concentrations of environmental *B. pseudomallei* published to date (Rattanavong et al. 2011). The comparison of these results showed that the presence of *B. pseudomallei* did not correlate with the elevation of the site nor the distance from the Mekong (Fig. 7.2).

The two sites in Saravane East and West were resampled in 2010 according to the same protocol, at the end of the dry season, whereas they had been sampled at the

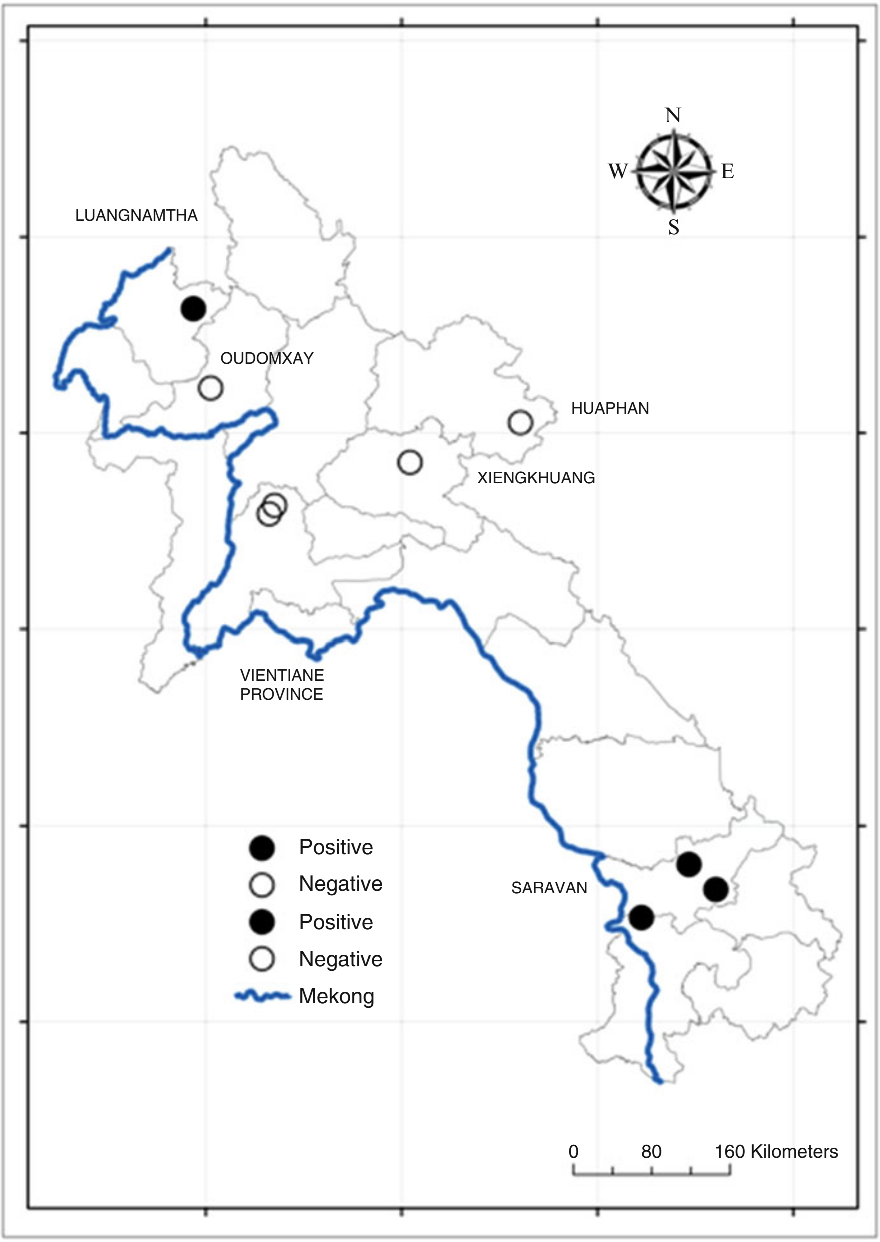


Fig. 7.1 Distribution of *Burkholderia pseudomallei* at nine sampling sites in Laos in 2009 (Data taken from Wuthiekanun et al. 2005)

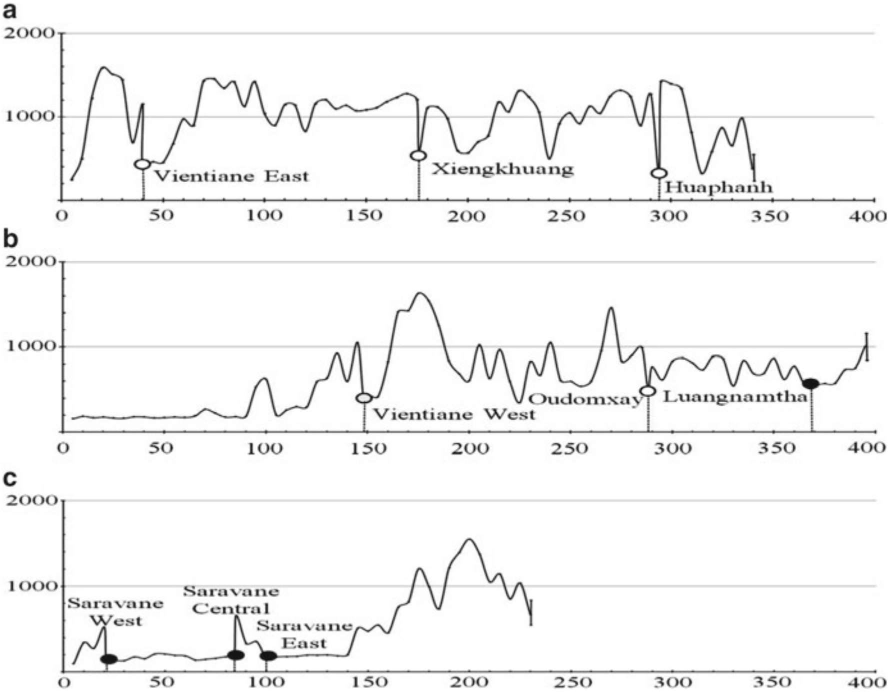


Fig. 7.2 Presence of *B. pseudomallei* in relation to elevation and distance from the Mekong River: (**a**) northeast, (**b**) northwest and (**c**) south. (●) positive for *B. pseudomallei*; (○) negative for *B. pseudomallei* (Data taken from Rattanavong et al. 2011)

start of the rainy season in 2009. The rates of contamination with *B. pseudomallei* were significantly lower with 76 % and 25 % of samples positive, respectively. Similarly, bacterial concentrations were lower with geometric means of 501 cfu/g [95 % CI: 314–797] in Saravane East and 147 cfu/g [95 % CI: 48–452] in Saravane West.

This first study (Rattanavong et al. 2011) suggested three conclusions: (i) the reservoir of melioidosis in Laos has a highly heterogeneous geographical distribution; (ii) it is not restricted to the Mekong basin and to low-lying regions; (iii) there are areas of high-level contamination with *B pseudomallei* in the province of Saravane.

7.3.2 Research into B. pseudomallei *in Surface Waters*

The second study [described in Vongphayloth et al. 2012) aimed to investigate the presence of *B. pseudomallei* in surface waters in the vicinity of contaminated sites and the use of Moore's swabs for the detection of the organism in water.

Table 7.2 Presence of *B. pseudomallei* in water samples collected around the sites in Saravane East and Saravane West

	Saravane East		Saravane West		
		No. positive		No positive	
Type of water	No. samples	n (%)	No. samples	n (%)	p
Boreholes and water tanks	3	1 (33)	35	0	0.07
Ponds and lakes	10	1 (10)	15	0	0.4
Rice fields	37	14 (38)	0	0	–
Sedone River	48	19 (39)	52	6 (11)	0.003
Total	98	35 (36)	102	6 (6)	0.000

The latter is a concentration technique using an immersed gauze swab that acts as a filter to capture and concentrate microorganisms in running or stagnant water. Developed by Moore (1948) more than 60 years ago to detect salmonellas in wastewater in urban settings, this method has proved an effective tool for isolation of enterobacteria, vibrios, mycobacteria and viruses from sewers and provides useful information for epidemiological investigations. It had been used once for the detection of *B. pseudomallei* in environmental waters, without success (Ketterer et al. 1986).

Based on the results of the study conducted in 2009 (Rattanavong et al. 2011), the sampling was undertaken close to the sites previously sampled in Saravane East and West. Water samples were collected within a radius of 2 km around each reference site. Four types of surface water were collected: (i) water from lakes or ponds, (ii) rice paddy water, (iii) river water and (iv) water from boreholes or domestic water tanks (Table 7.2). Water from the Sedone River, a tributary of the Mekong running within 100 m and 600 m of the sites at Saravane East and Saravane West, respectively, was also collected: 100 Moore's swabs were immersed every kilometre from 15 km upstream to 33 km downstream of the site at Saravane East and from 38 km upstream to 14 km downstream of the site at Saravane West. The two sites were about 140 km apart following the course of the Sedone River (Vongphayloth et al. 2012).

At each sampling point, Moore's swab was placed midway between the surface and bottom of the water source. Each swab was attached by two nylon strings, one fixed to a bamboo pole to ensure it was immersed at some distance from the bank and the other attached to a weight to ensure that the device sank. The pH, turbidity and temperature of the water were recorded: the pH and temperature were measured using a combined pH meter and thermometer (pHep-4, Hanna Instruments, Ann Arbor, MI, USA) and turbidity with a pocket turbidimeter (Hach, Loveland, CO, USA) and expressed in Nephelometric Turbidity Units (NTU). Once in place, the swab was left for 24–48 h before being recovered. After cutting the nylon strings aseptically, the swab was placed in 500 ml SBCT broth in a sterile container that was transported to the laboratory within 24 h. After aerobic incubation for 48 h at 40 °C, the broths were subcultured on Ashdown's agar. The identification of *B. pseudomallei* was carried out as described above. Note that this method is qualitative and does not permit enumeration of cfu.

Of the 98 samples of water collected around the site in Saravane East, 35 (36 %) were positive for *B. pseudomallei*. Of the 102 collected around the site in Saravane West, 6 (6 %) were positive (Table 7.2). The samples of water from ponds, lakes and domestic reservoirs were all found to be negative. Only one of the three samples of borehole water collected near Saravane East was positive. At both sites, water samples from the Sedone River were more frequently contaminated (39 % and 11 %, respectively) than rice paddy water (38 % at Saravane East). All the river water samples that were positive for *B. pseudomallei* were collected between the two reference sites (Figs. 7.3 and 7.4). The 15 swabs placed upstream of Saravane East and the 14 swabs downstream of Saravane West were all negative. The majority of the positive swabs were collected within 33 km downstream of the site in Saravane East (Fig. 7.3).

B. pseudomallei was more frequently isolated from water that was more acidic (pH median: 7.62 *versus* 8.16; $p<0.001$) and more turbid (median: 324 NTU *versus* 236 NTU; $p<0.001$), but there was no significant difference in temperature between positive and negative samples. In multivariate analysis, two parameters were independently associated with the presence of *B. pseudomallei*, a low pH (OR: 0.5 [95 % CI: 0.3–0.8]) and a high turbidity (OR: 1.0039 [95 % CI: 1.0006–1.0072]).

This second study suggested that the use of Moore's swabs is a simple, inexpensive and effective method of detecting *B. pseudomallei* in environmental water

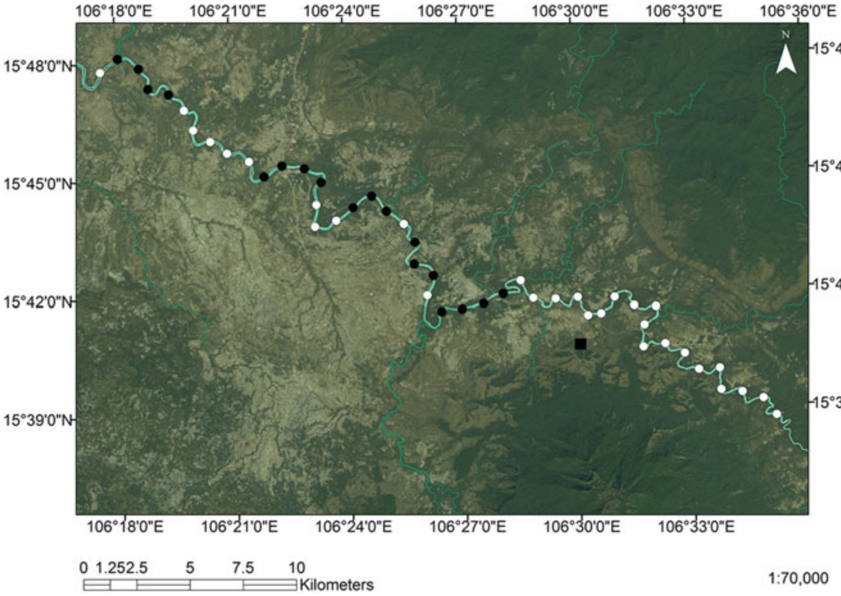


Fig. 7.3 Sampling points on the Sedone River upstream and downstream from the Saravane East reference site (*black square*). *White circles* represent points that were negative for *Burkholderia pseudomallei* and *black circles* represent points that were positive for *B. pseudomallei*. Water flows to the northwest (Data taken from Vongphayloth et al. 2012)

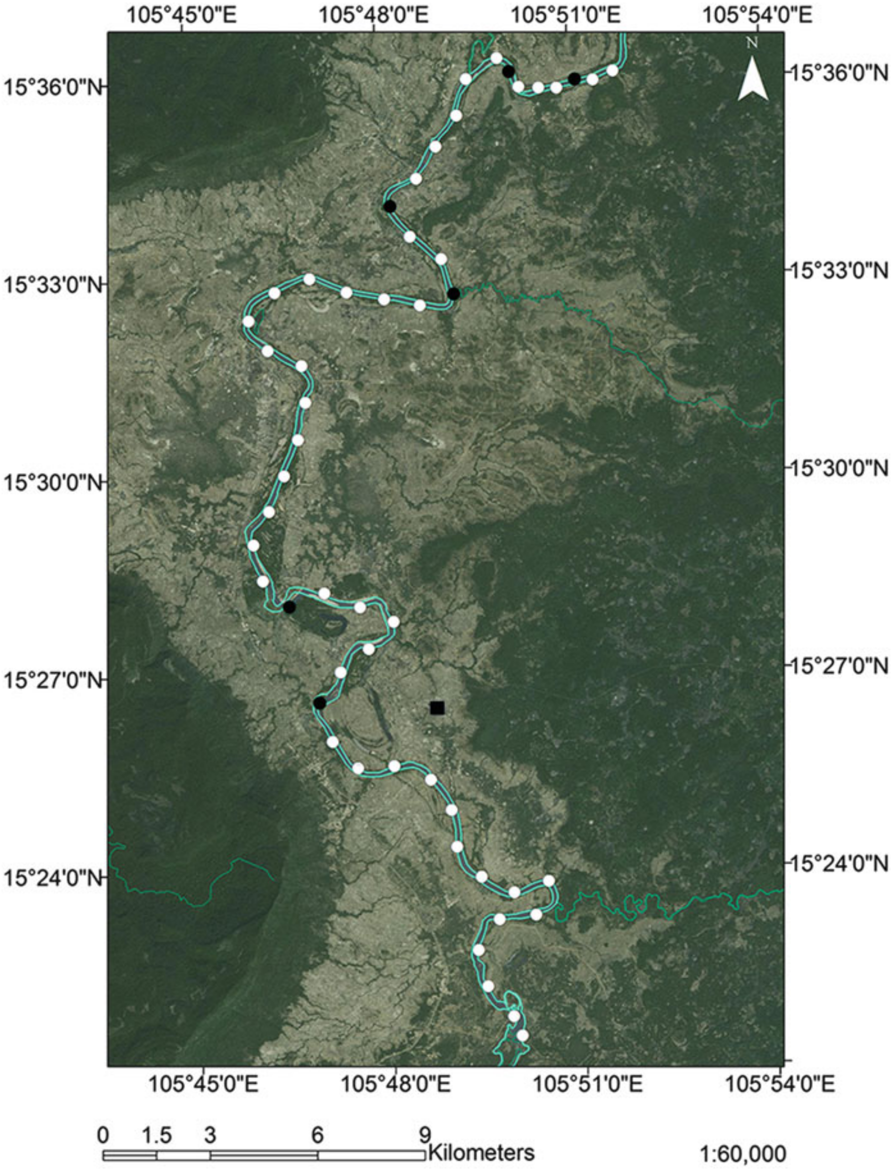


Fig. 7.4 Sampling points on the Sedone River upstream and downstream from the Saravane West reference site (*black square*). *White circles* represent points that were negative for *Burkholderia pseudomallei* and *black circles* represent points that were positive for *B. pseudomallei*. Water flows to the south (Data taken from Vongphayloth et al. 2012)

samples (Vongphayloth et al. 2012). Its main disadvantage is the inability to quantify the number of bacteria present. The high proportion of positive water samples around the highly contaminated site in Saravane East, in particular downstream on the Sedone River, suggests that surface waters are polluted by runoff from land-based reservoirs. A larger study is needed to confirm these results and analyse the relationship between the concentrations of *B. pseudomallei* in soil and the contamination of waters that drain it during the rainy season. The detection of this bacterium in river water with Moore's swabs could be good way of identifying the most contaminated watersheds and locating the main environmental reservoirs in areas where melioidosis is endemic.

7.4 Conclusion

Melioidosis is a common severe community-acquired infection in Laos. Still unknown by the majority of doctors 10 years ago, it is being more frequently recognised, thanks to the strengthening of diagnostic capacity in a few hospital laboratories, but it is probable that its true incidence is still grossly underestimated. Nearly 80 % of the population of Laos live in rural surroundings, the majority undertaking rice farming. This serious illness, frequently fatal, difficult to identify and treat, must be considered an important threat to public health.

Study of the environmental reservoir of *B. pseudomallei* would assist in defining areas that are melioidosis-free, low risk and high risk. Such stratification would enable health workers in rural areas to gauge the importance of this disease in their differential diagnosis of sepsis, guide empirical therapy and target possible prevention campaigns. Environmental research needs to be undertaken to analyse the physico-chemical parameters of soil that encourage the proliferation of the bacterium and whether any interventions could reduce bacterial density.

Acknowledgements We are grateful to all the staff of the Microbiology Laboratory, Mahosot Hospital, Vientiane, Lao PDR, who assisted with the laboratory studies, and to the Minister of Health and the Director of the Curative Department, Ministry of Health, for their support. This work was undertaken as part of the programme of the Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit funded by the Wellcome Trust of Great Britain.

References

Aldhous P (2005) Melioidosis? Never heard of it. Nature 434:692–693

Athan E, Allworth AM, Engler C, Bastian I, Cheng AC (2005) Melioidosis in tsunami survivors. Emerg Infect Dis 11:1638–1639

Cheng AC, Currie BJ (2005) Melioidosis: epidemiology, pathophysiology, and management. Clin Microbiol Rev 18:383–416

Currie BJ (2008) Advances and remaining uncertainties in the epidemiology of *Burkholderia pseudomallei* and melioidosis. Trans R Soc Trop Med Hyg 102:225–227

Currie BJ, Jacups SP, Cheng AC, Fisher DA, Anstey NM, Huffam SE, Krause VL (2004) Melioidosis epidemiology and risk factors from a prospective whole-population study in northern Australia. Trop Med Int Health 9:1167–1174

Currie BJ, Dance DAB, Cheng AC (2008) The global distribution of *Burkholderia pseudomallei* and melioidosis: an update. Trans R Soc Trop Med Hyg 102:S1–S4

Gilad J, Harary I, Dushnitsky T, Schwartz D, Amsalem Y (2007) *Burkholderia mallei* and *Burkholderia pseudomallei* as bioterrorism agents: national aspects of emergency preparedness. Isr Med Assoc J 9:499–503

Holden MTG, Titball RW, Peacock SJ, Cerdeño-Tárraga AM, Atkins T, Crossman LC et al (2004) Genomic plasticity of the causative agent of melioidosis, *Burkholderia pseudomallei*. Proc Natl Acad Sci U S A 101:14240–14245

Inglis TJJ, Sagripanti JL (2006) Environmental factors that affect the survival and persistence of *Burkholderia pseudomallei*. Appl Environ Microbiol 72:6865–6875

Inglis TJJ, Rigby P, Robertson TA, Dutton NS, Henderson M, Chang BJ (2000) Interaction between *Burkholderia pseudomallei* and *Acanthamoeba* species results in coiling phagocytosis, endamebic bacterial survival, and escape. Infect Immun 68:1681–1686

Kaestli M, Mayo M, Harrington G, Watt F, Hill J, Gal D, Currie BJ (2007) Sensitive and specific molecular detection of *Burkholderia pseudomallei*, the causative agent of melioidosis, in the soil of tropical northern Australia. Appl Environ Microbiol 73:6891–6897

Kaestli M, Mayo M, Harrington G, Ward L, Watt F, Hill J et al (2009) Landscape changes influence the occurrence of the melioidosis bacterium *Burkholderia pseudomallei* in soil in Northern Australia. PLoS Negl Trop Dis 3:e364

Ketterer PJ, Webster WR, Shield J, Arthur RJ, Blackall PJ, Thomas AD (1986) Melioidosis in intensive piggeries in south eastern Queensland. Aust Vet J 63:146–149

Kronmann KC, Truett AA, Hale BR, Crum-Cianflone NF (2009) Melioidosis after brief exposure: a serologic survey in US marines. Am J Trop Med Hyg 80:182–184

Le Hello S, Currie BJ, Godoy D, Spratt BG, Mikulski M, Lacasin F et al (2005) Melioidosis in New Caledonia. Emerg Infect Dis 11:1607–1609

Leelarasamee A (2000) Melioidosis in Southeast Asia. Acta Trop 74:129–132

Limmathurotsakul D, Wongratanacheewin S, Teerawattanasook N, Wongsuvan G, Chaisuksant S, Chetchotisakd P, Chaowagul W, Day NPJ, Peacock SJ (2010) Increasing incidence of human melioidosis in Northeast Thailand. Am J Trop Med Hyg 82:1113–1117

Moore B (1948) The detection of paratyphoid carriers in towns by means of sewage examination. Mon Bull Minist Health Public Health Lab Serv 7:241–248

Peacock SJ, Schweizer HP, Dance DAB, Smith TL, Gee JE, Wuthiekanun V et al (2008) Management of accidental laboratory exposure to Burkholderia pseudomallei and B mallei. Emerg Infect Dis 14:e2

Phetsouvanh R, Phongmany S, Newton P, Mayxay M, Ramsay A, Wuthiekanun V, White NJ (2001) Melioidosis and Pandora's box in the Lao People's Democratic Republic. Clin Infect Dis 32:653–654

Phetsouvanh R, Phongmany S, Soukaloun D, Rasachak B, Soukhaseum V, Soukhaseum S, Frichithavong K et al (2006) Causes of community-acquired bacteremia and patterns of antimicrobial resistance in Vientiane, Laos. Am J Trop Med Hyg 75:978–985

Rattanavong S, Wuthiekanun V, Langla S, Amornchai P, Sirisouk J, Phetsouvanh R, Moore CE, Peacock SJ, Buisson Y, Newton PN (2011) Randomized soil survey of the distribution of *Burkholderia pseudomallei* in rice fields in Laos. Appl Environ Microbiol 77:532–536

Rolim DB, Rocha MF, Brilhante RS, Cordeiro RA, Leitão NP Jr, Inglis TJ et al (2009) Environmental isolates of *Burkholderia pseudomallei* in Ceara state, Northeast Brazil. Appl Environ Microbiol 75:1215–1218

Shams AM, Rose LJ, Hodges L, Arduino MJ (2007) Survival of *Burkholderia pseudomallei* on environmental surfaces. Applied Environ Microbiol 73:8001–8004

Shih HI, Chuang YC, Cheung BM, Yan JJ, Chang CM, Chang K et al (2009) Sporadic and outbreak cases of melioidosis in southern Taiwan: clinical features and antimicrobial susceptibility. Infection 37:9–15

Sprague LD, Neubauer H (2004) Melioidosis in animals: a review on epizootiology, diagnosis and clinical presentation. J Vet Med B Infect Dis Vet Public Health 51:305–320

Su H-P, Chan T-C, Chang C-C (2011) Typhoon-related leptospirosis and melioidosis, Taiwan, 2009. Emerg Infect Dis 17:1322–1324

Thibault FM, Hernandez E, Vidal DR, Girardet M, Cavallo JD (2004) Antibiotic susceptibility of 65 isolates of *Burkholderia pseudomallei* and *Burkholderia mallei* to 35 antimicrobial agents. J Antimicrob Chemother 254:1134–1138

Vongphayloth K, Rattanavong S, Moore CE, Phetsouvanh R, Wuthiekanun V, Sengdouangphachanh A, Phouminh P, Newton PN, Buisson Y (2012) Burkholderia pseudomallei detection in surface water in southern Laos using Moore's swabs. Am J Trop Med Hyg 86:872–877

Vuddhakul V, Tharavichitkul P, Na-Ngam N, Jitsurong S, Kunthawa B, Noimay P, Noimay P, Binla A, Thamlikitkul V (1999) Epidemiology of *Burkholderia pseudomallei* in Thailand. Am J Trop Med Hyg 60:458–461

Wild S, Roglic G, Green A, Sicree R, King H (2004) Global prevalence of diabetes: estimates for the year 2000 and projections for 2030. Diabetes Care 27:1047–1053

Wuthiekanun V, Anuntagool N, White NJ, Sirisinha S (2002) Short report: a rapid method for the differentiation of Burkholderia pseudomallei and Burkholderia thailandensis. Am J Trop Med Hyg 66:759–761

Wuthiekanun V, Mayxay M, Chierakul W, Phetsouvanh R, Cheng AC, White NJ, Day NPJ, Peacock SJ (2005) Detection of *Burkholderia pseudomallei* in soil within the Lao People's Democratic Republic. J Clin Microbiol 43:923–924

Wuthiekanun V, Langa S, Swaddiwudhipong W, Jetsadapanpong W, Kaengnet Y, Chierakul W et al (2006) Melioidosis in Myanmar: forgotten but not gone. Am J Trop Med Hyg 75:945–946

Wuthiekanun V, Pheaktra N, Putchhat H, Sin L, Sen B, Kumar V et al (2008) Burkholderia pseudomallei antibodies in children, Cambodia. Emerg Infect Dis 14:301–303

Part III

Global Changes, Land Use Changes and Vector-Borne Diseases

Chapter 8
Adaptation of Mosquito Vectors to Salinity and Its Impact on Mosquito-Borne Disease Transmission in the South and Southeast Asian Tropics

Ranjan Ramasamy, Sinnathamby N. Surendran, Pavilupillai J. Jude, Sangaralingam Dharshini, and Muthuladchumy Vinobaba

Abstract Mosquito vector-borne diseases are a significant health problem in South and Southeast Asia. Some mosquito vectors in the region are well known to lay eggs and undergo pre-imaginal development in brackish water. However, a number of other important vectors, e.g. *Anopheles culicifacies* (malaria) and *Aedes aegypti* and *Aedes albopictus* (dengue and chikungunya), have previously been widely held to do so exclusively in freshwater. But recent evidence shows that these species can also lay eggs and undergo pre-imaginal development in brackish water collections in coastal areas of the region. This property produces a reservoir of vectors that are not targeted in larval control programmes. It can contribute to disease transmission in a previously unrecognised manner that can be compounded by environmental changes caused by expanding populations in coastal zones, climate change and rising sea levels due to global warming. Increased disease transmission in coastal areas will also lead to higher disease incidence in inland areas. Many countries in South and Southeast Asia have long coastlines, a high proportion of coastal zone relative to total land area and a large proportion of the population living in coastal areas. Hence, the region is particularly vulnerable to disease transmission by brackish water vectors. Appropriate policies and strategies need to be developed in a local, national and international context to counter this threat to human health in South and Southeast Asia.

R. Ramasamy (✉)
Department of Life Sciences, Faculty of Science and Technology,
Anglia Ruskin University, Cambridge, UK
e-mail: ranjan.ramasamy@anglia.ac.uk

S.N. Surendran • P.J. Jude
Department of Zoology, University of Jaffna, Jaffna, Sri Lanka
e-mail: noble@jfn.ac.lk; pjustinjude@gmail.com

S. Dharshini • M. Vinobaba
Department of Zoology, Eastern University, Chenkaladi, Sri Lanka
e-mail: dharshini1982@yahoo.com; laxmi@esn.ac.lk

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_8

8.1 Overview of Mosquito-Borne Human Diseases in Tropical South and Southeast Asia

Mosquito-borne human diseases are a cause of considerable mortality and morbidity worldwide. Diseases such as chikungunya, dengue and West Nile viral encephalitis are of great international concern because of their increasing incidence and global spread (Weaver and Reisen 2010). Mosquito vectors transmit many important human parasitic and arboviral diseases in tropical South and Southeast Asia. The World Health Organization (WHO) reported that there were approximately 130.6 million suspected cases of malaria caused by protozoan parasites of the genus *Plasmodium*, predominantly *P. falciparum* and *P. vivax*, in its Southeast Asian region in 2012 (WHO 2013a). This caused an estimated 1,226 deaths. The WHO Southeast Asian region includes countries with extensive coastal zones such as Bangladesh, India, Indonesia, Maldives, Myanmar, Sri Lanka, Thailand and Timor-Leste. In its Western Pacific region, which also contains many coastal countries regarded as part of Southeast Asia (Brunei, Cambodia, Malaysia, Papua New Guinea, the Philippines, Singapore and Vietnam), the WHO reported 10.8 million suspected cases and an estimated 458 malaria deaths in 2012 (WHO 2013a). The malaria situation in the greater South and Southeast Asian region is highly dynamic due to the increasing resistance of parasites to common antimalarial drugs and mosquito vectors to common insecticides, movement of human populations and changes in land use patterns, forest cover, health services and other pertinent factors. Several species of *Anopheles* mosquitoes are responsible for transmitting malaria in the region with some identified as dominant vectors (Sinka et al. 2011).

Lymphatic filariasis caused by the nematode parasites *Wuchereria bancrofti*, *Brugia malayi* and *Brugia timori* is widely prevalent in the region. It is responsible for considerable morbidity and disfigurement in infected persons. Recent WHO data suggest that approximately 60–65 million people in the two regions have lymphatic filariasis (WHO 2012). *Culex quinquefasciatus* in the Asian mainland and various species of *Anopheles* and *Mansonia* in the Southeast Asian archipelago are chiefly responsible for transmitting filariasis in the region (Walter Reed Biosystematics Unit 2013).

Dengue, the most common human arboviral disease, is widespread in South and Southeast Asia with 176,719 cases and 887 deaths reported in the WHO Southeast Asian region in 2010 and 242,424 cases with 784 deaths in the WHO Western Pacific region in 2009 (WHO 2012). *Aedes aegypti* and *Aedes albopictus* mosquitoes that are common throughout the region are predominantly responsible for transmitting dengue (Weaver and Reisen 2010; Walter Reed Biosystematics Unit 2013). Other mosquito-borne diseases that are endemic to the region include Japanese encephalitis and chikungunya. Yellow fever transmitted by *Ae. aegypti* and *Ae. albopictus* is endemic in parts of Africa and South America (WHO 2013b). An effective vaccine is available against yellow fever. The reasons for the absence of yellow fever from the South and Southeast Asian region, notwithstanding the presence of competent vectors, are not well understood. Increasing international travel and trade however poses the risk of its introduction to the region.

8.2 Vector Control Is Important for Reducing the Prevalence of Many Mosquito-Borne Diseases

A licensed vaccine is presently available against only Japanese encephalitis among all the major mosquito-borne diseases of the region. Vaccines for malaria, dengue and chikungunya are currently under development. The presence of four serotypes of the dengue virus hampers the production of a vaccine against dengue. In addition, a suboptimal immune response to any one of the serotypes can exacerbate disease caused by a subsequent infection with that serotype (Halstead 2003; Chun et al. 2007). Drugs for specific treatment of dengue are not presently available, and only symptomatic treatment is possible for the disease. On the other hand, specific and effective drugs are available to treat malaria and lymphatic filariasis. However, the Greater Mekong subregion in Southeast Asia is the origin of many strains of malaria parasites that have developed resistance to several antimalarial drugs and then spread worldwide. The recent emergence in this area of *P. falciparum* that is resistant to artemisinin combination therapies that are the first-line treatment for uncomplicated *falciparum* malaria is therefore of considerable international concern (Dondorp et al. 2010).

Minimising human-mosquito contact and reducing vector populations by the application of insecticides and through managing and eliminating pre-imaginal development sites therefore remain important components of mosquito-borne disease control programmes. The use of insecticide-impregnated bed nets and indoor residual spraying of insecticides is the mainstay of malaria vector control programmes throughout the world. These methods, together with early case detection and treatment as well as the management of larval habitats, have succeeded in reducing the incidence of malaria in many countries of the region over the past decade (WHO 2013b). However, the *Aedes* vectors of dengue can bite outdoors and during daytime making bed nets less effective against acquiring infections. Mosquito proofing houses, which has proved helpful in eliminating dengue from the southern United States, is not popular or widely affordable in the humid and densely populated countries of South and Southeast Asia. Therefore, reducing the *Aedes* vector populations through eliminating, minimising and larviciding pre-imaginal development habitats and the application of insecticide through fogging and residual spraying at infection foci are the principal methods used for controlling dengue in the region (WHO 2009). Such measures are additionally effective against chikungunya because *Ae. aegypti* and *Ae. albopictus* are also the principal vectors of chikungunya. *Aedes aegypti* is additionally capable of transmitting other Australasian arboviruses, such as Ross River and Murray Valley encephalitis viruses, as demonstrated in laboratory experiments (Ramasamy et al. 1990). It is also a potential vector of the filarial parasite *Brugia malayi* in Asia (Erickson et al. 2009).

8.3 Global Warming, Rising Sea Levels and Changes in Coastal Salinity

The United Nations Framework Convention on Climate Change described global climate change as long-term changes in commonly measured meteorological parameters, over and above natural variations, that are directly or indirectly attributable to human activity altering the composition of the atmosphere. Such parameters include temperature, rainfall and humidity. Global warming is the rise in average global temperatures due to the increasing emission of gases, principally carbon dioxide, causing a greenhouse effect in the atmosphere. Global warming leads to a rise in sea levels caused by the melting of polar ice and glaciers and the thermal expansion of seawater (Intergovernmental Panel on Climate Change 2013). The rise in sea levels, depending on the extent of the warming that is principally governed by the rate of burning of fossil fuels, is predicted to be about 82 cm by the end of the twenty-first century (Intergovernmental Panel on Climate Change 2013). Rising sea levels are anticipated to increase the extent of saline (>30 parts per thousand or ppt salt) or brackish (0.5–30 ppt salt) water bodies in coastal areas. These include coastal estuaries, lagoons, marshes and mangroves (Nicholls et al. 2007). The salinity of estuarine systems is projected to increase, and their boundaries move further inland with more pronounced tidal water flows into rivers (Nicholls et al. 2007). A proportion of coastal wetlands such as salt marshes and mangroves are expected to become inundated, but additional saline wetlands are anticipated to form further inland (Nicholls et al. 2007). Rising sea levels and higher water withdrawal rates from freshwater aquifers near the coast by expanding populations are also envisaged to increase saltwater intrusion into the aquifers (FAO 2007).

The tropical areas of South and Southeast Asia have extensive coastlines bordering the Indian and Pacific Oceans and various seas. Southeast Asia also has the largest archipelago in the tropics. Indonesia and the Philippines with 248 and 104 million persons, respectively, are the two most populous countries in this archipelago (CIA 2012). Table 8.1 presents data on the length of the coastline in relation to the land area for Indonesia and the Philippines and selected other countries in the region. A comparison is made with the Federated States of Micronesia, a collection of about 600 small islands in the Western Pacific tropics. India on the other hand has a long coastline but a low coast to land area ratio compared to countries composed of many islands.

Countries in South and Southeast Asia with extensive coastlines and high coast to land area ratios are particularly vulnerable to the consequences of rising sea levels on their biosphere and geosphere. One in ten persons worldwide lives in coastal areas that are less than 10 m above sea level (McGranahan et al. 2007). Such areas are prone to increasing salinisation caused by rising sea levels. The densely populated tropical South and Southeast Asian countries have a large proportion of their

Table 8.1 Coastline related to land area in selected South and Southeast Asian countries and Micronesia

Country/statistic	Land area Km^2	Coastline Km	Coast/area ratio m/Km^2
Bangladesh	130,168	580	4.5
India	2,973,193	7,000	2
Sri Lanka	64,630	1,340	20.7
Malaysia	328,657	4,675	14.2
Indonesia	1,811,569	54,716	30.2
Philippines	298,170	36,289	121.7
Micronesia (Western Pacific)	702	6,112	8,710

Data from Central Intelligence Agency (2012)

populations living in such vulnerable areas. For example, Vietnam, Bangladesh, Thailand and Indonesia, respectively, have 55, 46, 26 and 20 % of their population living on land that is less than 10 m above sea level (McGranahan et al. 2007).

8.4 Mosquito Vector Development in Brackish and Saline Waters

Global warming can alter the transmission of mosquito-borne diseases. This is due to the effects of changing temperature on mosquito survival and pre-imaginal development and the more rapid development of ingested pathogens in mosquitoes and shorter intervals between blood meals at moderately higher ambient temperatures (Ramasamy and Surendran 2012). However, global warming will also raise sea levels, leading to an increase in saline and brackish water bodies in coastal areas. We recently drew attention for the first time to the possible impacts of rising sea levels on the transmission of vector-borne diseases (Ramasamy and Surendran 2011).

There are about 3,500 species of mosquitoes that are present throughout the world, but only a few hundreds of them feed on humans. The pre-imaginal stages of several mosquito vectors of human disease are able to develop in brackish or saline water habitats. Larvae of such salinity-tolerant mosquitoes possess specific physiological mechanisms to overcome high osmolarity in their surrounding (Bradley 1987). A relatively thick cuticle that is impermeable to water and ions helps pupae to survive salinity (Bradley 1987). Details of the more important vector mosquitoes that possess salinity-tolerant pre-imaginal stages in South and Southeast Asia are summarised in Table 8.2.

We have postulated that an expansion of brackish/saline water bodies in coastal areas associated with rising sea levels can increase densities of salinity-tolerant vectors and lead to the adaptation of freshwater vectors to breed in brackish and saline waters (Ramasamy and Surendran 2011). Higher vector densities can increase transmission of diseases in coastal localities, which can then spread to inland areas through bridging vectors (Ramasamy and Surendran 2011, 2012). Because the tropical countries in South and Southeast Asia possess many lagoons, coastal

Table 8.2 Common salinity-tolerant mosquito vectors of human disease in South and Southeast Asia

Species	Distribution	Transmitted pathogens
Aedes togoi	SE Asia	Japanese encephalitis virus and filarial parasites
Ae. (Ochlerotatus) vigilax	Australasia, SE Asia	Barmah forest and Ross River viruses and filarial parasites
Anopheles farauti and An. annulipes	Australasia, SE Asia	Malaria parasites
An. subpictus	S and SE Asia	Malaria and filarial parasites
An. sundaicus	S and SE Asia	Malaria parasites
Culex sitiens	S and SE Asia, Australasia	Japanese encephalitis and Ross River viruses and filarial parasites
Cx. tritaeniorhynchus	S Asia	Japanese encephalitis virus

Adapted from Walter Reed Biosystematics Unit (2013), Ramasamy and Surendran (2011)

marshes, mangroves and estuaries and many have extensive coastlines or a high ratio of coastline to land area, they are particularly susceptible to an increase in disease transmission caused by salinity-tolerant mosquito vectors.

Evidence that has been discussed in detail elsewhere (Ramasamy and Surendran 2011, 2012) supports this new perspective on coastal transmission of mosquito-borne diseases. In particular, the inland incursion of seawater caused by the 2004 Asian tsunami and the effect of draining coastal marshland in Western Europe provide specific supportive evidence (Ramasamy and Surendran 2011, 2012). *Anopheles culicifacies*, the predominant freshwater vector of malaria in South Asia, was recently shown to undergo pre-imaginal development in brackish waters in Sri Lanka (Jude et al. 2010). *Anopheles sundaicus*, a well-known salinity-tolerant malaria vector in Southeast Asia, is now reported to be widespread in coastal areas of Sri Lanka (Surendran et al. 2010, 2011). Many mosquitoes identified through morphology as *Anopheles subpictus* sibling species B, which is reported to be salinity tolerant in Sri Lanka and elsewhere in the region, have been shown to be members of the *An. sundaicus* complex by DNA sequencing (Surendran et al. 2010). *An. sundaicus* is able to develop in nearly saline water, but the physiological mechanisms responsible for this ability have not been determined. It is possible that a capacity to differentially localise Na^+/K^+ ATPase in rectal cells that permits osmoregulation through ion excretion as reported for *Anopheles albimanus* (Smith et al. 2008), a salinity-tolerant malaria vector in the Americas, may also be a feature of *An. sundaicus*. This requires experimental verification. Genetic selection for salinity tolerance over a period is possible in anopheline vectors because sibling species that differ in salinity tolerance are reportedly present in the *Subpictus*, *Sundaicus* and *Farauti* vector complexes of the region (Sinka et al. 2011). Maps of the recent distributions of the three vector complexes and the *Culicifacies* complex, whose members may also adapt to salinity, in South and Southeast Asia, are shown in Fig. 8.1. Mosquitoes of the *Subpictus, Sundaicus* and *Farauti* complexes are widely distributed in the region. A future expansion of brackish water habitats with rising

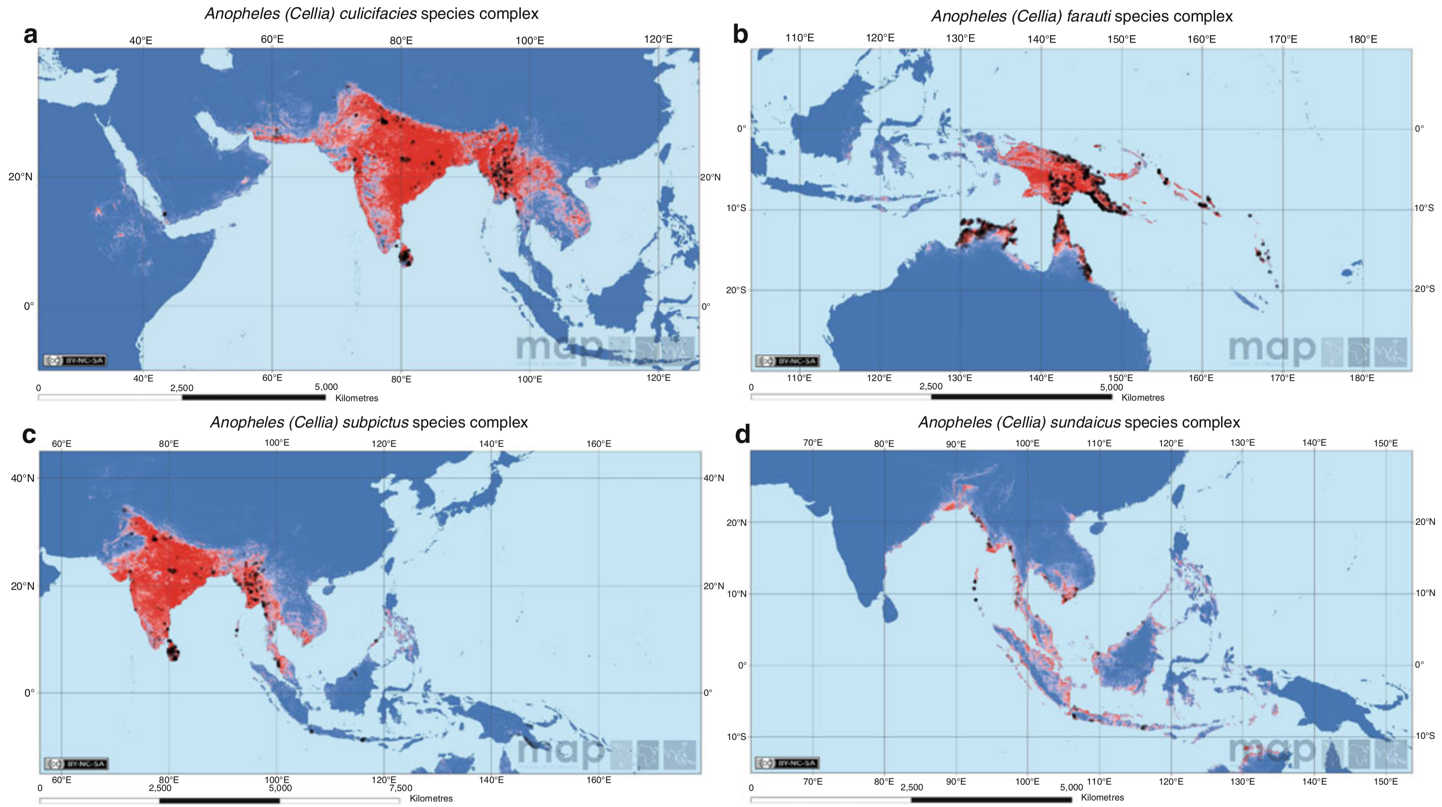


Fig. 8.1 The distributions of (**a**) *Anopheles (Cellia) culicifacies* species complex, (**b**) *Anopheles (Cellia) farauti species* complex, (**c**) *Anopheles (Cellia) subpictus* species complex in South and Southeast Asia (Reproduced with permission from Sinka et al. 2011, under the Creative Commons licence)

sea levels has the potential to increase malaria transmission by the salinity-tolerant members of the three complexes as well as brackish water-adapted freshwater species like *An. culicifacies*. This can increase the incidence and geographical spread of malaria in coastal areas that can subsequently be extended by bridging vectors to inland areas of the region.

We also recently showed that *Aedes aegypti* and *Aedes albopictus*, well known to be the vectors of dengue and chikungunya in the region, undergo pre-imaginal development in brackish water collections in coastal urban and peri-urban environments in the island of Sri Lanka (Ramasamy et al. 2011). Larvae and pupae were found in brackish water in discarded plastic and glass containers and disused boats and wells in beach areas. Figure 8.2 illustrates examples of such brackish water larval habitats. In the field surveys carried out in the northern and eastern provinces of Sri Lanka (Fig. 8.3), 17 % of brackish water containers in coastal beaches of Thannamunai in the eastern Batticaloa district were found to have *Ae. aegypti* and *Ae. albopictus* larvae, while 6 % of brackish water containers along the coast of Jaffna City in the north had *Ae. aegypti* larvae (Ramasamy et al. 2011). In Kurunagar, a coastal division of the city of Jaffna, 25 % of brackish water wells were found to have *Ae. aegypti* larvae in a salinity range of 2–9 ppt (Surendran et al. 2012). Such *Aedes* larval positivity rates in brackish water of up to 15 ppt salt in Jaffna (Ramasamy et al. 2011) are higher than the House Index (percentage of houses positive for *Aedes* larvae) or Breteau Index (number of containers with larvae per 100 houses) for freshwater habitats that have been typically associated with dengue epidemics in other countries (Sanchez et al. 2006). Pre-imaginal development in brackish water can play an unappreciated role in the transmission of dengue as

Fig. 8.2 Brackish water development habitats of *Aedes aegypti* and *Aedes albopictus* larvae in Sri Lanka. The photographs show the brackish water collections containing larvae in (**a**) and (**b**), disused boats; (**c**) and (**e**), abandoned wells; (**d**) and (**f**), discarded food and beverage containers (Reproduced with permission from Surendran et al. 2012)

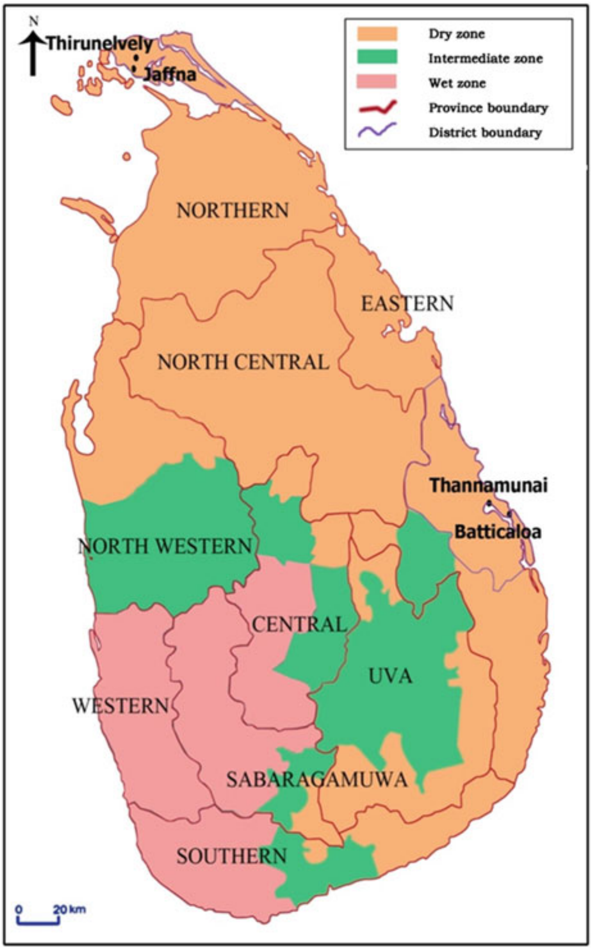


Fig. 8.3 Map of Sri Lanka showing the different provinces and the *Aedes* larvae collection sites in the Jaffna and Batticaloa districts. Sri Lanka is an island in the Indian Ocean with an area of 65,525 km^2 located between latitudes 5′55 and 9′50 North of the equator. The central hills of the island divide the surrounding plains into two distinct rainfall zones: the wet and dry zones. The wet zone receives an annual rainfall exceeding 2,500 mm in two main rainy seasons: the north-east monsoon in October–December and the south-west monsoon in May–July. Inter-monsoonal rains also occur in the wet zone. The dry zone, with an annual rainfall below 2,000 mm, receives maximal rainfall during the north-east monsoon and little or no rain during the rest of the year. An intermediate zone, with mixed characteristics, lies between the dry and wet zone. The *beige*, *green* and *pink* shaded areas show the dry, intermediate and wet rainfall zones, respectively (Reproduced with permission from Surendran et al. 2012)

dengue control efforts worldwide are presently directed only towards freshwater habitats of the two *Aedes* vectors because of the long and widely held view that they only develop naturally in freshwater (Barraud 1934; Chan et al. 1971; Kulatilaka and Jayakuru 1998; Ooi et al. 2006; WHO 2009, 2013c). The adaptation of

Ae. aegypti and *Ae. albopictus* to coastal brackish water habitats could have major consequences to human health since vaccines are presently not available against dengue and chikungunya that are increasing in incidence globally (Weaver and Reisen 2010). Small island countries like Singapore and Sri Lanka within the region have not been able to eliminate dengue despite well-resourced and long-established control programmes (Chan et al. 1971; Kulatilaka and Jayakuru 1998; Ooi et al. 2006). We hypothesise that the exclusive targeting of freshwater pre-imaginal habitats for vector source reduction and management until now has contributed to this failure. Our observations in Sri Lanka also suggest that *Ae. aegypti* and *Ae. albopictus* from different locations in the country may vary in their ability to tolerate salinity (Ramasamy et al. 2011). We observed that *Ae. albopictus* and *Ae. aegypti* first and third instar larvae from the Jaffna peninsula, where there is more extensive groundwater salinisation (Rajasooriyar et al. 2002), had significantly higher LC_{50} for salinity in developing into adults (11.9 and 13.0 ppt for first instar larvae of *Ae. aegypti* and *Ae. albopictus*, respectively) than the corresponding larvae from Batticaloa in mainland Sri Lanka (9.8 and 10.2 ppt for first instar larvae of *Ae. aegypti* and *Ae. albopictus*, respectively) (Ramasamy et al. 2011).

In Brunei Darussalam, which is 3,775 km away from Sri Lanka, we observed larvae of *Ae. albopictus* in discarded plastic food and beverage containers in beach areas in water with salinity of up to 8 ppt (Idris et al. 2013). The laboratory determined LC_{50} for the development of first instar *Ae. albopictus* larvae to adults in Brunei Darussalam in brackish water was approximately 9 ppt salinity (Idris et al. 2013). *Aedes aegypti* was however found in brackish water in a house from a water village on the Brunei river estuary (Ramasamy and Surendran 2013). The failure to detect *Ae. aegypti* pre-imaginal stages in brackish water containers along beaches in Brunei Darussalam may be due to the peri-urban nature of the beaches and the greater endophilicity of *Ae. aegypti* in Brunei Darussalam, a country that is less densely populated than the surveyed coastal areas of Sri Lanka. The observations in Brunei Darussalam and Sri Lanka suggest that the development of *Ae. aegypti* and *Ae. albopictus* in brackish water may be a widespread phenomenon in tropical countries that can contribute to dengue transmission.

We speculate that *Ae. aegypti* and *Ae. albopictus* may be evolving strains that are adapting to brackish water habitats in the urban or peri-urban environment by a process that may be driven by anthropogenic changes that increase such habitats, the exclusive application of larval control methods to freshwater habitats and the use of insecticides in mainly inland locations for agriculture and vector control. *Aedes albopictus* has spread from Asia to Africa, America and Europe since the 1980s (Rezza 2012). It recently caused a chikungunya epidemic in northern Italy and dengue transmission in southern France (Rezza et al. 2007; Cavrini et al. 2009; La Ruche et al. 2010). We hypothesise that salinity-tolerant and diapausing *Ae. albopictus* will further increase the potential for arboviral disease transmission in coastal areas of the temperate zone in Asia and elsewhere.

The physiological mechanisms that permit *Ae. aegypti* and *Ae. albopictus* to oviposit and for the eggs to hatch into larvae that then develop into adults are not known. Larvae of the American brackish water mosquito *Aedes taeniorhynchus*, a vector of Eastern equine encephalitis virus, osmoregulate by drinking the surrounding fluid and excreting Na + and Cl− from the posterior rectum to produce a hyperosmotic urine (Bradley 1987). Early laboratory studies show that *Ae. aegypti* larvae are able to tolerate a limited increase in salinity in their surroundings by increasing the concentrations of free amino acids and ions in their haemolymph in order to osmoconform to their environment (Edwards 1982). Recent evidence suggests that the pre-imaginal development of *Ae. aegypti* in brackish water of up to 15 ppt salinity in Sri Lanka is accomplished by a combination of reversible and irreversible physiological changes (Ramasamy et al. 2014).

Many tropical South and Southeast Asian countries are experiencing a rapid growth of populations living in coastal areas (McGranahan et al. 2007; UNEP 2007). Discarded containers along coasts that can accumulate brackish water and serve as habitats for the pre-imaginal development of mosquito vectors will become more common if refuse collection becomes increasingly inadequate because the relevant government authorities fail to cope with the rising need. Such a scenario, coupled with the application of mosquito control methods only to inland, urban and freshwater habitats, can favour the adaptation of vector mosquitoes to undergo pre-imaginal development in coastal brackish water habitats. This can additionally increase the prevalence of mosquito-borne diseases in the region.

The Jaffna peninsula is located at the apex of northern Sri Lanka (Fig. 8.3). Jaffna is traditionally an agricultural area with an extensive coastline. It is largely composed of sedimentary limestone of the Miocene period (Rajasooriyar et al. 2002), has a maximum altitude of 10.4 m and contains many lagoons and other seawater inlets. Almost all locations in the peninsula are <10 km from the sea, lagoon or other seawater inlets. Therefore, the entire peninsula may be considered to be a coastal zone. Dengue is endemic (Ramasamy and Surendran 2012, 2013), and there have been recent epidemics of malaria (Ramasamy and Surendran 2012, 2013) and chikungunya (Surendran et al. 2007) in the Jaffna peninsula. There are no reports of the local transmission of Japanese encephalitis and filariasis in the Jaffna peninsula in recent times although their respective primary vectors *Culex tritaeniorhynchus* and *Culex quinquefasciatus* are present in the peninsula (Rajendram and Antony 1991; Jude et al. 2012). Furthermore, the larvae of *Culex sitiens*, a known vector of arboviruses including the Japanese encephalitis virus, are present in domestic wells with salinity ranging from 10 to 20 ppt in the islands off the peninsula (Jude et al. 2012). We propose that the Jaffna peninsula is therefore a model location for studying the future impact of global climate change and rising sea levels on mosquito vector populations and disease transmission in tropical coastal zones of Asia. The availability of relevant expertise and resources in the University of Jaffna makes a systems-based approach for studying the primary and secondary effects of different climate change parameters, changing salinity and other ecological and socio-economic factors, on mosquito populations and disease transmission possible in the Jaffna peninsula.

In summary, several mosquito vector species that have traditionally been regarded as developing exclusively in freshwater habitats are now known to be able to undergo pre-imaginal development in brackish water in the peri-urban and urban

Table 8.3 Examples of freshwater mosquito vectors of human disease that are able to undergo pre-imaginal development in brackish water

Species	Location	Maximum salinity tolerance (ppt)	Reference
Aedes aegypti	Brunei Darussalam, Sri Lanka	10	Ramasamy and Surendran (2013)
		15	Ramasamy et al. (2011, 2014), Surendran et al. (2012)
Aedes albopictus	Brunei Darussalam	8	Idris et al. (2013)
	Sri Lanka	14	Ramasamy et al. (2011)
Anopheles culicifacies	India	7	Gunasekaran et al. (2005)
	Sri Lanka	4	Jude et al. (2010)
Anopheles stephensi	India	17	Gunasekaran et al. (2005)

environments. The data are summarised in Table 8.3. The relative contribution of brackish water-developing vectors, compared to vectors developing in freshwater habitats, towards disease transmission in coastal areas remains to be elucidated in detailed epidemiological studies. An analysis of dengue incidence in relation to rainfall in Jaffna and the rest of Sri Lanka is compatible with the hypothesis that brackish water vectors are a perennial source of dengue transmission and act as a virus source to help generate the increase in dengue transmission that follows soon after the onset of monsoonal rains (Ramasamy and Surendran 2013).

8.5 Impact of Increased Disease Transmission on Coastal Communities in South and Southeast Asia

Rising sea levels can therefore act synergistically with climate change and then interact in a complex manner with other environmental and socio-economic factors near coasts to generate a greater potential for the transmission of malaria, dengue and other mosquito-borne diseases. More than half the world's population lives within 60 km of a shoreline, and population densities in coastal areas will increase markedly in disease-endemic countries of the region (McGranahan et al. 2007; UNEP 2007). Growing numbers of people will therefore be at risk of acquiring infections from increasing vector populations in coastal areas. Greater host density, by increasing vector-host contact, will also contribute to an increase in disease transmission rates.

Factors such as climate, agricultural practice, forest cover, animal reservoirs of disease, efficiency of garbage collection in coastal locations and human population changes can influence the greater mosquito-borne disease transmission risk in coastal areas (Ramasamy and Surendran 2012). Higher incidence of such disease in coastal areas can serve as a focus to spread the disease inland through efficient freshwater vectors. The resulting health impacts may be particularly significant in the more resource-poor countries of the South and Southeast Asian region.

8.6 Mitigating Measures

Controlling the transmission of malaria, dengue and other mosquito-borne diseases and providing medical care to the corresponding patients consume a significant part of the health and national budgets of several South and Southeast Asian countries. This diverts scarce resources from improving medical services in other areas. Illness due to mosquito-borne diseases also reduces economic productivity. Therefore, improved control of dengue and other mosquito-borne diseases, through targeting brackish water larval habitats, is an important consideration for health authorities and governments in the region.

There is a clear need for supporting more research at local, national and international levels into the impact of rising sea levels and climate change on mosquito vector populations in coastal areas of the region. The impact of rising sea levels on the expansion of brackish and saline water bodies along coasts is subject to local geosphere factors, occurs over a timescale of decades and is therefore best studied at local levels. The bionomics of salinity-tolerant mosquito vector populations needs to be investigated in more detail. Present methods of identifying sibling species in malaria vector species complexes based on morphology or karyotyping have proved unreliable and unsuitable for field studies (Surendran et al. 2010). Robust and readily usable methods for differentiating sibling species that differ in salinity tolerance in the field need to be developed for different localities of the region. Mathematical models of disease transmission that take into consideration vector development in brackish water habitats have to be developed. The physiological mechanisms employed by mosquitoes such as *An. culicifacies* and *Ae. aegypti* that were considered to be freshwater species in adapting to brackish water need to be elucidated. Besides furthering knowledge on mosquito biology, this research can lead to the development of specific larvicides that can be used in brackish water habitats.

Therefore, greater attention needs to be devoted to monitoring disease incidence and mosquito vector development in coastal brackish and saline water habitats. Countermeasures to prevent an expansion of such habitats and reduce vector development therein are required. The extension of vector source reduction and management programmes to the brackish water habitats of the *Aedes* vectors of dengue and chikungunya is likely to immediately improve disease control in coastal areas. Pilot studies are needed in dengue-endemic areas to confirm this. Similarly, greater attention to brackish and saline water development of malaria vectors may also be helpful in further reducing malaria transmission in the region. Larval source reduction in defined habitats is effective in controlling dengue (WHO 2009) and malaria in many situations (Fillinger and Lindsay 2011). Managing and eliminating brackish water mosquito vector habitats may assume even greater importance in a future context of global warming, as sea levels rise and increase the extent of such habitats (Ramasamy and Surendran 2011, 2012). In this context, the stability and effectiveness of larvicides that are developed for freshwater use need to be examined in brackish and saline waters (Jude et al. 2012).

Community understanding and action have contributed to minimising freshwater larval development sites of dengue vectors in many disease-endemic countries. It is expected that this can be usefully extended to the brackish water habitats of the vectors. Governments can publicise the importance of brackish water mosquito vectors for transmitting disease through newspapers, radio, television and appropriate websites. This can include, for example, highlighting the additional importance of brackish water habitats of dengue vectors in national dengue awareness campaigns.

It is also important that the many local and national authorities responsible for different concerned sectors, e.g. health, agriculture, coastal planning, environment, irrigation, livestock development, etc., are made aware of the increased risk of mosquito-borne diseases in coastal areas due to rising sea levels, in order to incorporate it into their strategic development plans. Application of appropriate countermeasures can greatly reduce the potential for increased transmission of mosquito-borne diseases in coastal areas of South and Southeast Asia in the context of climate change and a rise in sea levels.

References

Barraud PJ (1934) Diptera Vol V Family Culicidae. Tribes Megarhinini and Culicini. In: Sewell RBS, Edwards PW (eds) The fauna of British India, including Ceylon and Burma. Taylor and Francis, London

Bradley TJ (1987) Physiology of osmoregulation in mosquitoes. Annu Rev Entomol 32:439–462

Cavrini F, Gaiban P, Pierro AM et al (2009) Chikungunya: an emerging and spreading arthropod-borne viral disease. J Infect Dev Ctries 3:744–752

Central Intelligence Agency (2012) The world factbook. Washington, DC, USA

Chan KL, Ho BC, Chan YC (1971) *Aedes aegypti* (L.) and *Aedes albopictus* (Skuse) in Singapore City. Bull World Health Organ 4:629–633

Chun L, Telisinghe PU, Hossain MM et al (2007) Vaccine development against dengue and shigellosis and implications for control of the two diseases in Brunei Darussalam. Brunei Darussalam J Health 2:60–71

Dondorp AM, Yeung S, White L et al (2010) Artemisinin resistance: current status and scenarios for containment. Nat Rev Microbiol 8:272–280

Edwards HA (1982) Free amino acids as regulators of osmotic pressure in aquatic insect larvae. J Exp Biol 101:153–160

Erickson SM, Xi Z, Mayhew GF et al (2009) Mosquito infection responses to developing filarial worms. PLoS Negl Trop Dis 3:e529

Fillinger U, Lindsay SW (2011) Larval source management for malaria control in Africa: myths and reality. Malar J 10:353

Food and Agricultural Organisation (2007) Seawater intrusion in coastal aquifers – guidelines for study, monitoring and control. FAO, Rome

Gunasekaran K, Jambulingam P, Srinivasan R et al (2005) Malaria receptivity in the tsunami-hit coastal villages of southern India. Lancet Infect Dis 5:531–532

Halstead SB (2003) Neutralisation and antibody-dependent enhancement of dengue viruses. Adv Virus Res 60:421–467

Idris FH, Usman A, Surendran SN et al (2013) Detection of *Aedes albopictus* pre-imaginal stages in brackish water habitats in Brunei Darussalam. J Vect Ecol 38:197–199

Intergovernmental Panel on Climate Change (2013) Working group I contribution to the IPCC Fifth Assessment Report Climate Change 2013: the physical science basis. Summary for policymakers. http://www.climatechange2013.org/images/uploads/WGIAR5-PM_Approved27Sep2013.pdf. Accessed 17 Oct 2013

Jude PJ, Dharshini S, Vinobaba M et al (2010) *Anopheles culicifacies* breeding in brackish waters in Sri Lanka and implications for malaria control. Malar J 9:106

Jude PJ, Tharmasegaram T, Sivasubramaniyam G et al (2012) Salinity-tolerant larvae of mosquito vectors in the tropical coast of Jaffna, Sri Lanka and the effect of salinity on the toxicity of *Bacillus thuringiensis* to *Aedes aegypti* larvae. Parasit Vectors 5:269

Kulatilaka TA, Jayakuru WS (1998) Control of dengue/dengue haemorrhagic fever in Sri Lanka. Dengue Bull 22:53–61

La Ruche G, Souares Y, Armengaud A et al (2010) First two autochthonous dengue virus infections in metropolitan France. Euro Surveill 15:19676

McGranahan G, Balk D, Anderson B (2007) The rising tide: assessing the risks of climate change and human settlements in low elevation coastal zones. Environ Urban 19:17

Nicholls RJ, Wong PP, Burkett VR (2007) Coastal systems and low-lying areas. Climate change 2007: impacts, adaptation and vulnerability. In: Parry ML, Canziani OF, Palutikof JP et al (eds) Contribution of working group II to the fourth assessment report of the intergovernmental panel on climate change. Cambridge University Press, Cambridge, pp 315–356

Ooi EE, Goh KT, Gubler DJ (2006) Dengue prevention and 35 years of vector control in Singapore. Emerg Infect Dis 12:887–893

Rajasooriyar LD, Mathavan V, Dharmagunewardene HA et al (2002) Groundwater quality in the Valigamam region of the Jaffna Peninsula, Sri Lanka. In: Hiscock KM, Rivett MO, Davison RM (eds) Sustainable groundwater development. Geological Society, London, pp 181–197, Special publications 193

Rajendram G, Antony NR (1991) Survey of peri-domestic mosquito species of Jaffna peninsula in Sri Lanka. Southeast Asian J Trop Med Public Health 22:637–642

Ramasamy R, Surendran SN (2011) Possible impact of rising sea levels on vector-borne infectious diseases. BMC Infect Dis 11:18. doi:10.1186/1471-2334-11-18

Ramasamy R, Surendran SN (2012) Global climate change and its potential impact on disease transmission by salinity-tolerant mosquito vectors in coastal zones. Front Physiol 3:198

Ramasamy R, Surendran SN (2013) Global environment changes and salinity adaptation in mosquito vectors. Lambert Academic Publishing, Saarbrucken

Ramasamy MS, Sands M, Kay BH et al (1990) Anti-mosquito antibodies reduce the susceptibility of *Aedes aegypti* to arbovirus infection. Med Vet Entomol 4:49–55

Ramasamy R, Surendran SN, Jude PJ et al (2011) Larval development of *Aedes aegypti* and *Aedes albopictus* in peri-urban brackish water and its implications for transmission of arboviral diseases. PLoS Negl Trop Dis 5:e1369

Ramasamy R, Jude PJ, Veluppillai T et al (2014) Biological differences between brackish and fresh water-derived *Aedes aegypti* from two locations in the Jaffna peninsula of Sri Lanka and the implications for arboviral disease transmission. PLoS One 9:e104977

Rezza G (2012) *Aedes albopictus* and the re-emergence of dengue. BMC Public Health 12:72

Rezza G, Nicoletti L, Angelini R et al (2007) Infection with chikungunya virus in Italy: an outbreak in a temperate region. Lancet 370:1840–1846

Sanchez L, Vanlerberghe V, Alfonso L et al (2006) *Aedes aegypti* larval indices and risk of dengue epidemics. Emerg Infect Dis 12:800–806

Sinka ME, Bangs MJ, Manguin S et al (2011) The dominant *Anopheles* vectors of human malaria in the Asia-Pacific region: occurrence data, distribution maps and bionomic précis. Parasit Vectors 4:89

Smith KE, Van Ekeris LA, Okech BA et al (2008) Larval anopheline mosquito recta exhibit a dramatic change in localization patterns of ion transport proteins in response to shifting salinity: a comparison between anopheline and culicine larvae. J Exp Biol 211:3067–3076

Surendran SN, Kannathasan S, Kajatheepan A et al (2007) Chikungunya type fever outbreak: some aspects related to this new epidemic in Jaffna district, northern Sri Lanka. Trop Med Health 35:249–252

Surendran SN, Singh OP, Jude PJ et al (2010) Genetic evidence for malaria vectors of the *Anopheles sundaicus* complex in Sri Lanka with morphological characteristics attributed to *Anopheles subpictus* species B. Malar J 9:343

Surendran SN, Jude PJ, Ramasamy R (2011) Variations in salinity tolerance of malaria vectors of the *Anopheles subpictus* complex in Sri Lanka and the implications for malaria transmission. Parasit Vectors 4:117

Surendran SN, Jude PJ, Thabothiny V et al (2012) Pre-imaginal development of *Aedes aegypti* in brackish and fresh water urban domestic wells in Sri Lanka. J Vector Ecol 37:471–473

United Nations Environment Programme (2007) Global programme of action for the protection of the marine environment from land-based activities: physical alteration and destruction of habitats. UNEP, Nairobi. http://gpa.unep.org/content.html?id=199&ln=6. Accessed 15 Jun 2010

Walter Reed Biosystematics Unit (2013) Keys to medically important mosquito species. Smithsonian Institution, Silver Spring, http://wrbu.org/command_aors_MQ.html. Accessed 26 Dec 2013

Weaver SC, Reisen WK (2010) Present and future arboviral threats. Antiviral Res 85:328–345

World Health Organization (2009) Dengue guidelines for diagnosis, treatment, prevention and control. http://www.whqlibdoc.who.int/publications/2009/9789241547871_eng.pdf. Accessed 13 Jun 2013

World Health Organisation (2012) http://www.searo.who.int and http://www.wpro.who.int. Accessed 15 May 2012

World Health Organisation (2013a) Fact sheet No 100. Yellow fever. WHO, Geneva, http://www.who.int/mediacentre/factsheets/fs100/en/. Accessed 26 Dec 2013

World Health Organisation (2013b) World malaria report 2012. http://www.who.int/malaria/publications/world_malaria_report_2013/report/en/. Accessed 27 Feb 2014

World Health Organization (2013c) Fact sheet No. 117 – Dengue and severe dengue. http://www.who.int/mediacentre/factsheets/fs117/en/. Accessed 26 Jan 2014

Chapter 9
The Malaria Landscape: Mosquitoes, Transmission, Landscape, Insecticide Resistance, and Integrated Control in Thailand

Hans J. Overgaard, Wannapa Suwonkerd, and Jeffrey Hii

Abstract This chapter presents results on the effect of land use on malaria vector density, species diversity, and insecticide resistance in northern Thailand. Entomological data from 1977 to 1999 was analysed to understand spatio-temporal variations in vector density and potential effects on malaria transmission. Landscape analysis can potentially be used as a tool in vector control strategy development, particularly to understand local vector behaviour and habitat characteristics for stratification of vector control areas. Our results show that an increase in landscape diversity, particularly forest fragmentation, reduces malaria vector diversity and density. Such land use changes in non-malaria transmission areas were the potential cause for reductions in malaria mosquito densities. Similar land use changes were not observed in areas with permanent malaria transmission. The landscape analysis further shows that agricultural intensification increases the likelihood of insecticide resistance development in malaria mosquitoes. We therefore argue for intersectoral collaboration, especially between the public health and agricultural sectors, to develop and implement integrated insecticide resistance

---

H.J. Overgaard (✉)
Department of Mathematical and Technological Sciences, Norwegian University of Life Sciences, Ås, Norway

Institut de Recherche pour le Développement (IRD), Maladies Infectieuses et Vecteurs, Ecologie, Génétique, Evolution et Contrôle (IRD 224-CNRS 5290 UM1-UM2), Montpellier Cedex 5, France

Department of Entomology, Kasetsart University, Bangkok, Thailand
e-mail: hans.overgaard@nmbu.no

W. Suwonkerd
Office of Disease Prevention and Control #10, Ministry of Public Health, 50200 Chiang Mai, Thailand

J. Hii
School of Public Health, Tropical Medicine and Rehabilitative Sciences, James Cook University, 4811 Townsville, QLD, Australia

Malaria Consortium Asia, Mahidol University, 420/6 Rajavidhi Road, Bangkok 10400, Thailand

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_9

management plans and integrated control. Integration of pest and vector control strategies should build on the integrated pest and vector management (IPVM) strategies described in this chapter. Such a strategy should be implemented through the Farmer Field School approach. For future research topics we suggest studies on the bionomics of the sibling species of the malaria vectors in the region to more effectively implement vector control actions. Furthermore, the effect of IPVM strategies on vector populations and disease outcome should be evaluated through large-scale trials.

9.1 Introduction

Malaria in Thailand occurs in forested regions, along the borders of the country, where it is transmitted by forest-associated malaria vectors of the *Anopheles minimus*, *An. dirus*, and *An. maculatus* species groups. Malaria has decreased drastically in Thailand during the last 60 years. During this time, Thailand has undergone large changes in terms of socioeconomical development, including improved access to health services. Large changes in land use have also occurred, e.g. deforestation and agricultural intensification. Such land use changes may cause changes in distribution patterns of the malaria vectors. This chapter is a summary of research that we carried out using data from the late 1970s up to 2005 in northern Thailand. In Sect. 9.2 we give an overview of malaria in Thailand. The taxonomy of the malaria mosquito fauna in Southeast Asia is complicated. There are many morphologically indistinguishable species, large species complexes, and groups. In Sect. 9.3 we briefly describe the current status of malaria mosquito taxonomy relevant for Thailand. Thereafter, in Sect. 9.4, we assess the effect of landscape structure, i.e. land use composition and configuration, on malaria mosquito density and diversity. As the structure of a landscape may, indeed, affect malaria mosquitoes, we further compare variations in mosquito density in transmission and non-transmission areas in order to evaluate the influence of landscapes on malaria transmission (Sect. 9.5). The landscape analyses also show that mosquito densities are lower in landscapes with a high proportion of insecticide-intensive land uses. This prompted us to assess if mosquitoes (survivors) collected in such insecticide-intensive land use systems have a higher degree of resistance to agricultural insecticides than mosquitoes collected in land uses with less insecticide inputs (Sect. 9.6). The fact that insecticide resistance in malaria mosquitoes is affected by agriculture, in addition to public health insecticides, suggests that the public health and agricultural sectors could collaborate for effective control of both malaria mosquitoes and agricultural pests. Such integrated pest and vector management options are discussed in Sect. 9.7.

9.2 Malaria in Thailand

The malaria landscape particular for Thailand and many other Southeast Asian countries is commonly identified as forested or forest-fringe regions along national borders, where malaria is transmitted by forest-associated malaria vectors (Sharma and Kondrashin 1991; Chareonviriyaphap et al. 2000). In this sense malaria transmission is unique compared to other malaria-endemic areas around the globe. For example, there are many confirmed and potential malaria vectors. Anopheline taxonomy is complicated by difficulties for morphologic identification because of many species complexes and groups. Malaria disproportionately affects vulnerable populations such as migrants, forest workers, border rangers, miners, ethnic minorities, soldiers, etc. In Thailand, it is estimated that more than half of all malaria cases occur among the non-Thai people (Konchom et al. 2003). Malaria transmission in Thailand also occurs along the southern border to Malaysia, where civil unrest during recent years has inhibited effective malaria control.

The incidence of malaria in 1947 was about 286 per 1,000 and mortality was 351 per 100,000 population (Malikul 1988). In 1984 the malaria incidence had decreased to about 6 per 1,000 and mortality to 1.7 in 1997 (Malaria Division 1998). In 2009 the number of reported malaria cases was 22,844 (0.41/1,000 population), and in 2012 there were 27,744 cases (0.39/1,000 population) (Bureau of Vector Borne Disease 2013) (Fig. 9.1). In Thailand it is estimated that about 5.6 million people

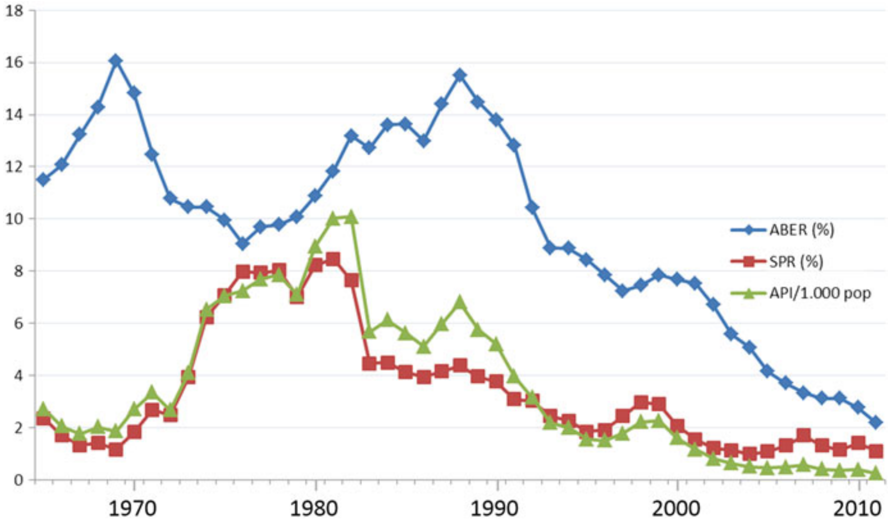


Fig. 9.1 Malaria incidence in Thailand: annual parasite incidence per 1,000 population (API), annual blood examination rate (ABER %), and slide positivity rate (%) (SPR) from 1965 to 2011 (Bureau of Vector Borne Disease 2013)

(8 % of the Thai population) live in areas with >1 case per 1,000 population (high transmission) and 29.2 million people (42 %) live in areas with <1 cases per 1,000 population (low transmission) (WHO 2013). The rest, about 50 %, live in malaria-free areas. Malaria is still considered a problem in about 22 provinces along the border areas to Myanmar, Cambodia, Malaysia, and Laos. The major problems to control malaria in Thailand today are multidrug resistance, emergence of *Plasmodium falciparum* resistance to artemisinins along the Thai-Cambodian border, exophilic behaviour of malaria vectors, insecticide resistance, and migration of people for social, economic, and political reasons (WHO 2010; Satimai et al. 2012).

It is interesting to note that the malaria decline in Thailand based on reports 60–70 years ago until today coincides with large historical land use changes. In fact, it has been suggested that the reduction of malaria could have been as much an effect of deforestation as of malaria control efforts (Rosenberg et al. 1990). Deforestation and environmental change can reduce availability of breeding habitats, thus affecting mosquito propagation of anopheline species that breed in shaded water bodies, such as many of the malaria vectors in Southeast Asia (Yasuoka and Levins 2007). We have shown that land use change and encroachment of fruit orchards into forest areas reduced the mosquito fauna (Overgaard et al. 2003; Suwonkerd et al. 2002).

In 1938 it was estimated that the forest cover in Thailand was approximately 70 % of the country's total land area (Elkington and Ingkasuwan 1988). In 1995 the forest cover had been reduced to 23 % (FAO 1999). In an assessment for the year 2000 for the Greater Mekong Subregion (Myanmar, Thailand, Laos, Kampuchea, and Vietnam), the total forest area was estimated at ca. 75 million ha or 39 % of the total land area; in Thailand the estimate was 14.3 million ha or 28 % of the country's land area (Stibig et al. 2007). Southeast Asia has the highest relative rate of deforestation of any major tropical region in the world and could deplete three quarters of its native forest cover by 2100, effectively removing up to 42 % of its fauna and flora biodiversity (Sodhi et al. 2004).

Forest resources have contributed to the rapid economic development of Thailand in terms of export and wood and other forest resources. In some areas the livelihood of people is still dependent on forests. People use forests for hunting and collecting edible and medicinal plants and wood for housing and cooking. Forests also retain soil nutrients in the traditional shifting cultivation systems of numerous ethnic groups in the uplands. Forests are important for soil and watershed protection, agricultural productivity, and conservation of biodiversity. The main reasons for the loss of forests are over-exploitation of forest resources by national and international enterprises for timber, agricultural expansion, and conversion to intensive cash crop farming, such as rubber, fruits, sugar cane, cassava, etc. (Stibig et al. 2007). Forest degradation is caused by unsustainable and illegal logging. Deciduous forests are also threatened by forest fires that are common for land clearing, cattle grazing, and hunting (Rundel and Boonpragob 1995). The accelerated economic development of Thailand has affected human settlement and migration patterns leading to increased pressure on land resources and changes in rural economic structures (Singhanetra-Renard 1993).

9.3 Malaria Vectors in Thailand

There are approximately 74 species of the genus *Anopheles* reported from Thailand (Harrison 1980; Walter Reed Biosystematics Unit 2012; Tainchum et al. 2015). However, only six species are officially recognized as malaria vectors (WHO 2011). They comprise members of the Dirus and Minimus complexes and Maculatus and Barbirostris groups. The primary vectors are *An. dirus*, *An. baimaii*, *An. minimus*, and *An. maculatus*, while *An. aconitus*, *An. pseudowillmori*, and *An. epiroticus* are considered as secondary vectors, based on the recovery of sporozoites from salivary glands and their geographic distribution (Saeung 2012). *An. barbirostris/campestris* group is considered as potential vectors that play an important role in increased *P. vivax* transmission (Saeung 2012). All these complexes or groups are often not possible to distinguish morphologically from one another (Rattanarithikul and Panthusiri 1994) and have thus depended on techniques such as chromosomal analysis (Baimai et al. 1984; Baimai 1988), allozyme typing (Green et al. 1992), and allele-specific polymerase chain reaction (AS-PCR) techniques (Walton et al. 1999) for species identification. The vectorial capacity of the sibling species often varies, affected by behaviour and geographical distribution, thus resulting in different abilities to transmit malaria in different areas of the country.

9.3.1 Dirus Complex

This species complex is represented by five species in Thailand. Currently they are *An. dirus* s.s. (formerly *An. dirus* sp. A), *An. cracens* (*An. dirus* sp. B), *An. scanloni* (*An. dirus* sp. C), and *An. baimaii* (*An. dirus* sp. D) and *An. nemophilous* (*An. dirus* sp. F). Because of taxonomic confusions, they were all previously regarded as *An. dirus* s.l. with sporozoite rates of up to 10 % (Peyton 1989; Sallum et al. 2005; Tainchum et al. 2015). Two members, *An. baimaii* and *An. dirus* s.s., are considered to be among the more important primary malaria vectors in Thailand (Rattanarithikul et al. 2006; Manguin et al. 2008a, b) because of their endophagic and anthropophilic behaviour. *Anopheles dirus* s.s. occurs mainly in the eastern part of Thailand through Laos, Cambodia and Vietnam (south of the Red River), while *An. baimaii* spreads predominantly to the west of Thailand through Myanmar and southern China (Hunan) (Obsomer et al. 2007; Sallum et al. 2005).

Species of the Dirus complex inhabit forested mountains and foothills, cultivated forests, rubber plantations, and forest fringes. Typical larval habitats include small, shallow, usually temporary, mostly shaded bodies of fresh, stagnant water, such as pools, puddles, small gem pits, animal footprints, wheel ruts, hollow logs, streams, and wells (Sinka et al. 2011). Water habitats can be clear or turbid with nitrogenous waste, due to animal excreta or rotten leaves. These species are most abundant during the rainy (monsoon) season (Rattanarithikul et al. 2006; Sinka et al. 2011).

9.3.2 Funestus Group

Minimus Complex This complex comprises of three species, namely, *An. minimus* s.s. Theobald (formerly *An. minimus* A), *An. harrisoni* Harbach and Manguin (*An. minimus* C), and *An. yaeyamaensis* Somboon and Harbach (*An. minimus* species E) (Harbach et al. 2006, 2007; Sinka et al. 2011), with only the first two species known to occur in Thailand. *An. minimus* s.s. occurs throughout the country and southward to the Thai-Malay peninsula (Manguin et al. 2008b), while *An. harrisoni* is confined to the western and northern subregions, including Tak, Chiang Mai, and Kanchaburi provinces (Rattanarithikul et al. 2006; Tainchum et al. 2015). Vectorial status is uncertain, although *An. minimus* s.s. seems to be a more efficient malaria vector than *An. harrisoni* (Trung et al. 2004; Garros et al. 2005). Both species have been reported to be sympatric in mainland Asia (Garros et al. 2006, 2008; Manguin et al. 2008b), in northern Vietnam (Van Bortel et al. 1999; Trung et al. 2005), and in Kanchanaburi Province, western Thailand (Sungvornyothin et al. 2006). Misidentification of *An. minimus* s.s. is problematic for public health personnel conducting vector control due to the high morphological variability and habitat similarities with other members of the Myzomyia series, particularly in the Aconitus subgroup (*An. aconitus* Dönitz, *An. pampanai* Buttiker and Beales, and *An. varuna* Iyengar).

Anopheles minimus s.l. immatures occur principally in stream pools and stream margins, with cool unpolluted water with partial shade and grassy margins (Muirhead Thompson 1940a, b; Overgaard et al. 2002). In northern Vietnam and western Thailand, *An. minimus* habitats vary from dense canopy forest to open agricultural fields, particularly traditional rice agroecosystems. Using remote sensing geographical information systems (GIS) and Landsat satellite data, Rongnoparut et al. (2005) showed that *An. minimus* s.s. has a wide habitat preference, from dense canopy forest to open agricultural fields, while *An. minimus* C has a narrow habitat preference. In the Thai-Myanmar border area, light forests were defined as areas covered by trees that are accessible to people. Multivariate analysis revealed that light forest cover was a significant factor only for *P. falciparum* and the mean distance from an individual house to a stream was about 200 m with a range of 200–500 m (Lawpoolsri et al. 2010). This relatively small variation suggests that vector abundance is similar among houses. The risk of *P. falciparum* malaria attack among people in a hamlet increased by 1.03 for every 1% increase in the hamlet's light forest cover, but this association is uncertain due to the limited number of landscape data for comparison at hamlet level (Lawpoolsri et al. 2010).

Aconitus Subgroup This subgroup is represented in Thailand by *An. aconitus* Dönitz, *An. pampanai* Buttiker and Beales, and *An. varuna* Iyengar (Tainchum et al. 2015), and immatures have been collected from groundwater habitats near foothills and forest fringe areas similar to those of *An. minimus* (Rattanarithikul et al. 2006).

9.3.3 Maculatus Group

This group includes three subgroups with a total of eight species which are found in Thailand, i.e. *An. maculatus* s.s. Theobald (Form B), *An. sawadwongporni* Rattanarithikul and Green (Form A), *An. dravidicus* Christophers (formerly Form C), *An. notanandai* Rattanarithikul and Green (Form G), *An. pseudowillmori* (Theobald) (Form I), *An. willmori* (James) (Form H) (Saeung 2012), *An. maculatus* Form E, and *An. maculatus* Form K (Hii and Rueda 2013). Recently *An. maculatus K* was formally named *An.* (*Cellia*) *rampae* Harbach & Somboon (Somboon et al. 2011). *Anopheles maculatus* s.s. occurs in six regions in Thailand, whereas *An. sawadwongporni* is recorded in the north-eastern and southern regions, and *An. maculatus* Form E is found throughout the peninsular region (Rattanarithikul et al. 2006; Saeung 2012). *Anopheles maculatus* and *An. pseudowillmori* were incriminated as primary and secondary vectors of malaria in the southern and western regions, respectively, while *An. sawadwongporni* is regarded as a suspected malaria vector (Green et al. 1991; Saeung 2012).

Species in the Maculatus group are found in or near hilly forested zones and in rubber plantation areas where the larvae occur in shaded puddles in drying streams and other temporary habitats such as rock pools, drying streams, etc. (Rattanarithikul et al. 1995; Chareonviriyaphap et al. 2000; Jaichapor et al. 2005).

9.3.4 Barbirostris Group

The Barbirostris subgroup of this group includes five species: *An. barbirostris* van der Wulp s.l., *An. campestris* Reid, *An. donaldi* Reid, *An. hodgkini* Reid, and *An. pollicaris* Reid (Saeung et al. 2007, 2008; Saeung 2012; Rattanarithikul et al. 2006; Walter Reed Biosystematics Unit 2012). *Anopheles barbirostris* and *An. campestris* are the most common species of this group, and they are closely associated with humans. Larvae are usually found in rice fields, stagnant ditches, earthen wells, swamps, canals, and other groundwater habitats (Reid 1962; Rattanarithikul et al. 1994). *Anopheles campestris* and *An. donaldi* are considered vectors of malarial parasites in Thailand, and both malarial parasites and filarial worms in other non-Greater Mekong Subregion (GMS) countries (Rattanarithikul et al. 2006; Walter Reed Biosystematics Unit 2012). The capture of an oocyst-positive specimen of *An. barbirostris/campestris* in the prolonged absence of the dominant vector species (Sinka et al. 2011) highlighted the role of *An. barbirostris* s.l., an outdoor biting vector, in maintaining malaria transmission in Sae Kaeo province (Limrat et al. 2001; Apiwathnasorn et al. 2002) and in Kanchanburi province (Green et al. 1991). *Anopheles campestris* and *An. hodgkini* were naturally infected with sporozoites (Coleman et al. 2002), suggesting their potential roles of secondary vectors in habitats experiencing land use and environmental changes in Thailand.

9.3.5 Sundaicus Complex

This complex is represented by *An. epiroticus* (*sundaicus* A) based on morphological cytological, isoenzyme and molecular markers (Linton et al. 2001, 2005) and is considered a secondary vector in coastal areas of eastern and southern Thailand (Saeung 2012; Ritthison et al. 2014). Larvae of *An. epiroticus* are typically found in sunlit brackish pools containing algae as well as freshwater pools (Rattanarithikul et al. 2006).

9.4 Effect of Landscape Structure on Malaria Vector Density and Diversity

By linking mosquito vector population dynamics with spatial and temporal habitat quality, it might be possible to make predictions about how landscapes affect the production and density of disease vectors. In agriculture this has been long acknowledged for assessing severity of pest attack (Gould and Stinner 1984; Ekbom 2000). The location of mosquito breeding sites, blood and nectar sources, resting places, and variations in the landscape between these sources likely influence mosquito movement and spatial distribution. Such variations in the landscape can be quantified by landscape structure analysis. Landscape structure is the pattern of a landscape and consists of landscape composition and configuration (Turner 1989; Turner and Gardner 1990; Dunning et al. 1992). Landscape composition is the presence and proportion of different land uses and landscape elements or habitat patches. Landscape configuration is the spatial arrangements of those elements. Landscape structure is quantified by various metrics, such as landscape diversity, percentage of specific land use covers, mean patch size, fractal dimensions, etc.

We used data from six landscapes, three predominantly agricultural landscapes and three forested landscapes (Fig. 9.2), to assess if landscape structure could be used to explain anopheline density (particularly *An. minimus*, *An. maculatus*, and *An. aconitus*) and diversity (Overgaard et al. 2003). Based on previous observations (Scanlon and Sandhinand 1965; Rosenberg et al. 1990; Kondrashin et al. 1991), it was hypothesized that malaria mosquito density would be lower in more developed, urbanized locations with a high landscape diversity than in less developed forest locations with a low landscape diversity. Adult malaria mosquitoes were collected by monthly outdoor human landing catches during the wet and dry seasons from October 1997 to December 1999. The number of collection months per location varied from 12 to 21. Landscape and land use class metrics were calculated for each landscape using the spatial statistical software FRAGSTATS*ARC (McGarigal and Marks 1995).

The agricultural locations had significantly higher landscape diversity, more patches, smaller mean patch sizes, and more complex patch shapes than the forest locations. Both adult malaria mosquito density and diversity were lower in landscapes with high landscape diversity, low forest cover, and high agricultural and

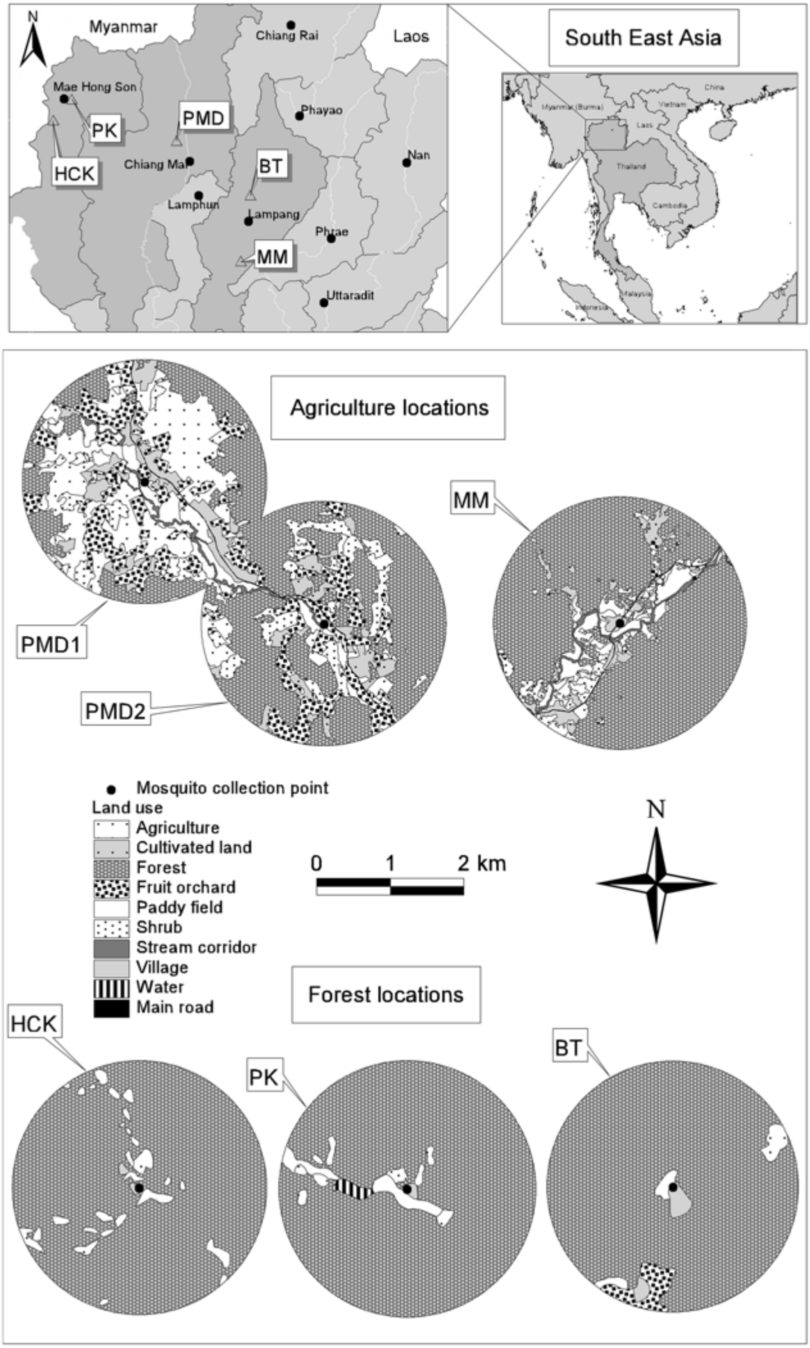


Fig. 9.2 Land use maps of six landscapes in northern Thailand. Pang Mai Daeng village (*PMD1* and *PMD2*), Chiang Mai Province; Mae Mok village (*MM*), Lampang Province; Ban Tae village (*BT*), Lampang Province; Huay Chang Kham village (*HCK*), Mae Hong Son Province, and Pakkolo village (*PK*), Mae Hong Son Province (Overgaard et al. 2003)

fruit orchard cover. In contrast, Vanwambeke et al. (2007a) showed that sites located in the most diverse landscapes, as indicated by the modified Simpson index >1.2, had a fivefold higher chance of harbouring *An. minimus* larvae than those with the least diverse landscape, but the association with malaria transmission was inconclusive. Forest fragmentation, resulting from human economic activities, increases landscape heterogeneity. Specifically, anopheline species diversity was negatively related to landscape diversity (Fig. 9.3). *Anopheles minimus* s.l. was the most abundant mosquito species. The densities of *An. minimus* s.l. and *An. maculatus* s.l. were both significantly higher in the forest locations in at least one season. The density of *An. minimus* s.l. was positively related to forest mean patch size, percentage of several water, and paddy field landscape metrics and negatively related to landscape diversity.

Both fruit orchard cover and agricultural cover appeared to affect anopheline species density and diversity. The generally observed pattern was that landscapes with large fruit orchard patch sizes seemed to be associated with low *An. minimus* s.l. density and low malaria mosquito diversity. This result could be explained by the intensively managed fruit cropping systems in northern Thailand, where particularly tangerine pest management is highly dependent on insecticide pest control (Chalermphol and Shivakoti 2009). Malaria vectors are likely affected negatively by these insecticides resulting in reduced abundance of both larvae and adults. In northern Thailand, Vanwambeke et al. (2007a) showed that turbid and temporary water and the presence of algae and excrement decreased the probability of finding *An. minimus* s.l. larvae. Similar effects were observed in northern Vietnam where

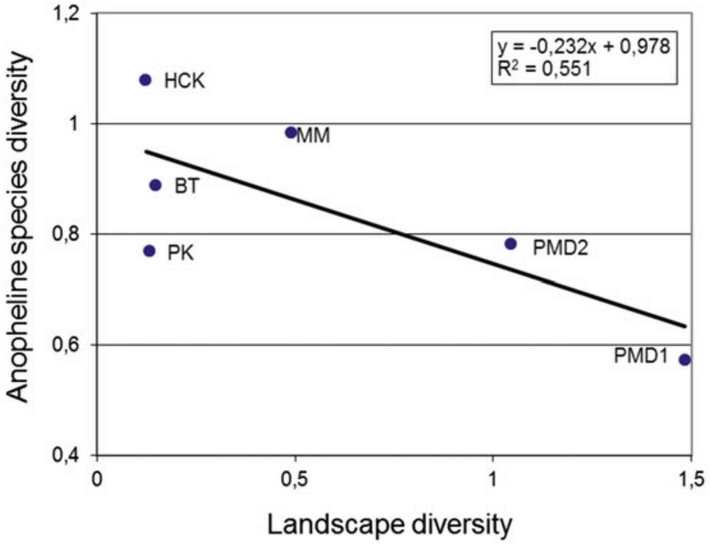


Fig. 9.3 Relationship between anopheline species diversity (Shannon-Weaver diversity index) and landscape diversity (modified Simpson's diversity index) in six landscapes in northern Thailand (See Fig. 9.1 for landscape acronyms) (Overgaard et al. 2003)

recent agricultural development linked to modified irrigation might have disturbed mosquito habitats causing low density of *An. minimus* s.l. (only three specimens) (Garros et al. 2008). Human economic activities often increase landscape heterogeneity, and application of pesticides in the dry season may result in a reduction of anopheline species diversity and density (Overgaard et al. 2003).

The conversion of forests to fruit orchards, a major land use change in northern Thailand, was promoted during the late 1990s by the Thai government (Ampunpong 1996; Chalermphol and Shivakoti 2009). Results from landscape analyses, as carried out here, can point to the importance of the quality of a landscape for sustaining anopheline presence. Landscape analysis can be used to predict changes in anopheline fauna as response to landscape changes and may inform on potential landscape management strategies for suppressing disease vector populations. The results presented here show that the vector status in northern Thailand is complex and that vector and agriculture pest control are intricately interrelated. It is therefore important to include both the public health and agricultural sectors in controlling malaria vectors in the country.

9.5 Spatio-temporal Variations in Vector Density: Effects on Malaria Transmission

Environmental heterogeneity in time and space may have an impact on several aspects of mosquito vector biology and ecology. Adaptation to environmental variations may cause for selection of insect behaviour and physiology. For example, differences in host preference (Nuthsathapana et al. 1986a) and susceptibility to insecticides (Nuthsathapana et al. 1986b; McKenzie 1996; Chareonviriyaphap et al. 1999) have been observed, potentially caused by environmental change and variation. Chiang Mai Province in northern Thailand displays a large variation in terms of ecology, land use, topography, human population density, and social and economic development. The highest mountain of Thailand, Doi Inthanon, is located in Chiang Mai Province, and the province is a popular tourist destination. The pace of urbanization and general development, particularly in and around the largest city Chiang Mai, is rapid and causes large disparities with other areas of the province.

Analysis of mosquito data from the last two decades of the twentieth century in neighbouring Mae Hong Son Province indicated that the densities of the main malaria vectors were stable or increasing (Suwonkerd et al. 2004). Every year Mae Hong Son Province is one of the top five provinces in terms of number of malaria cases (Childs et al. 2006; Congpuon et al. 2011), and the high mosquito densities are one probable factor contributing to this (Suwonkerd et al. 2004). Malaria in Chiang Mai Province, on the other hand, is not as pronounced. The annual parasite incidence per 1,000 population in Chiang Mai was 1.11 and 1.08 in 2003 and 2004, respectively, whereas in Mae Hong Son the corresponding numbers were 14.20 and 10.04 (Suwonkerd et al. 2010). In 2010–2011 the annual malaria incidence per 1,000 population in Chiang Mai was less than 1/1,000 population, but it increased to 1.4 in 2012. In Mae Hong Son, this incidence was 5.4 in 2010, 7.1 in 2011, and 14.7 in 2012 (ODPC 2012). Chiang Mai is more populated and developed and environmentally and geographically more heterogeneous compared to Mae Hong Son. This means that there is a larger variation in landscape diversity and forests are more fragmented. As discussed above, malaria mosquitoes are affected by landscape diversity and fragmentation.

To understand the spatial and temporal patterns in vector density and their potential roles in malaria transmission, we analysed long-term mosquito collection data from the Ministry of Public Health in Chiang Mai Province (Suwonkerd et al. 2002). The available data were from indoor and outdoor human bait collections and cow-baited collections from 1977 to 1999. The data were separated into two time periods, 1977–1989 and 1990–1999, and into transmission areas (TA) and non-transmission areas (NTA). Aerial photos and satellite images were used to analyse changes in land use during the same periods.

Malaria control and vector management in Thailand is based on area stratification. Therefore, the country is divided into different areas based on malaria transmission and vector presence (Malaria Division 1993). The different strata are (A) control area with transmission (TA), (B) control area without transmission (NTA), (C) pre-integration areas, and (D) integration areas. The control area with transmission is divided into perennial transmission areas (A1), where transmission occurs >6 months per year, and periodic transmission areas (A2), where transmission occurs <6 months per year. The control area without transmission is divided into high-risk non-transmission areas (B1), where no transmission has been observed for at least 3 years and where primary malaria vectors are present, and low-risk non-transmission areas (B2), where no transmission has taken place for at least 3 consecutive years and only suspected vectors are present. In this study, 25 subdistricts were selected as representative for the transmission area and one subdistrict as representative of non-transmission areas. The reason for this large difference in number of subdistricts is that mosquito surveillance has been prioritized in transmission areas and only one subdistrict in the non-transmission area had sufficient entomological data to be analysed.

We hypothesized that the densities of the main malaria vectors would be consistently higher in transmission areas than in non-transmission areas. We also hypothesized that during the study period, mosquito densities would be stable or increase in the transmission areas, as observed in Mae Hong Son (Suwonkerd et al. 2004), and that they would decrease in non-transmission areas. We further assumed that a decrease in vector density in non-transmission areas might be explained by an increase in landscape diversity (Overgaard et al. 2003). Available data on changes in landscape structure in the non-transmission area allowed us to explore if landscape change might have had an impact on vector densities. Landscape changes in transmission areas were also investigated.

There were a total of 27 different anophelines collected during the study period. The three most abundant malaria mosquito species collected were *An. minimus* s.l., *An. maculatus* s.l., and *An. dirus*. During the whole study period, *An. dirus* was mainly collected on human bait, but its density was generally very low; therefore, no significant trends could be seen for this species. For *An. minimus* s.l. on the other hand, there was no significant difference in indoor mosquito density between NTA and TA areas for both periods combined.

However, there were significantly more *An. minimus* s.l. mosquitoes collected in the second period (1990s) compared to the first period (1980s) in the TA, whereas the opposite was observed in the NTA. This suggests that the environmental conditions in the TA were favourable for mosquito propagation and collection. In the NTA, on the contrary, mosquito density significantly decreased from the first to the second period. Land use change between the two periods was greater in NTA than in TA, i.e. landscape diversity, forest fragmentation, cover of agriculture and fruit orchards increased, and stream corridor area decreased (Fig. 9.4). In the TA the forest cover remained around 80 % during both periods.

The overall results suggest that land use changes were responsible for changes in malaria mosquito densities, which, in turn, were responsible for the observed differences in malaria transmission. However, other important factors such as malaria control activities, human movement and behaviour, and socioeconomic conditions also influence malaria transmission (Singhanetra-Renard 1986; Singhasivanon 1999; Vanwambeke et al. 2007b). The exact effect of land use change on mosquito populations and disease transmission cannot be easily predicted without local-scale contextual information.

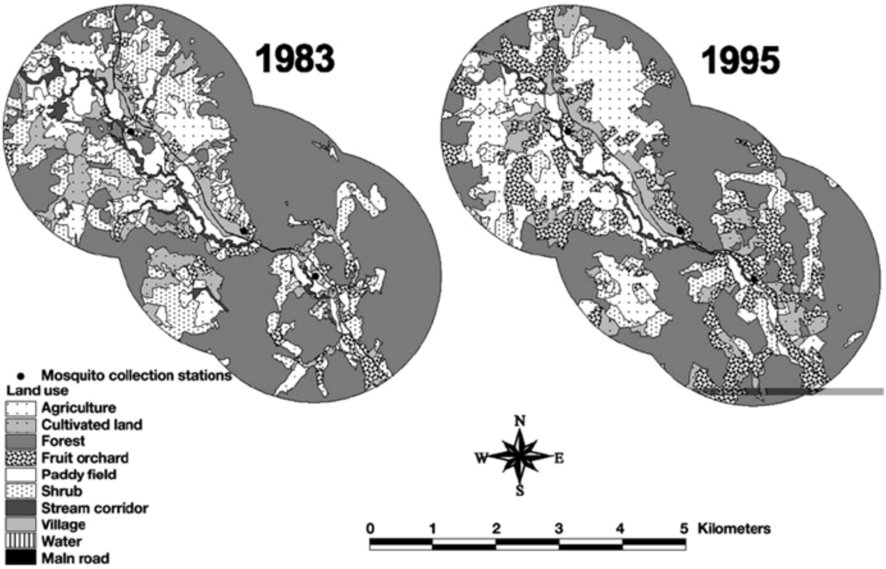


Fig. 9.4 Land use change between 1983 and 1995 in Pang Mai Daeng village (non-transmission area), Chiang Mai Province, northern Thailand (Suwonkerd et al. 2002)

9.6 Land Use and Insecticide Resistance in Mosquito Vectors

Insecticide resistance in mosquito vectors is a serious threat to vector-borne disease control (Hemingway and Ranson 2000; Ranson et al. 2011). Evolution of insecticide resistance in an insect population arises when there is an increase in the frequency of one or more resistance genes in the population following exposure to insecticides. The dynamics of resistance development in mosquito vectors is complex and varies from species to species and from area to area. However, the fundamental requirements for an insect population to develop resistance are exposure to insecticides and intrinsic genetic variation in susceptibility to insecticides. Natural selection and genetic drift act on the inherent genetic variation in the population that is created by mutation, genetic recombination, and gene flow.

The main methods to control malaria mosquitoes are chemical based, e.g. indoor residual spraying (IRS) and insecticide-treated nets (ITN), or long-lasting insecticide-treated nets (LLINs). In Thailand the main malaria vector control methods have been IRS with DDT. However, in 1995 DDT was banned and gradually replaced by pyrethroids. At the beginning deltamethrin was used for IRS and permethrin for treated bed nets (Chareonviriyaphap et al. 2004). Fenitrothion was mainly used in some particular areas and in the areas along the Thai-Cambodia border during 1982–1987 (Suwonkerd et al. 1990). Wide-scale use of permethrin-treated bed nets (0.3 g./sq.m) was initiated in 1997 (Chareonviriyaphap et al. 1999). After the partial integration programme was implemented in 2003 (also for other vector-borne disease control), the bed net coverage was 91–97 % in Mae Hong Son and 89–98 % in Chiang Mai, and households having at least one net were higher in Mae Hong Son (95.3 %) than Chiang Mai (52.2 %) (Suwonkerd et al. 2010). The available insecticides used to control malaria mosquitoes are increasingly becoming less effective due to resistance development in mosquito populations (Van Bortel et al. 2008; Ranson et al. 2011). However, the malaria vectors in Thailand are still susceptible to various kinds of insecticides (Chareonviriyaphap et al. 1999; Somboon et al. 2003), although *An. maculatus* s.s. was found resistant to the agrochemical methyl parathion (Overgaard et al. 2005); *An. minimus* and *An. harrisoni* showed avoidance behaviour to agrochemicals (carbaryl, malathion, cypermethrin) (Pothikasikorn et al. 2007); and *An. maculatus* and *An. sawadwongporni* avoided DDT and permethrin (Muenworn et al. 2006).

As have been discussed above, landscape structure acts as a determinant of the distribution of malaria vectors (Suwonkerd et al. 2002; Overgaard et al. 2003). The land use cover of fruit orchards and agriculture appears to affect both anopheline species density and diversity. Fruit orchards were associated with fewer mosquitoes and lower anopheline diversity, potentially caused by high agricultural pesticide input in fruit orchards (Overgaard et al. 2003; Chalermphol and Shivakoti 2009). Approximately 90 % of all insecticides worldwide are used for agricultural purposes (WHO 1996). This intensive use of insecticides in agriculture has caused concern for increased selection pressure for insecticide resistance development in disease vectors. Several studies suggest that insecticide-intensive agriculture is an important cause for insecticide resistance development in malaria vectors (Georghiou et al. 1972; Chapin and Wasserstrom 1981; Brogdon et al. 1988; Diabate et al. 2002; Fane et al. 2012; Yadouleton et al. 2011).

In a small study from northern Thailand, we found that malaria vectors collected in insecticide-intensive fruit orchards were less susceptible to insecticides than those collected in fruit orchards with low insecticide input (Overgaard et al. 2005). The malaria vector control activities were the same in both areas, ruling out the possibility that mosquitoes were affected by public health insecticides. In summary, mortality of the progeny of *Anopheles maculatus* s.s. collected in the high-insecticide-input area and subjected to discriminating doses of the agricultural insecticide methyl parathion was 74 %. The progeny of same species collected from the low-insecticide-input area subjected to the same concentration of methyl parathion had a mortality of 92 %. Also for *An. sawadwongporni* a similar pattern was found, 94 % mortality in the high-input area and 99 % in the low-input area. Unfortunately, it was not possible to collect a sufficient number of *An. minimus*, the main vector in the area, for susceptibility tests. The lethal times (LT_{50} and LT_{90}) of *An. maculatus* s.s. were significantly higher in mosquitoes collected from the high-insecticide-input area than in those collected in the low-input area ($p < 0.05$) (Table 9.1). There was no indication of resistance to cypermethrin to either of the species tested. The study concluded that reduced susceptibility of malaria mosquitoes in this area was caused by intensive agricultural pest control and not by vector control activities. Further, mosquitoes were still susceptible to pyrethroids; therefore, this resistance did not pose a direct threat to malaria vector control activities; however, increased use of pyrethroids in agriculture may compromise future malaria vector control.

Table 9.1 Lethal times (in minutes) producing 50 % (LT50) and 90 % (LT90) mortalities and lethal time ratios (LTR) with 95 % confidence intervals (in parenthesis) for *An. maculatus* s.s. subjected to diagnostic doses of methyl parathion. Mosquitoes were collected from a fruit orchard with high insecticide use, Muang Na village (HIGH), and a fruit orchard with low insecticide use, Huay Mae Kiang village (LOW) in Chiang Mai Province, northern Thailand (Overgaard et al. 2005)

Lethal time	HIGH	LOW	LTR[a]
LT_{50}	14.4 (11.2–18.1)	13.1 (12.5–13.8)	1.096 (1.007–1.193)
LT_{90}	25.5 (20.0–39.1)	19.3 (18.2–20.7)	1.321 (1.180–1.478)

[a] If LTR confidence limits do not include 1, there is a significant difference in response between the two populations at the 0.05 level

9.7 Integrated Pest and Vector Management

The fact that agricultural insecticides affect insecticide resistance in malaria mosquitoes suggests that, in some areas, it may be advantageous for the agricultural and public health sectors to collaborate. Joint planning of integrated insecticide resistance management and development of alternative vector and pest control strategies could be advantageous for reducing resistance development. The first step would be to identify such areas where there is a risk for high insecticide resistance selection pressure in mosquito vectors due to exposure to both agricultural and public health insecticides.

The geographical extent of insecticide exposure in malaria mosquitoes can be assessed by mapping intensive agricultural cropping systems and malaria vector distribution or vector control stratification. This spatial approach makes use of GIS technology to identify overlapping areas where the two attributes coexist. Although the results give a general indication of potential risk areas, this indirect approach is easier than to assess the geographical extent of variations in insecticide resistance and population genetic characteristics. Attempts to identify such risk areas have been made in Thailand and Vietnam (Overgaard 2006; Thongdara et al. 2009; Nguyen et al. 2009). The main obstacle of this approach is to know the exact amounts of pesticides that farmers apply in their fields. This often depends on the individual farmer and the cropping system. The situation is further complicated by the fact that sometimes different crops, requiring different pesticide regimes, are grown in the same fields and vary from year to year. Statistics on pesticide use are often very general and are usually based on the amount of pesticides imported to a country. One way to overcome this obstacle is to make decisions based on experience and evidence from detailed studies that certain crops require more pesticides than others and thereafter range crops in terms of pesticide intensity (Overgaard 2006).

Identifying risk areas should focus on land use specifically pesticide use to determine local or regional variations in pesticide use and intensity. Maps showing risk areas may be particularly helpful for assessing potential locations for the implementation of resistance management and integrated control strategies. Such strategies could be action plans to reduce or replace insecticides used in pest and disease vector control or coordination of integrated pest management (IPM) and integrated vector management (IVM) activities (WHO 2006).

As an example, we carried out a risk area mapping analysis for Thailand (Thongdara et al. 2009). First we identified the 20 highest malaria provinces in the country, and then, out of those, we selected 12 provinces that had the highest number of pesticide-using land holders (Fig. 9.5). We then performed a GIS analysis by overlaying high and medium insecticide-intensive land uses over the malaria transmission areas A1 and A2. Chanthaburi Province had the highest feasible area for implementing IPVM of the 12 examined provinces. About 121,600 ha or 19 % of the provincial area of Chanthaburi could be suitable for IPVM implementation (Table 9.2 and Fig. 9.6a). This high percentage is due to the large number of fruit

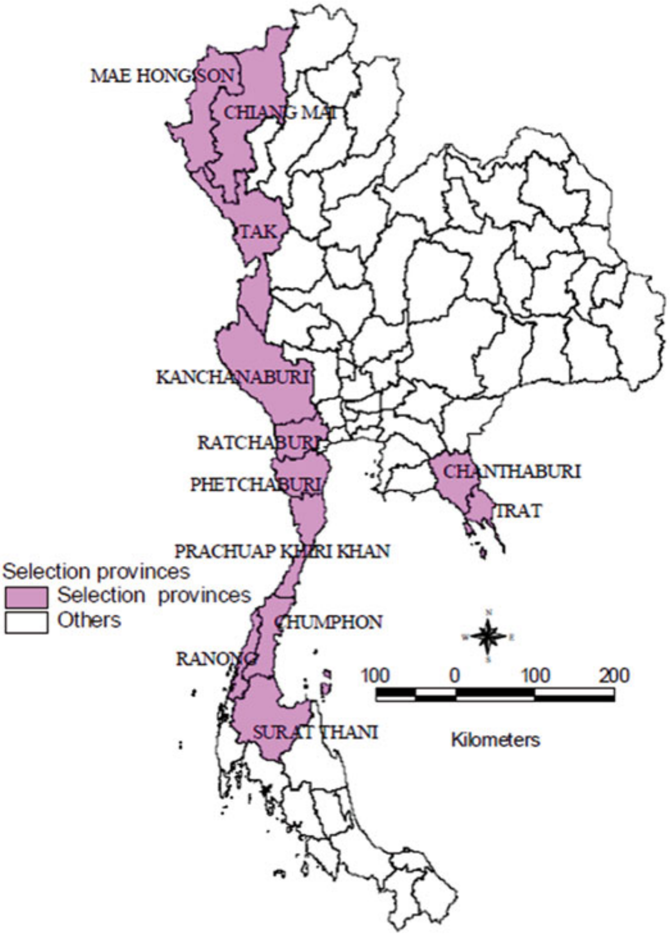


Fig. 9.5 Map of Thailand showing 12 provinces with high malaria transmission and agricultural pesticide use (Thongdara et al. 2009)

orchards in the province. In Chiang Mai Province, another fruit-growing province, the feasible area for implementing IPVM was calculated to be 127,300 ha or 5.7 % of the provincial area (Table 9.2 and Fig. 9.6b).

Coordination of IPM and IVM, or integrated pest and vector management (IPVM), depends on the fact that agricultural pests and vector-borne diseases overlap geographically (WHO 2006). Integrated pest and vector management is an extension of the IPM-based Farmer Field School (FFS) approach and is a potential solution to the control of both agricultural pests and disease vectors, while simultaneously improving public health and promoting community empowerment. The FFS is a season-long training activity for farmers to implement IPM (Pontius et al. 2002). It started in 1989–1990 in Indonesia, but has been implemented in more than

Table 9.2 Calculation of implementation areas for integrated pest and vector management in 12 provinces in Thailand (Thongdara et al. 2009)

Province	Province area (ha)	Potential IPVM area in province	
		ha	%
Chanthaburi	635,091	121,673	19.1
Prachuap Khiri Khan	642,416	77,764	13.0
Chumphon	598,243	81,254	12.6
Trat	286,409	24,184	8.4
Ranong	314,001	26,451	8.4
Chiang Mai	2,202,781	127,339	5.7
Mae Hong Son	1,272,529	44,046	3.4
Phetchaburi	615,439	16,217	2.6
Ratchaburi	517,834	13,448	2.6
Tak	1,726,865	38,373	2.2
Surat Thani	1,312,804	24,653	1.8
Kanchanaburi	1,940,760	19,694	1.0

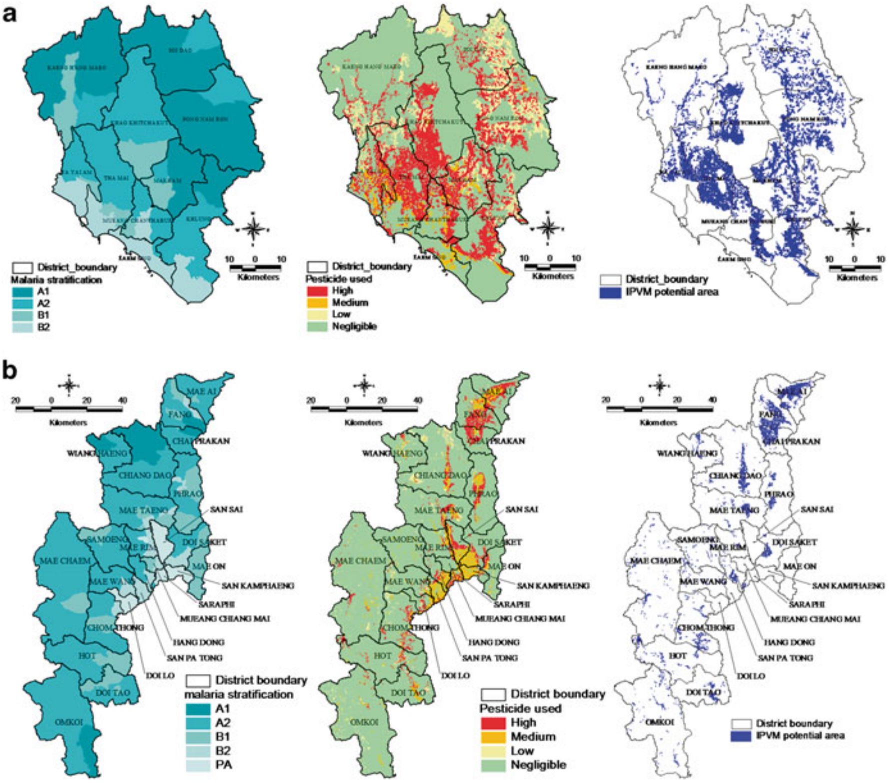


Fig. 9.6 Identifying risk areas for insecticide resistance in mosquitoes and potential implementation areas for integrated pest and vector management. (**a**) Chanthaburi Province, (**b**) Chiang Mai Province. From *left* to *right*: malaria area stratification map, insecticide-intensive land use map, and potential area for implementing IPVM (overlay of A1/A2 stratification areas and high/medium insecticide use) (Thongdara et al. 2009)

80 countries. The Farmer Field School is usually carried out in farmer's fields and focuses on participatory learning. It is not top-down lecturing but a social learning process, by doing, observing, and discussing, involving group dynamics to improve local decision-making and empowerment. It also builds on experimentation, e.g. by comparing observations and results in IPM plots with non-IPM plots. The principles of IPM are to grow a healthy crop, conserve natural enemies, observe crops regularly, and make farmers agricultural experts in their own fields. The most important result of the IPM FFS is reduction of pesticide use, both when comparing before and after implementation of FFS programmes and between FFS and non-FFS farmers. Further results are improved health, community empowerment, and improved livelihoods (e.g. van den Berg et al. 2003).

IVM is defined as a rational decision-making process to optimize the use of resources for vector control (WHO 2004, 2012a). This means that vector control should build on combinations of interventions; that methods are selected based on local vector biology, disease transmission, and morbidity; and that interventions should include intersectoral collaboration and engaging local communities and the public health framework. The similarities between IPM and IVM, therefore, are to preserve healthy ecosystem for pest control, consider all available control methods, use and select pesticides wisely, and encourage local participation. The differences between IPM and IVM are that IPM is a decentralized system, whereas IVM has a centralized approach. IPM has a strong link to farmer occupation and provides an economic incentive to farmers, but IVM has no such occupational link and has no direct economic effects. Furthermore, IPM is implemented through the Farmer Field Schools, whereas IVM is realized through the general health infrastructure.

The purpose of combining IPM and IVM into IPVM through the FFS approach is to achieve a multipronged strategy with four specific effects on vector-borne disease (Fig. 9.7): (1) reduction of disease transmission through reduced vector populations achieved by environmental management of vector breeding, (2) reduced risk of insecticide resistance in vector mosquitoes by reduced agro-pesticide use, (3) improved personal protection measures and treatment-seeking behaviour through increased awareness and understanding about malaria, and (4) improved nutrition and housing conditions by increased profits from agriculture.

The validity of the IPVM approach has been demonstrated in the Sri Lanka IPVM project (2002–2007) financed by the FAO, UNEP, and WHO (WHO 2006). Farmers were educated and motivated to carry out source reduction and to restore and maximize rice ecosystem functions. It was shown that farmers can improve their knowledge of mosquito ecology and disease epidemiology and change their agricultural practices in favour of environmentally sound measures for mosquito control and disease prevention (Yasuoka et al. 2006a, b). The WHO evaluation of the project also showed that farmers became masters in analysing their agroecosystems, the use of mosquito bed nets increased, and they were empowered to proactively approach specialized health teams on issues related to vector-borne diseases, creating opportunities for better integration of community health programmes (WHO 2006). The IPVM intervention and its field-level effects and outcomes, with potential health impacts, are summarized in Fig. 9.8.

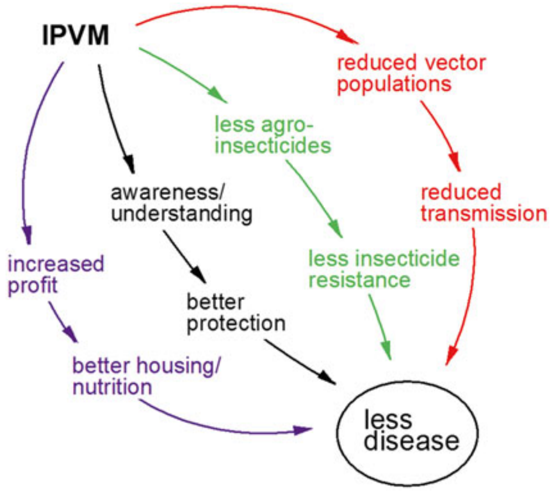


Fig. 9.7 Multipronged strategy of integrated pest and vector management (IPVM) through Farmer Field Schools (FFS) (van den Berg and Knols 2006)

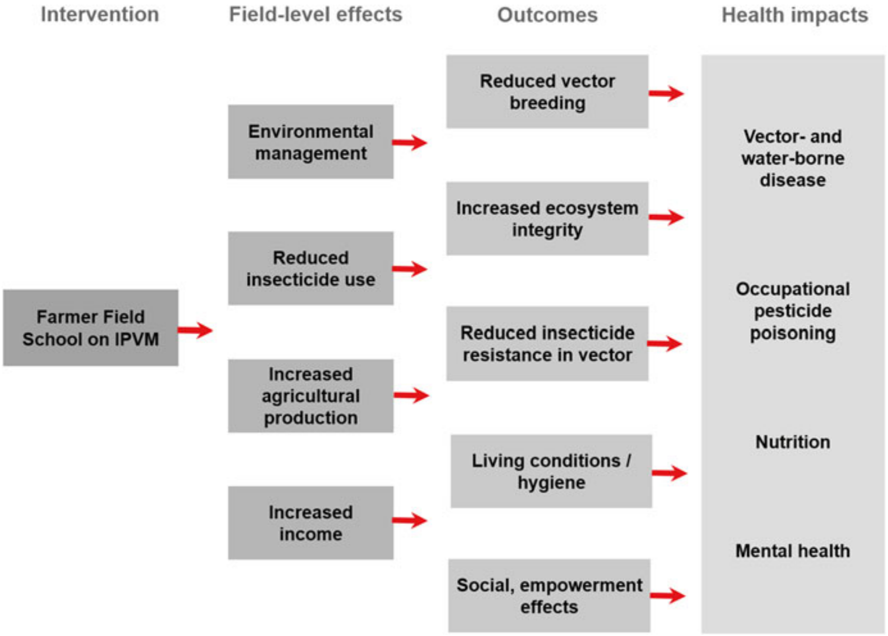


Fig. 9.8 Field-level effects, indirect outcomes, and ultimate health effects of Farmer Field Schools on IPVM (WHO 2006)

Integrated pest and vector management for malaria is probably most effective in cropping systems where agricultural pests and malaria vectors overlap, e.g. paddy rice fields. Rice field-associated vectors, such as *An. sinensis* in China and Korea (Ree 2005; Sinka et al. 2011); *An. culicifacies* and *An. fluviatilis* in India (Sahu et al.

1990); *An. aconitus* in Indonesia, Vietnam, and other Southeast Asian countries (Stoops et al. 2008; Manh et al. 2010; Harrison 1980); and *An. arabiensis* in Tanzania (Ijumba et al. 2002) and Kenya (Muturi et al. 2008), could potentially be efficiently controlled through the IPVM approach. However, also in insecticide-intensive cropping system, such as fruit orchards and flower production, could this approach prove to be valuable.

9.8 Discussion

Our research on malaria mosquitoes in northern Thailand indicates a complex vector situation. We have shown that malaria vectors are affected by the landscape that they encounter and live in. For example, when the diversity of a landscape increases, i.e. becomes complex in terms of number of land uses and the arrangement of land use patches, both the diversity and density of mosquito vectors decrease (Overgaard et al. 2003). Also, in areas with no or little malaria transmission, mosquito densities decline in response to land use changes, particularly where forest cover declines. On the other hand, in areas with annual malaria transmission, mosquito density is not largely affected by land use change (Suwonkerd et al. 2002). Furthermore, intensive agricultural cropping systems, such as fruit orchards, increase the likelihood of insecticide resistance development in malaria mosquitoes (Overgaard et al. 2005). Landscape structure in general, therefore, has an impact on malaria transmission scenarios that potentially could be exploited for more efficient malaria control strategies.

Landscape Analysis The number of studies on geographical risk mapping of diseases, their vectors, or etiological agents has increased dramatically during the last decade. Studies have been carried out to find associations between landscape patterns and vector-borne diseases, such as malaria, dengue, Chagas disease, leishmaniasis, West Nile virus, and Saint Louis encephalitis (e.g. Hemme et al. 2010; Roux et al. 2011; Sudhakar et al. 2006; Brown et al. 2008; Cid et al. 2013). The aim of these studies has mainly been to understand vector ecology and behaviour to assist in control efforts of governments and organizations so that limited funds can be used in locations where they have the greatest impact. The analysis of landscape structure, as carried out here, is not common in disease vector research. Particularly landscape configuration is difficult to assess in terms of its effect on vectors, and it is unclear of how this knowledge can be meaningfully utilized in vector control. Landscape configuration and habitat fragmentation are naturally of more importance in agricultural pest control where pest insects are specifically associated with a certain crop or landscape element. However, plant community composition may have an effect on vectorial capacity and the fitness of malaria mosquitoes because mosquitoes also feed on nectar (Stone et al. 2012). The presence and absence of nectariferous plants in the environment could potentially be an important factor in vector control (Stone et al. 2012). Plant patches that are attractive for mosquitoes could be of similar importance as specific food crop patches are to some agricultural pests. Such patches could be used actively as attractants to mosquitoes and then treated with toxic sprays, such as boric acid (Muller et al. 2010; Beier et al. 2012; Naranjo et al. 2013). The effect of attractive toxic sugar bait plant spraying in Mali showed that malaria mosquito density and number of completed gonotrophic cycles were reduced compared to the controls (Muller et al. 2010).

IPVM As far as we know, the IPVM approach has not been widely implemented apart from a trial in Sri Lanka (WHO 2006; Yasuoka et al. 2006a, b). It is not clear why this is so, but it could relate to the complexity of concepts and methods, difficulties to incite collaboration across ministries, involvement of potentially reluctant farmers, etc. Agricultural IPM has not always been successful either and sustainability of IPM programmes seems to be difficult to achieve, mainly due to technological transfer, implementation complexity, and maintenance and reinforcement of farmer's knowledge (Wearing 1988; Ekstrom and Ekbom 2011). Lack of funds and loss of interest or endurance may be other causes for failure. While a framework for implementing IVM at district level is available (WHO 2004, 2012a), there are major challenges for the national vector control programmes. The main problems in the implementation of IVM are that programmes do not ideally target vector-borne diseases, methods are not adapted to local circumstances, and opportunities are not taken for integrating disease control. National policies support disease-specific programme and do seldom take into account the role of local communities. The significance of the IPVM approach is that it may cancel out and reconcile the differences between IPM and IVM mentioned earlier. Thus, IPVM should aim to find a balance between decentralized and centralized systems, through a combination of on-the-ground FFS supported by the agriculture and health authorities. Currently, intersectoral collaboration is generally poor and mainly on an ad hoc basis and dependent on individuals, not institutions. Opportunities for different ministries to collaborate should be strengthened. Community participation is not aimed at community empowerment, and vector control programmes are delinked from the farmer's economy. While ideal, integration of IPM and IVM to generate income is not always feasible. However, the occupational and economical aspects for farmer participation must be maintained without disregarding the vector component.

In southern Yunnan Province in China, inhabitants from remote mountain areas have moved into new villages and lack the skills in rice field management. This has resulted in high mosquito densities and dominance of *An. minimus* and increased malaria incidence (Meide et al. 2008). In such a setting, IPVM and FFS could be a suitable intervention for farmers to improve their knowledge in pest and vector identification and control and their understanding in irrigation water supply and innovative ways to implement environmental modification (Keiser et al. 2005).

Mosquito Taxonomy The development of molecular tools to identify mosquito sibling species has probably occurred quicker than the speciation process itself, i.e. the sibling species we know of today were likely already existing when the fundamental knowledge of the biology and ecology of many vector species was established. Interpreting results from outdated studies on mosquito bionomics and behavioural characteristics may affect the development of vector control strategies negatively. Given the behavioural heterogeneity and plasticity of many *Anopheles* species complexes and sibling species which avoid exposure to both IRS and LLINs, many control programmes recognize that a single strategy for an entire country, and even for a single province/district, is not applicable. This requires the deployment of situation-specific and, at times, even species-specific strategies. Current vector control strategies and activities are targeting the entire species complexes based on their local overall behavioural characteristics rather than taking into consideration species-specific behaviour and vectorial capacity.

Lessons for Vector Control New findings on composition of *Anopheles* species complexes and their varying bionomics have undoubtedly important implications for the epidemiology and strategies for malaria elimination. In many transmission areas in the region, the proportion of primary vectors biting outdoors, in the early evening and/or on animals, is relatively increasing; these vectors are responsible for residual transmission (Durnez and Coosemans 2013). Mosquitoes biting outdoors and at times when people are unprotected by bed nets or other vector control tools present serious challenges for vector and disease control in the region. For example, rubber plantations have been associated with higher risk for malaria, due to the practice of nocturnal rubber tapping and presence of malaria vectors, e.g. *An. minimus* and *An. maculatus* (Bhumiratana et al. 2013). Specific vector control strategies are needed for migrant and mobile populations, people that have their livelihoods from forest-associated work, e.g. hunting, gathering, forestry, rubber plantation workers, etc. With increasing *An. minimus* populations in some transmission areas, control strategies should incorporate both indoor and outdoor control tools which will help in significantly reducing the levels of malaria transmission. In addition to LLINs or IRS, treated materials or space repellents coupled with stakeholder involvement and community engagement, packaged in IPVM, would be ideal to significantly reduce indoor and outdoor resting vectors.

Future Research Currently, molecular capability for analysis of sibling species is well developed; consequently further studies are needed to assess the distribution and abundance of sibling species of the Dirus, Minimus, Maculatus, and Barbirostris complexes and groups. Priority research questions extracted from a Roll Back Malaria meeting in 2011 (RBM 2011) were strongly focused on vector bionomics, such as determining the bionomics and distribution of *An. dirus* at local scale taking into account seasonal and environmental changes and the role of secondary vectors in maintenance of transmission on *P. falciparum* and *P. vivax* in different environmental settings. Such studies should include mapping of land use/cover and other geographical attributes.

It is often argued that landscape analysis, spatial statistics, and GIS can be used as valuable tools in vector and disease control. Many studies have attempted to link various landscape elements and spatial patterns with high disease transmission risk with the aim to assist in vector and disease control. There is potential to incorporate the results of these studies with malaria stratification, using good case studies demonstrating tangible and causal links. However, the evidence is lacking regarding the application of the outcomes and knowledge of this research by control programmes. It is likely that the technical nature of these methods and lack of knowledge of how to attain and interpret results prohibits uptake of this technology in malaria control. It would be valuable to review and assess if landscape spatial analysis research has, indeed, benefited the implementation of control measures. We believe that a large-scale cluster randomized controlled trial should be carried out in a suitable location to confirm if the IPVM FFS approach is actually reducing vector abundance and disease incidence compared to non-IPVM, i.e. business as usual, or perhaps compared with IPM only.

9.9 Conclusion

This review attempts to consolidate various studies exploring the effects of landscape structure on mosquito density and diversity and insecticide resistance carried out in northern Thailand using data from the 1970s up to around 2005. We have shown that landscape analysis could potentially be used as a tool in vector control strategy development, particularly to understand local vector behaviour and habitat characteristics for stratification of vector control areas. We found a positive relationship between landscape diversity and malaria vector diversity and density. Land use changes, particularly forest fragmentation, reduced vector densities. Such land use changes were more pronounced in non-transmission areas than in transmission areas. Furthermore, agricultural intensification increases the likelihood of insecticide resistance development in malaria mosquitoes, and as a consequence public health-agricultural sector collaboration in a regional context should be encouraged and strengthened. Landscape analysis can be used to identify areas for integrated insecticide resistance management. Such strategies are in line with the recently published Global Plan for Insecticide Resistance Management (GPIRM) in malaria vectors (WHO 2012b). Integration of pest and vector control strategies should build on the integrated pest and vector management strategies described in this chapter and implemented on the ground through Farmer Field Schools. However, before large-scale IPVM interventions are carried out, we suggest that a well-designed research project should verify the potentials for vector and disease reduction and under which circumstances it would work. Future research should also investigate the ecological and biological characteristics of the sibling species of the malaria vectors in the region.

References

Ampunpong C (1996) Analysis of tangerine handling and marketing in Thailand. Thesis No AE-96-36, Asian Institute of Technology

Apiwathnasorn C, Prommongkol S, Samung Y, Limrat D, Rojruthai BJ, Entomol M (2002) Potential for *Anopheles campestris* (Diptera: Culicidae) to transmit malaria parasites in Pa Rai subdistrict (Aranyaprathet, Sa Kaeo province), Thailand. J Med Entomol 39(4):583–586

Baimai V (1988) Population cytogenetics of the malaria vector *Anopheles leucosphyrus* group. Southeast Asian J Trop Med Public Health 19(4):667–680

Baimai V, Green CA, Andre RG, Harrison BA, Peyton EL (1984) Cytogenetic studies of some species complexes of *Anopheles* in Thailand and Southeast Asia. Southeast Asian J Trop Med Public Health 15(4):536–546

Beier JC, Muller GC, Gu W, Arheart KL, Schlein Y (2012) Attractive toxic sugar bait (ATSB) methods decimate populations of *Anopheles* malaria vectors in arid environments regardless of the local availability of favoured sugar-source blossoms. Malar J 11:31. doi:10.1186/1475-2875-11-31

Bhumiratana A, Sorosjinda-Nunthawarasilp P, Kaewwaen W, Maneekan P, Pimnon S (2013) Malaria-associated rubber plantations in Thailand. Travel Med Infect Dis 11(1):37–50. doi:10.1016/j.tmaid.2012.11.002

Brogdon WG, Beach RF, Stewart JM, Castanaza L (1988) Microplate assay analysis of the distribution of organophosphate and carbamate resistance in Guatemalan *Anopheles albimanus*. Bull World Health Organ 66(3):339–346

Brown H, Duik-Wasser M, Andreadis T, Fish D (2008) Remotely-sensed vegetation indices identify mosquito clusters of West Nile virus vectors in an urban landscape in the northeastern United States. Vector Borne Zoonotic Dis 8(2):197–206. doi:10.1089/vbz.2007.0154

Bureau of Vector Borne Disease (2013) Annual Vector Borne Disease Reports. Bureau of Vector Borne Disease, Department of Disease Control, Ministry of Public Health, Nonthaburi

Chalermphol J, Shivakoti GP (2009) Pesticide use and prevention practices of tangerine growers in northern Thailand. J Agric Educ Ext 15(1):21–38

Chapin G, Wasserstrom R (1981) Agricultural production and malaria resurgence in Central America and India. Nature 293(5829):181–185

Chareonviriyaphap T, Aum-aung B, Ratanatham S (1999) Current insecticide resistance patterns in mosquito vectors in Thailand. Southeast Asian J Trop Med Public Health 30(1):184–194

Chareonviriyaphap T, Bangs MJ, Ratanatham S (2000) Status of malaria in Thailand. Southeast Asian J Trop Med Public Health 31(2):225–237

Chareonviriyaphap T, Prabaripai A, Bangs MJ (2004) Excito-repellency of deltamethrin on the malaria vectors, *Anopheles minimus, Anopheles dirus, Anopheles sawadwongporni*, and *Anopheles maculatus*, in Thailand. J Am Mosq Control Assoc 20(1):45–54

Childs DZ, Cattadori IM, Suwonkerd W, Prajakwong S, Boots M (2006) Spatiotemporal patterns of malaria incidence in northern Thailand. Trans R Soc Trop Med Hyg 100(7):623–631. doi:10.1016/j.trstmh.2005.09.011

Cid CV, Estallo EL, Almiron WR, Contigiani MS, Spinsanti LI (2013) Landscape determinants of Saint Louis encephalitis human infections in Cordoba city, Argentina during 2010. Acta Trop 125(3):303–308. doi:10.1016/j.actatropica.2012.12.005

Coleman RE, Sithiprasasna R, Kankaew P, Kiaattiut C, Ratanawong S, Khuntirat B et al (2002) Naturally occurring mixed infection of *Plasmodium vivax* VK210 and *P. vivax* VK247 in anopheles mosquitoes (Diptera: Culicidae) in western Thailand. J Med Entomol 39(3):556–559

Congpuon K, Satimai W, Sujariyakul A, Intanakom S, Harnpitakpong W, Pranuth Y et al (2011) In vivo sensitivity monitoring of chloroquine for the treatment of uncomplicated vivax malaria in four bordered provinces of Thailand during 2009–2010. J Vector Borne Dis 48(4):190–196

Diabate A, Baldet T, Chandre F, Akoobeto M, Guiguemde TR, Darriet F et al (2002) The role of agricultural use of insecticides in resistance to pyrethroids in *Anopheles gambiae* s.l. in Burkina Faso. Am J Trop Med Hyg 67(6):617–622

Dunning JB, Danielson BJ, Pulliam HR (1992) Ecological processes that affect populations in complex landscapes. Oikos 65(1):169–175. doi:10.2307/3544901

Durnez JB, Coosemans M (2013) Residual transmission of malaria: an old issue for new approaches. In: Manguin S (ed) Anopheles mosquitoes – new insights into malaria vectors. Intech, Croatia. Open access book: http://www.intechopen.com/books/anopheles-mosquitoes-new-insights-into-malaria-vectors

Ekbom B (2000) Interchanges of insects between agricultural and surrounding landscapes. In: Ekbom B, Irwin ME, Robert Y (eds) Interchanges of insects between agricultural and surrounding landscapes. Kluwer, Dordrecht, pp 1–3

Ekstrom G, Ekbom B (2011) Pest control in agro-ecosystems: an ecological approach. Crit Rev Plant Sci 30(1-2):74–94. doi:10.1080/07352689.2011.554354

Elkington J, Ingkasuwan P (1988) Natural resources of South East Asia. Oxford University Press, Oxford

Fane M, Cisse O, Traore CS, Sabatier P (2012) *Anopheles gambiae* resistance to pyrethroid-treated nets in cotton versus rice areas in Mali. Acta Trop 122(1):1–6. doi:10.1016/j.actatropica.2011.11.013

FAO (1999) State of the world's forests 1999. Food and Agricultural Organization, Rome

Garros C, Marchand RP, Quang NT, Hai NS, Manguin S (2005) First record of *Anopheles minimus* C and significant decrease of *An. minimus* A in central Vietnam. J Am Mosq Control Assoc 21(2):139–143

Garros C, Van Bortel W, Trung HD, Coosemans M, Manguin S (2006) Review of the Minimus complex of Anopheles, main malaria vector in Southeast Asia: from taxonomic issues to vector control strategies. Trop Med Int Health 11(1):102–114. doi:10.1111/j.1365-3156.2005.01536.x

Garros C, Van Nguyen C, Trung HD, Van Bortel W, Coosemans M, Manguin S (2008) Distribution of Anopheles in Vietnam, with particular attention to malaria vectors of the *Anopheles minimus* complex. Malar J 7:11. doi:10.1186/1475-2875-7-11

Georghiou GP, Ariaratnam V, Breeland SG (1972) Development of resistance to carbamates and organophosphorus compounds in *Anopheles albimanus* in nature. Bull World Health Organ 46(4):551–554

Gould F, Stinner RE (1984) Insects in heterogeneous habitats. In: Huffaker CB, Tabb RL (eds) Ecological entomology. Wiley, New York, pp 427–449

Green CA, Rattanarithikul R, Pongparit S, Sawadwongporn P, Baimai V (1991) A newly-recognized vector of human malarial parasites in the Oriental region, *Anopheles (Cellia) pseudowillmori* (Theobald, 1910). Trans R Soc Trop Med Hyg 85(1):35–36

Green CA, Rattanarithikul R, Charoensub A (1992) Population genetic confirmation of species status of the malaria vectors *Anopheles willmori* and *An. pseudowillmori* in Thailand and chromosome phylogeny of the Maculatus group of mosquitoes. Med Vet Entomol 6(4):335–341

Harbach RE, Parkin E, Chen B, Butlin RK (2006) *Anopheles (Cellia) minimus* Theobald (Diptera: Culicidae): neotype designation, characterization, and systematics. Proc Entomol Soc Wash 108:198–209

Harbach RE, Garros C, Manh ND, Manguin S (2007) Formal taxonomy of species C of the *Anopheles minimus* sibling species complex (Diptera: Culicidae). Zootaxa 1654:41–54

Harrison BA (1980) Medical entomology studies – XIII. The Myzomyia Series of Anopheles (Cellia) in Thailand, with emphasis on intra-interspecific variations (Diptera: Culicidae). Contr Am Ent Inst 17:1–195

Hemingway J, Ranson H (2000) Insecticide resistance in insect vectors of human disease. Annu Rev Entomol 45:371–391. doi:10.1146/annurev.ento.45.1.371

Hemme RR, Thomas CL, Chadee DD, Severson DW (2010) Influence of urban landscapes on population dynamics in a short-distance migrant mosquito: evidence for the dengue vector *Aedes aegypti*. PLoS Negl Trop Dis 4(3), e634. doi:10.1371/journal.pntd.0000634

Hii J, Rueda LM (2013) Malaria vectors in the Greater Mekong Subregion: overview of malaria vectors and remaining challenges. Southeast Asian J Trop Med Public Health 44(Suppl 1):73–165; discussion 306–167

Ijumba JN, Mosha FW, Lindsay SW (2002) Malaria transmission risk variations derived from different agricultural practices in an irrigated area of northern Tanzania. Med Vet Entomol 16(1):28–38

Jaichapor B, Kengluecha A, Rongnoparut P, Rueda LM, Jones JW, Sithiprasasna R (2005) Morphological variations of *Anopheles minimus* A in Tak Province, Thailand. Southeast Asian J Trop Med Public Health 36(3):609–615

Keiser J, Singer BH, Utzinger J (2005) Reducing the burden of malaria in different eco-epidemiological settings with environmental management: a systematic review. Lancet Infect Dis 5(11):695–708. doi:10.1016/s1473-3099(05)70268-1

Konchom S, Singhasivanon P, Kaewkungwal J, Chupraphawan S, Thimasarn K, Kidson C et al (2003) Trend of malaria incidence in highly endemic provinces along the Thai borders, 1991–2001. Southeast Asian J Trop Med Public Health 34(3):486–494

Kondrashin AV, Jung RK, Akiyama J (1991) Ecological aspects of forest malaria in Southeast Asia. An informal consultative meeting WHO/MRC, World Health Organization/Malaria Research Centre, New Delhi, 18–22 Feb 1991, pp 1–28

Lawpoolsri S, Chavez IF, Yimsamran S, Puangsa-Art S, Thanyavanich N, Maneeboonyang W et al (2010) The impact of human reservoir of malaria at a community-level on individual malaria occurrence in a low malaria transmission setting along the Thai-Myanmar border. Malar J 9:143. doi:10.1186/1475-2875-9-143

Limrat D, Rojruthai B, Apiwathnasorn C, Samung Y, Prommongkol S (2001) *Anopheles barbirostris/campestris* as a probable vector of malaria in Aranyaprathet, Sa Kaeo Province. Southeast Asian J Trop Med Public Health 32(4):739–744

Linton YM, Harbach RE, Seng CM, Anthony TG, Matusop A (2001) Morphological and molecular identity of *Anopheles (Cellia) sundaicus* (Diptera: Culicidae), the nominotypical member of a malaria vector species complex in Southeast Asia. Syst Entomol 26(3):357–366. doi:10.1046/j.1365-3113.2001.00153.x

Linton YM, Dusfour I, Howard TM, Ruiz F, Nguyen DM, Trung HD et al (2005) *Anopheles (Cellia) epiroticus* (Diptera: Culicidae), a new malaria vector species in the Southeast Asian Sundaicus Complex. Bull Entomol Res 95(4):329–339. doi:10.1079/ber2005364

Malaria Division (1993) Thailand country report on malaria control strategy. Ministry of Public Health, Bangkok

Malaria Division (1998) Annual report of Ministry of Public Health. Thai Government, Bangkok

Malikul S (1988) The current situation of the anti-malaria programme in Thailand. Southeast Asian J Trop Med Public Health 19(3):355–359

Manguin S, Carnevale P, Mouchet F (2008a) Biodiversity of malaria. John Libbey Eurotext, Montrouge

Manguin S, Garros C, Dusfour I, Harbach RE, Coosemans M (2008b) Bionomics, taxonomy, and distribution of the major malaria vector taxa of Anopheles subgenus Cellia in Southeast Asia: an updated review. Infect Genet Evol 8(4):489–503. doi:10.1016/j.meegid.2007.11.004

Manh CD, Beebe NW, Van VN, Quang TL, Lein CT, Nguyen DV et al (2010) Vectors and malaria transmission in deforested, rural communities in north-central Vietnam. Malar J 9:259. doi:10.1186/1475-2875-9-259

McGarigal K, Marks BJ (1995) FRAGSTATS: spatial pattern analysis for quantifying landscape structure. General technical report PNW-GTR-351. US Department of Agriculture, Forest Servie, Pacific Northwest Research Station, Portland

McKenzie JA (1996) Ecological and evolutionary aspects of insecticide resistance, Environmental intelligence unit. RG Landes, Austin

Meide L, Xuezhong W, Tongyan Z, Du Z, Yande D, Baolin L (2008) Analysis of the relationship between density and dominance of *Anopheles minimus* (Diptera: Culicidae) with environmental parameters in southern Yunnan Province, Peoples Republic of China. J Med Entomol 45(6):1007–1010

Muenworn V, Akaratanakul P, Bangs MJ, Parbaripai A, Chareonviriyaphap T (2006) Insecticide-induced behavioral responses in two populations of *Anopheles maculatus* and *Anopheles sawadwongporni*, malaria vectors in Thailand. J Am Mosq Control Assoc 22(4):689–698. doi:10.2987/8756-971x(2006)22[689:ibritp]2.0.co;2

Muirhead Thompson RC (1940a) Studies on the behaviour of *Anopheles minimus.* Part I. The selection of the breeding place and the influence of light and shade. J Malar Inst India 3:265–294

Muirhead Thompson RC (1940b) Studies on the behaviour of *Anopheles minimus.* Part II. The influence of water movement on the selection of the breeding place. J Malar Inst India 3:295–325

Muller GC, Beier JC, Traore SF, Toure MB, Traore MM, Bah S et al (2010) Successful field trial of attractive toxic sugar bait (ATSB) plant-spraying methods against malaria vectors in the *Anopheles gambiae* complex in Mali, West Africa. Malar J 9:210. doi:10.1186/1475-2875-9-210

Muturi EJ, Muriu S, Shililu J, Mwangangi J, Jacob BG, Mbogo C et al (2008) Effect of rice cultivation on malaria transmission in central Kenya. Am J Trop Med Hyg 78(2):270–275

Naranjo DP, Qualls WA, Muller GC, Samson DM, Roque D, Alimi T et al (2013) Evaluation of boric acid sugar baits against *Aedes albopictus* (Diptera: Culicidae) in tropical environments. Parasitol Res 112(4):1583–1587. doi:10.1007/s00436-013-3312-8

Nguyen D, Nguyen M, Le V, Ho L, Tran A, Nguyen K et al (2009) Pesticides, agriculture and health in Vietnam. Identification of potential implementation sites for integrated pest and vector management. Bioforsk RAPPORT 4(105):86s, Ås. http://www.bioforsk.no/ikbViewer/page/tjenester/publikasjoner/publikasjon?p_document_id=61663

Nuthsathapana S, Sawadwongphorn P, Chitprarop U, Cullen JR, Gass RF, Green CA (1986a) A mark-release-recapture demonstration of host-preference heterogeneity in *Anopheles minimus* Theobald (Diptera: Culicidae) in a Thai village. Bull Entomol Res 76:313–320

Nuthsathapana S, Sawadwongphorn P, Chitprarop U, Cullen JR (1986b) The behaviour of *Anopheles minimus* Theobald (Diptera: Culicidae) subjected to differing levels of DDT selection pressure in northern Thailand. Bull Entomol Res 76:303–312

Obsomer V, Defourny P, Coosemans M (2007) The *Anopheles dirus* complex: spatial distribution and environmental drivers. Malar J 6. doi:10.1186/1475-2875-6-26

ODPC (2012) Annual report 2012. Office of Disease Prevention and Control no. 10. Ministry of Public Health, Chiang Mai

Overgaard HJ (2006) Malaria mosquito resistance to agricultural insecticides: risk area mapping in Thailand. Research report 103. International Water Management Institute, Colombo. ISSN 1026–0862. http://www.iwmi.cgiar.org/pubs/pub103/RR103.pdf

Overgaard HJ, Tsuda Y, Suwonkerd W, Takagi M (2002) Characteristics of *Anopheles minimus* (Diptera: Culicidae) larval habitats in northern Thailand. Environ Entomol 31(1):134–141. doi:10.1603/0046-225x-31.1.134

Overgaard HJ, Ekbom B, Suwonkerd W, Takagi M (2003) Effect of landscape structure on anopheline mosquito density and diversity in northern Thailand: implications for malaria transmission and control. Landsc Ecol 18(6):605–619. doi:10.1023/a:1026074910038

Overgaard HJ, Sandve SR, Suwonkerd W (2005) Evidence of anopheline mosquito resistance to agrochemicals in northern Thailand. Southeast Asian J Trop Med Public Health 36(Suppl 4):152–157

Peyton EL (1989) A new classification for the Leucosphyrus group of Anopheles (Cellia). Mosq Syst 21:97–205

Pontius JC, Dilts R, Bartlett A (2002) From farmer field school to community IPM: ten years of IPM training in Asia. Food and Agricultural Organization Regional Office for Asia and the Pacific, RAP/2002/15, Bangkok, 106 pp

Pothikasikorn J, Overgaard H, Ketavan C, Visetson S, Bangs MJ, Chareonviriyaphap T (2007) Behavioral responses of malaria vectors, *Anopheles minimus* complex, to three classes of agrochemicals in Thailand. J Med Entomol 44(6):1032–1039

Ranson H, N'Guessan R, Lines J, Moiroux N, Nkuni Z, Corbel V (2011) Pyrethroid resistance in African anopheline mosquitoes: what are the implications for malaria control? Trends Parasitol 27(2):91–98. doi:10.1016/j.pt.2010.08.004

Rattanarithikul R, Panthusiri P (1994) Illustrated keys to the medically important mosquitos of Thailand. Southeast Asian J Trop Med Public Health 25(Suppl 1):1–66

Rattanarithikul R, Mongkolpanya K, Noigamol C, Chanaimongkol S, Mahapibul P, Nakngen S (1994) Dry season distribution of mosquito larvae in the bed of the Mekong river, Northeastern Thailand. J Am Mosq Control Assoc 10(2):197–201

Rattanarithikul R, Green CA, Panyim S, Noigamol C, Chanaimongkol S, Mahapibul P (1995) Larval habitats of malaria vectors and other *Anopheles* mosquitoes around a transmission focus in northwestern Thailand. J Am Mosq Control Assoc 11(4):428–433

Rattanarithikul R, Harrison BA, Harbach RE, Panthusiri P, Coleman RE, Panthusiri P (2006) Illustrated keys to the mosquitoes of Thailand. IV. Anopheles. Southeast Asian J Trop Med Public Health 37(Suppl 2):1–128

RBM (2011) Strategies for prevention of outdoor transmission of malaria. Roll back malaria vector control working group (VCWG) technical workshop report. 2nd annual strategy meeting Phnom Penh, 28 Nov 2011. http://www.rbm.who.int/partnership/wg/wg_itn/docs/ws2/minutes2outdoorTransmissionWSmeeting.pdf. Accessed May 2013

Ree HI (2005) Studies on *Anopheles sinensis*, the vector species of vivax malaria in Korea. Korean J Parasitol 43(3):75–92

Reid JA (1962) The *Anopheles barbirostris* group (Diptera: Culicidae). Bull Entomol Res 53:1–57

Ritthison W, Tainchum K, Manguin S, Bangs MJ, Chareonviriyaphap T (2014) Biting patterns and host preference of Anopheles epiroticus in Chang Island, Trat Province, Thailand. J Vector Ecol 39:361–371

Rongnoparut P, Ugsang DM, Baimai V, Honda K, Sithiprasasna R (2005) Use of a remote sensing-based geographic information system in the characterizing spatial patterns for *Anopheles minimus* A and C breeding habitats in western Thailand. Southeast Asian J Trop Med Public Health 36(5):1145–1152

Rosenberg R, Andre RG, Somchit L (1990) Highly efficient dry season transmission of malaria in Thailand. Trans R Soc Trop Med Hyg 84(1):22–28

Roux E, Venancio AD, Girres JF, Romana CA (2011) Spatial patterns and eco-epidemiological systems – part II: characterising spatial patterns of the occurrence of the insect vectors of Chagas disease based on remote sensing and field data. Geospat Health 6(1):53–64

Rundel PW, Boonpragob K (1995) Dry forest ecosystems of Thailand. In: Bullock SH, Mooney HA, Medina E (eds) Seasonally dry tropical forests. Cambridge University Press, Cambridge, UK, pp 93–123

Saeung A (2012) Anopheles (Diptera: Culicidae) species complex in Thailand: identification, distribution, bionomics and malaria-vector importance. Int J Parasitol Res 4:75–82

Saeung A, Otsuka Y, Baimai V, Somboon P, Pitasawat B, Tuetun B et al (2007) Cytogenetic and molecular evidence for two species in the *Anopheles barbirostris* complex (Diptera: Culicidae) in Thailand. Parasitol Res 101(5):1337–1344. doi:10.1007/s00436-007-0645-1

Saeung A, Baimai V, Otsuka Y, Rattanarithikul R, Somboon P, Junkum A et al (2008) Molecular and cytogenetic evidence of three sibling species of the *Anopheles barbirostris* form a (Diptera:Culicidae) in Thailand. Parasitol Res 102(3):499–507. doi:10.1007/s00436-007-0788-0

Sahu SS, Parida SK, Sadanandane C, Gunasekaran K, Jambulingam P, Das PK (1990) Breeding habitats of malaria vectors: *A. fluviatilis*, *A. annularis* and *A. culicifacies*, in Koraput district, Orissa. Indian J Malariol 27(4):209–216

Sallum MA, Peyton EL, Wilkerson RC (2005) Six new species of the *Anopheles leucosphyrus* group, reinterpretation of *An. elegans* and vector implications. Med Vet Entomol 19(2):158–199. doi:10.1111/j.0269-283X.2005.00551.x

Satimai W, Sudathip P, Vijaykadga S, Khamsiriwatchara A, Sawang S, Potithavoranan T et al (2012) Artemisinin resistance containment project in Thailand. II: responses to mefloquine-artesunate combination therapy among falciparum malaria patients in provinces bordering Cambodia. Malar J 11:300. doi:10.1186/1475-2875-11-300

Scanlon JE, Sandhinand U (1965) The distribution and biology of *Anopheles balabacensis* in Thailand (Diptera: Culicidae). J Med Entomol 2:61–69

Sharma VP, Kondrashin AV (1991) Forest malaria in Southeast Asia. In: Proceedings of an informal consultative meeting. World Health Organization/Medical Research Council, New Delhi

Singhanetra-Renard A (1986) Population movement, socio-economic behavior and the transmission of malaria in northern Thailand. Southeast Asian J Trop Med Public Health 17(3):396–405

Singhanetra-Renard A (1993) Malaria and mobility in Thailand. Soc Sci Med 37(9):1147–1154

Singhasivanon P (1999) Mekong malaria. Malaria, multi-drug resistance and economic development in the greater Mekong subregion of Southeast Asia. Southeast Asian J Trop Med Public Health 30(Suppl 4):i–iv, 1–101

Sinka ME, Bangs MJ, Manguin S, Chareonviriyaphap T, Patil AP, Temperley WH et al (2011) The dominant Anopheles vectors of human malaria in the Asia-Pacific region: occurrence data, distribution maps and bionomic precis. Parasit Vectors 4:89. doi:10.1186/1756-3305-4-89

Sodhi NS, Koh LP, Brook BW, Ng PKL (2004) Southeast Asian biodiversity: an impending disaster. Trends Ecol Evol 19(12):654–660. doi:10.1016/j.tree.2004.09.006

Somboon P, Prapanthadara LA, Suwonkerd W (2003) Insecticide susceptibility tests of *Anopheles minimus* s.l., *Aedes aegypti*, *Aedes albopictus*, and *Culex quinquefasciatus* in northern Thailand. Southeast Asian J Trop Med Public Health 34(1):87–93

Somboon P, Thongwat D, Harbach RE (2011) *Anopheles (Cellia) rampae* n. sp., alias chromosomal form K of the Oriental Maculatus Group (Diptera: Culicidae) in Southeast Asia. Zootaxa 2810:47–55

Stibig HJ, Belward AS, Roy PS, Rosalina-Wasrin U, Agrawal S, Joshi PK et al (2007) A land-cover map for South and Southeast Asia derived from SPOT-VEGETATION data. J Biogeogr 34(4):625–637. doi:10.1111/j.1365-2699.2006.01637.x

Stone CM, Jackson BT, Foster WA (2012) Effects of plant-community composition on the vectorial capacity and fitness of the malaria mosquito *Anopheles gambiae*. Am J Trop Med Hyg 87(4):727–736. doi:10.4269/ajtmh. 2012.12-0123

Stoops CA, Gionar YR, Shinta, Sismadi P, Rachmat A, Elyazar IF et al (2008) Remotely-sensed land use patterns and the presence of *Anopheles* larvae (Diptera: Culicidae) in Sukabumi, West Java, Indonesia. J Vector Ecol 33(1):30–39. doi:10.3376/1081-1710(2008)33[30:rlupat]2.0.co;2

Sudhakar S, Srinivas T, Palit A, Kar SK, Battacharya SK (2006) Mapping of risk prone areas of kala-azar (Visceral leishmaniasis) in parts of Bihar State, India: an RS and GIS approach. J Vector Borne Dis 43(3):115–122

Sungvornyothin S, Muenvorn V, Garros C, Manguin S, Prabaripai A, Bangs MJ et al (2006) Trophic behavior and biting activity of the two sibling species of the *Anopheles minimus* complex in western Thailand. J Vector Ecol 31(2):252–261

Suwonkerd W, Amg-Ung B, Rimwangtrakul K, Wongkattikul S, Kattiyamongkool B, Chitprarop U et al (1990) A field study on the response of *Anopheles dirus* to DDT and Fenitrothion sprayed to huts in Phetchabun province, Thailand. Trop Med 32(1):1–5

Suwonkerd W, Overgaard HJ, Tsuda Y, Prajakwong S, Takagi M (2002) Malaria vector densities in transmission and non-transmission areas during 23 years and land use in Chiang Mai province, Northern Thailand. Basic Appl Ecol 3(3):197–207. doi:10.1078/1439-1791-00108

Suwonkerd W, Tsuda Y, Overgaard HJ, Chawprom S, Tuno N, Prajakwong S et al (2004) Changes in malaria vector densities over a twenty-three year period in Mae Hong Son Province, northern Thailand. Southeast Asian J Trop Med Public Health 35(2):316–324

Suwonkerd W, Vryheid R, Suwannachote N (2010) Progress of partial integration of malaria control with other vector borne diseases control in northern Thailand. Southeast Asian J Trop Med Public Health 41(6):1297–1305

Tainchum K, Kongmee M, Manguin S, Bangs MJ, Chareonviriyaphap T (2015) Anopheles species diversity and distribution of the malaria vectors of Thailand. Trends Parasitol 31(3):109–119

Thongdara R, Limsoontorn T, Imvitthaya C, Samarakoon L, Ranamukhaarachchi S, Almvik M et al (2009) Pesticides, agriculture and health in Thailand. Identification of potential implementation sites for integrated pest and vector management. Bioforsk report 4(103): 194 p. Ås. http://www.bioforsk.no/ikbViewer/page/tjenester/publikasjoner/publikasjon?p_document_id=52573

Trung HD, Van Bortel W, Sochantha T, Keokenchanh K, Quang NT, Cong LD et al (2004) Malaria transmission and major malaria vectors in different geographical areas of Southeast Asia. Trop Med Int Health 9(2):230–237

Trung HD, Van Bortel W, Sochantha T, Keokenchanh K, Briet OJT, Coosemans M (2005) Behavioural heterogeneity of *Anopheles* species in ecologically different localities in Southeast Asia: a challenge for vector control. Trop Med Int Health 10(3):251–262. doi:10.1111/j.1365-3156.2004.01378.x

Turner MG (1989) Landscape ecology. The effect of pattern on process. Annu Rev Ecol Syst 20:171–197. doi:10.1146/annurev.ecolsys.20.1.171

Turner MG, Gardner RH (1990) Quantitative methods in landscape ecology: the analysis and interpretation of landscape heterogeneity, vol 82, Ecological studies series. Springer, Berlin

Van Bortel W, Trung HD, Manh ND, Roelants P, Verle P, Coosemans M (1999) Identification of two species within the *Anopheles minimus* complex in northern Vietnam and their behavioural divergences. Trop Med Int Health 4(4):257–265

Van Bortel W, Trung HD, le Thuan K, Sochantha T, Socheat D, Sumrandee C et al (2008) The insecticide resistance status of malaria vectors in the Mekong region. Malar J 7:102. doi:10.1186/1475-2875-7-102

Van den Berg H, Knols BGJ (2006) The farmer field school: a method for enhancing the role of rural communities in malaria control? Malar J 5. doi:10.1186/1475-2875-5-3

Van den Berg H, Senerath H, Amarasinghe L (2003) Farmer field schools in Sri Lanka: assessing the impact. Pestic News 61:14–16

Vanwambeke SO, Somboon P, Harbach RE, Isenstadt M, Lambin EF, Walton C et al (2007a) Landscape and land cover factors influence the presence of *Aedes* and *Anopheles* larvae. J Med Entomol 44(1):133–144. doi:10.1603/0022-2585(2007)44[133:lalcfi]2.0.co;2

Vanwambeke SO, Lambin EF, Eichhorn MP, Flasse SP, Harbach RE, Oskam L et al (2007b) Impact of land-use change on dengue and malaria in northern Thailand. Ecohealth 4(1):37–51. doi:10.1007/s10393-007-0085-5

Walter Reed Biosystematics Unit (2012) Systematic catalog of Culicidae. Walter Reed Biosystematics Unit, Walter Reed Army Institute of Research, Smithsonian Institution, Suitland. http://www.mosquitocatalog.org/default.aspx. Accessed May 2013

Walton C, Sharpe RG, Pritchard SJ, Thelwell NJ, Butlin RK (1999) Molecular identification of mosquito species. Biol J Linn Soc 68(1-2):241–256. doi:10.1111/j.1095-8312.1999.tb01168.x

Wearing CH (1988) Evaluating the IPM implementation process. Annu Rev Entomol 33:17–38. doi:10.1146/annurev.ento.33.1.17

WHO (1996) Resistance of vectors and reservoirs of disease to pesticides, vol 737, WHO technical report series. World Health Organization, Geneva, pp 1–87

WHO (2004) Global strategic framework for integrated vector management. WHO/CDS/CPE/PVC/2004.10. World Health Organization, Geneva, 12 pp

WHO (2006) Evaluation report of the integrated pest and vector management project in Sri Lanka. World Health Organization, Southeast Asia Regional Office, New Dehli. http://209.61.208.233/EN/Section23/Section1001/Section1110_12796.htm. Accessed May 2013

WHO (2010) Malaria Thailand profile. World Health Organization, Southeast Asia Regional Office, New Dehli. http://whothailand.healthrepository.org/bitstream/123456789/1443/6/Thailand%20malaria%20report.pdf. Accessed May 2013

WHO (2011) World Malaria report 2011. World Health Organization, Geneva. http://www.who.int/malaria/world_malaria_report_2011/9789241564403_eng.pdf. Accessed May 2013

WHO (2012a) Handbook for integrated vector management. WHO/HTM/NTD/VEM/2012.3. World Health Organization, Geneva, 12 pp

WHO (2012b) Global plan for insecticide resistance management in malaria vectors (GPIRM). http://www.who.int/malaria/vector_control/ivm/gpirm/en/index.html. WHO/HTM/GMP/2012.5. World Health Organization, Geneva

WHO (2013) World malaria report 2013. World Health Organization, Geneva

Yadouleton A, Martin T, Padonou G, Chandre F, Asidi A, Djogbenou L et al (2011) Cotton pest management practices and the selection of pyrethroid resistance in *Anopheles gambiae* population in Northern Benin. Parasit Vectors 4. doi:10.1186/1756-3305-4-60

Yasuoka J, Levins R (2007) Impact of deforestation and agricultural development on anopheline ecology and malaria epidemiology. Am J Trop Med Hyg 76(3):450–460

Yasuoka J, Levins R, Mangione TW, Spielman A (2006a) Community-based rice ecosystem management for suppressing vector anophelines in Sri Lanka. Trans R Soc Trop Med Hyg 100(11):995–1006. doi:10.1016/j.trstmh.2005.12.014

Yasuoka J, Mangione TW, Spielman A, Levins R (2006b) Impact of education on knowledge, agricultural practices, and community actions for mosquito control and mosquito-borne disease prevention in rice ecosystems in Sri Lanka. Am J Trop Med Hyg 74(6):1034–1042

Chapter 10
Rubber Plantations as a Mosquito Box Amplification in South and Southeast Asia

Padikkala Kandiyil Sumodan, Ronald Morales Vargas,
Jinrapa Pothikasikorn, Anchana Sumanrote, Régine Lefait-Robin,
and Jean-Pierre Dujardin

Abstract Using simple species richness index and geometric morphospaces, we compared the mosquito fauna in rubber plantations from Thailand and India and contrasted it with a fragmented forest fauna from northern Thailand. In rubber plantations, *Aedes albopictus* was the most frequent mosquito, together with a high proportion of filarial and malaria vectors. Because of the many breeding sites represented by the latex cups, heavy downpour during the rainy season probably transforms the rubber plantation ecosystems into mosquito-borne disease-transmitting systems. In the forest, a different composition of the mosquito fauna was observed, but *A. albopictus* was also the most frequent mosquito. Its presence and its different metric properties in the forest could suggest the possible existence of native populations in Thailand, in accordance with the hypothesis of its Southeast Asian origin.

P.K. Sumodan
Post Graduate Department of Zoology, Government College,
Madappally, Vadakara-2, Kerala, India

R.M. Vargas • A. Sumanrote
Department of Medical Entomology, Faculty of Tropical Medicine, University of Mahidol,
Salaya, Thailand

J. Pothikasikorn
Department of Microbiology, Faculty of Science, University of Mahidol, Salaya, Thailand

R. Lefait-Robin
Haut Conseil de la santé publique, Ministère des affaires sociales et de la santé, Paris, France

J.-P. Dujardin (✉)
UMR177 IRD-CIRAD INTERTRYP, TA A 17/G Campus International de Baillarguet,
34398 Montpellier cedex 5, France
e-mail: dujardinbe@gmail.com

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_10

10.1 Introduction

Mosquito-borne diseases have been staging a vengeful comeback all over the world, especially Asian countries since the 1980s. Among these resurged diseases, dengue and chikungunya are the most important in Asian countries, especially those under the Southeast Asian region of the World Health Organization (Gübler 1996). To what extent could be the resurgence related to some environmental changes affecting the mosquito populations? Here, we focus on the mosquito vectors and rubber plantation (RP) development, with special emphasis to *Aedes albopictus*, responsible for the recent outbreak of chikungunya in the Indian Ocean (Paupy et al. 2009) and Southeast Asian (SEA) countries (Tawatsin et al. 2009).

Chikungunya started to appear in epidemic proportions in 2005 after extensive outbreaks in Indian Ocean islands (Charrel et al. 2007). Since then, it has been spreading to the entire Southeast Asian region (Hapuarachchi et al. 2010) and could reach distant regions outside Southeast Asia (Reiter et al. 2006) like Italy (Rezza et al. 2007) and France (Paupy et al. 2001). The worldwide extension of chikungunya has been attributed to the invasive behavior of the vector (Benedict et al. 2007; Paupy et al. 2009). The cause of its increasing importance in Southeast Asia (SEA) is less obvious. SEA is supposed to be the source of *A. albopictus*: unless it was reinvaded by migrating populations of *A. albopictus* (see the “invaders” hypothesis of Delatte et al. 2011) or together with this possibility, a likely cause of the local spread of chikungunya could be an increased abundance of its vector populations.

Sumodan (2003) provided the first evidence for a possible relationship between the chikungunya spread in India and the development of RPs. These observations are summarized here, suggesting that RP would act as amplification boxes for *A. albopictus*.

In addition to the Indian evidence, we provide some original data on the mosquito fauna found in RPs from Thailand (Fig. 10.1). A comparison of the fauna between northern and central Thailand plantations confirms that RPs have a typical diversity structure. Supporting this observation, a morphometric study of *A. albopictus* suggests different patterns of morphological variation between RP and forest habitats.

Our data lend support to the idea that RPs could represent a source of emerging populations of *A. albopictus* for both local disease transmission and, possibly, “invader” production.

10.2 Rubber Plantations in India and Their Likely Association with Chikungunya

The relation between mosquito breeding and RPs in Kerala was noticed in 2002 during an investigation on suspected dengue outbreak in North Kerala. It was observed that during southwest monsoon seasons, latex tapping was suspended in several RPs and led to the accumulation of rainwater in the latex-collecting

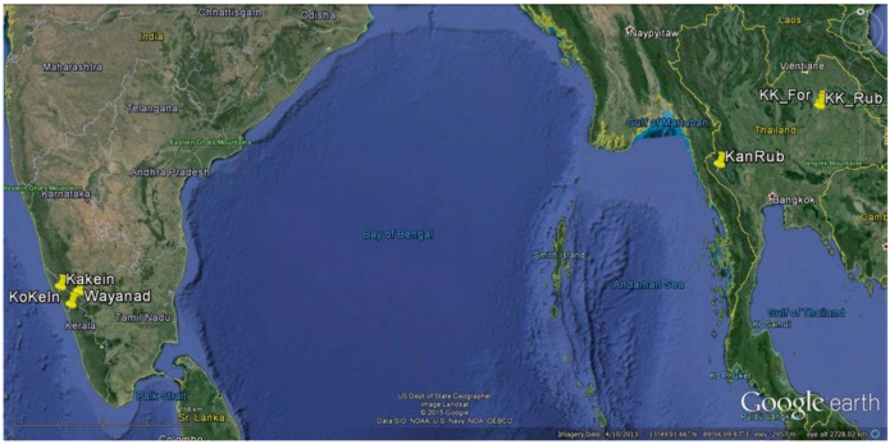


Fig. 10.1 Our data were obtained from collections from India (Kerala state) and two areas of Thailand (Kanchanaburi and Khon Kaen)

containers and breeding of different mosquito species including *A. albopictus*, the vector of dengue and chikungunya (Sumodan 2003). With 670,000 ha, India ranks fifth in total area under RPs in the world. The share of Kerala is 517,475 ha, which is more than 76 % total area under rubber cultivation in the country. There are two categories of RPs in Kerala: holdings (area 20 ha and less) and estates (area more than 20 ha). Out of 517,475 ha of RPs, 480,240 (92.80 %) are holdings in the state (Source: Rubber Board, India).

Resurgence of chikungunya in India began during 2005–2006 after a gap of 32 years causing 1.3 million cases in 13 states (Yergolkar et al. 2006). The South Indian state of Kerala experienced the first wave of chikungunya in 2006 (Manju and Sushamabai 2009). Considering the role of *A. albopictus* in the transmission of diseases and also the experience of its breeding in RPs, a detailed survey was done in three districts, viz., Kannur, Kozhikode, and Wayanad, from June 2005 to September 2010 to study the extent of *A. albopictus* breeding and factors involved in transforming the rubber plantation ecosystems into *Aedes*-borne disease (dengue and chikungunya) transmission systems.

10.2.1 Status of Rubber Plantations

During the study period, 4,028 RPs were surveyed for the status of tapping. Out of this, 3,812 were holdings and 216 were estates. Latex tapping was found uninterrupted in the estates in the rainy season. Rain guards were used to prevent rain from

Table 10.1 Tapping status of rubber plantations during southwest monsoon, with average yield per hectare rubber plantation (2005–2006)

	Number surveyed		Plantations where tapping is suspended (%)			
District	Holdings	Estates	Holdings	Estates	Total	Average yield (kg/ha)
Kozhikode	966	162	316 (33 %)	0	28 %	1,642
Kannur	2,323	54	1,412 (61 %)	0	59 %	1,616
Wayanad	523	0	476 (91 %)	–	91 %	864

falling into the cups. Percentage of holdings, where tapping was discontinued, varied from 28 % to 91 % in the three districts (Table 10.1). It was found that the tapping workforce in the estates was regular employees, while in the holdings the workforce was employed purely on temporary basis.

Yield of RPs per hectare also varied from district to district. Kozhikode district had the highest yield, while Wayanad had the least (Table 10.1).

10.2.2 *Mosquito Breeding*

During the survey, out of 23,486 latex-collecting containers surveyed, 17,856 (76 %) were with rainwater collection (Fig. 10.2a, b). 15,531 (87 %) of these cups were positive for mosquito immature stages (larva and pupa). Emergence data have shown that there were 12 species of mosquitoes including *A. albopictus. A. albopictus* breeding was observed in 10,856 (60.8 %) cups.

10.2.3 *Human Dwellings*

175 plantations were surveyed for the presence of human dwellings within the plantations or within 100 m perimeter from the periphery of the plantations. While 26 out of 175 (14.9 %) plantations had human dwellings within the plantations, human dwellings were observed within 100 m perimeter from the periphery of all 175 plantations.

10.2.4 *Chikungunya Outbreaks*

There were major outbreaks of chikungunya in Ernakulam (2006, 2007), Kottayam (2007), Malappuram (2007, 2009), Kozhikode (2009), and Kannur (2009) districts (Table 10.2).

Fig. 10.2 (**a**) Forest and rubber plantation (**b**) at Khon Kaen (northern Thailand). BG traps were used in both environments following the same time protocol. (**c**) Human-landing collections at Kanchanaburi (Thailand). (**d**) Geometric morphometrics. The first step after dissection and mounting is to take a picture of each wing, together with the relevant size scale apparent on the picture. These pictures will then be submitted to specialized morphometric analysis (Dujardin and Slice 2006)

Table 10.2 Outbreaks of dengue and chikungunya in major rubber-growing districts (2006–2009)

Year	District	Area under rubber plantation (hectare)	Chikungunya cases
2006	Ernakulam	57,040	1,840
2007	Kottayam	112,069	10,662
2009	Malappuram	29,905	1,886
	Ernakulam		1,882
	Malappuram		3,930
	Kozhikode	17,681	3,339
	Kannur	34,672	3,246

10.3 Rubber Plantations in Thailand and Their Mosquito Fauna

10.3.1 Collection Site

10.3.1.1 Kanchanaburi

The study sites are located in an endemic area for *Wuchereria bancrofti*. The selected village (about 20 households) had low pesticide agricultural use and is located in Huay Ka Yeng subdistrict, Thong Pha Phum district, Kanchanaburi province, near the western border of Thailand and close to Myanmar. There are mixed cultivation farms with rice, cassavas, and several kinds of fruits, but nowadays, almost the complete surrounding area is transformed to RP. The collection site was situated at latitude 14.35° and longitude 98.36°, approximately 200 km from Tha Muang district of Kanchanaburi province and about 330 km from Bangkok.

10.3.1.2 Khon Kaen

The Khon Kaen province is located in the northeastern plateau of Thailand, approximately 450 km from Bangkok. Mosquitoes were collected from two different habitats near the city of Khon Kaen: forest (Fig. 10.2a) and RP (Fig. 10.2b). The natural primary deciduous forest is located in the main campus of the Khon Kaen University, covered with more than 80 different plant species, with the nearest building with student activities at ca. 500 m. The RP was located at a distance of 18.2 km from the natural primary deciduous forest. There was a permanent resident family at the entrance of the plantation.

10.3.2 Collection Techniques

10.3.2.1 Kanchanaburi

Wild adult females of various mosquitoes were collected 2 days per month (3 months per season, wet and dry) throughout 1 year by human-landing catches in RP about 300 m apart from the village (Fig. 10.2c). Mosquito collections were undertaken for 24 h by two persons at the same sites, for each period. The first period was collecting mosquitoes from 06.05 to 12.00 h, the second period was collecting from 12.05 to 18.00 h, the third period was 18.05 to 24.00 h, and the fourth period was 24.05 to 06.00 h; torches were used to observe mosquitoes at night and aspirators for collecting them. Collected mosquitoes were kept in separate marked plastic cups and covered with netting material, one for each hour. All alive mosquito specimens were provided with 10 % sugar solution and transported to the laboratory for morphological identification.

10.3.2.2 Khon Kaen

Female and male mosquitoes were collected during 2 days and 3 nights three times between April 2011 and April 2012 using two BG (Biogent)-Sentinel traps baited with human skin extract (BG-Lure\s\up5I). Mosquitoes were transported at low temperature to the laboratory for morphological identification and further analyses.

Females were identified on the base of their external morphology following the illustrated keys of Rattanarithikul et al. (2005a, b, 2006a, b, 2010), and their wings were dissected and photographed for morphometric analyses (Fig. 10.2d).

10.3.3 Species Richness in Mosquitoes

In Kanchanaburi, mosquito captures made from December 2009 to August 2010 provided 4,495 specimens representing 42 mosquito species (3,857 samples of 32 Culicinae and 638 samples of 11 Anophelinae). The greatest proportion of mosquitoes was recorded in wet season of August, and the lowest population was in January in dry season. In Khon Kaen, the collections provided a total of 750 specimens, from which 351 females are detailed on Table 10.3.

Although the percentage of *A. albopictus* was similar whichever the habitat (forest, plantation), it was the most frequent species in the RPs (from 25 % to 30 %), while it ranked second (25 %) in the forest after *C. brevipalpis* (36 %). RP showed no or low presence of two species which were among the most frequent in the forest: *C. brevipalpis* and *C. quinquefasciatus*, the latter being recognized as a potent vector of the filarial *W. bancrofti* (Triteeraprapab et al. 2000). RPs also were distinguished from the forest by the relatively higher abundance of *Armigeres subalbatus*.

Table 10.3 Summary of the taxonomic diversity of the mosquito fauna as collected in two different areas of Thailand, Kanchanaburi (4,495 specimens) and Khon Kaen (351 specimens), and two different habitats: the rubber plantation and the forest (244 mosquitoes). The 351 mosquitoes presented here from Khon Kaen were females only. RP, rubber plantation

		RP	RP	Forest
Genus	species	Kanchanaburi	Khon Kaen	Khon Kaen
Aedes	*albopictus*	25 %	30 %	25 %
Aedes	*sp.*	11 %	5 %	8 %
Armigeres	*subalbatus*	16 %	9 %	6 %
Culex	*brevipalpis*	0.0 %	7 %	36 %
Culex	*quinquefasciatus*	0.4 %	6 %	19 %
Culex	*vishnui*	4 %	24 %	2 %
Culex	*whitmorei*	0.1 %	7 %	0 %
Mansonia	*sp.*	13 %	0 %	0 %
Anopheles	*sp.*	11 %	3 %	0 %
remaining	*sp.*	20 %	9 %	3 %
Total	*sp.*	4,495	107	244

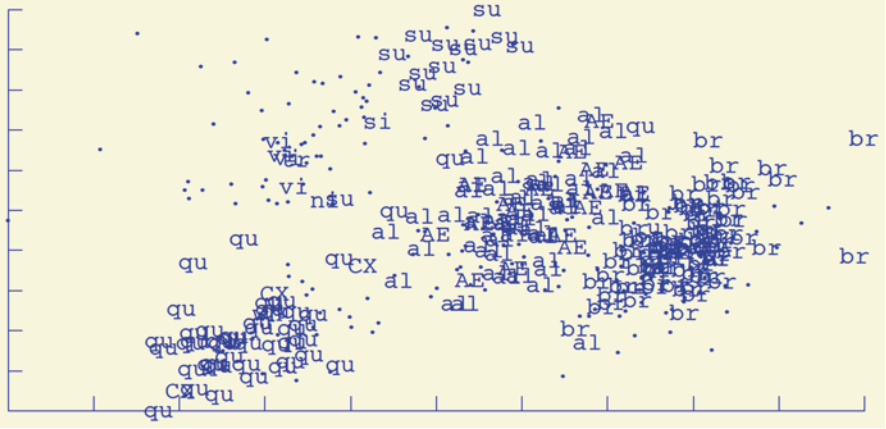


Fig. 10.3 Morphospace of mosquitoes collected from the forest. Horizontal and vertical axes are the first and second principal components of shape variables (wings), respectively; they quantify the morphological similarity between species. Three clouds are visible, a right one restricted to *Cx. brevipalpis* (br), a left one containing various *Culex* species, particularly *Cx. quinquefasciatus* (qu), and a central one containing *Aedes albopictus* (al) and *Armigeres subalbatus* (su). Dots represent specimens from the other habitat (RP). vi, *Cx. vishnui*; si, *Cx.* sitiens; AE, undetermined Aedes, CX, undetermined *Culex*

10.3.4 Morphological Diversity

The study examining the range of size and shape variation of the mosquitoes was performed in the Khon Kaen collection only using the landmark-based approach for *Aedes* sp. (Henry et al. 201; Jirakanjanakit et al. 2007; Morales Vargas et al. 2013). It allowed to produce a one-year morphospace of the mosquito fauna (Dujardin et al. 2012) from either the RP or the forest (see Figs. 10.3 and 10.4). The statistical comparison of the *A. albopictus* metric properties in the forest versus RP was performed using nonparametric permutation tests (5,000 runs).

10.4 Conclusion

10.4.1 Species Diversity

In Thailand, the two RP sites did not show exactly the same range of species. These differences are likely to be attributed to unequal sample sizes, to the techniques of capture, to the local environment of each RP, or simply to the current geographic repartition of the species in Thailand. The same kind of reasons could explain different species richness of RP mosquitoes in India (12) versus Thailand (from 13 to 42). However, one significant trait was shared by each RP: be the collection effort

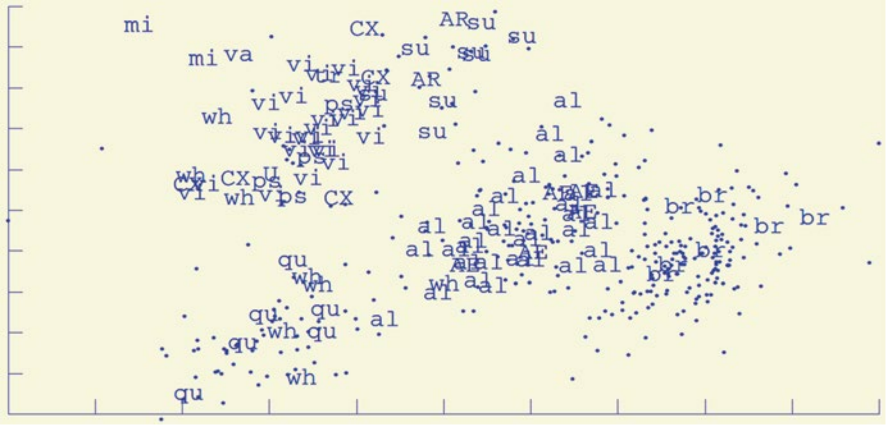


Fig. 10.4 Morphospace of mosquitoes collected from the rubber plantation (RP). Horizontal and vertical axes are the first and second principal components of shape variables (wings), respectively; they quantify the morphological similarity between species. The clouds observed in the forest (Fig. 9.4) are still visible, with however the right one (*Cx. brevipalpis*) depopulated, and a wide left one containing also some other Culex species than *Cx.* quinquefasciatus (qu), particularly Cx. vishnui (vi), *Cx whitmorei* (wh) and *Cx. vagus* (va). The central top cloud contains *Aedes albopictus* (al) and *Armigeres subalbatus* (su). Dots represent specimens from the other habitat (forest). br, *Cx. brevipalpis*; ps, *Cx pseudovishnui*; mi, *Anopheles minimus*; AE, undetermined *Aedes*; AR, undetermined *Armigeres*; CX, undetermined *Culex*. The capital letter « U » stands for unknown

extensive (15,531 latex containers in India, 4,495 specimens in central Thailand) or not (107–244 females in northern Thailand), about one specimen out of four was *A. albopictus*.

It is also worth mentioning the similar prevalence of *A. albopictus* in the forest area, where no artificial containers such as the latex collection cups could serve as breeding sites. Such abundance in a sylvatic environment suggests again the possible existence of native populations in Thailand, in accordance with the hypothesis of a SEA origin of the species.

Finally, the significant differences in shape ($P = 0.022$) and size (forest specimens were smaller, $P < 0.001$) between *A. albopictus* from forest and RP suggest local populations adapting to different ecotopes in spite of possible exchanges or simply lack of frequent exchanges between these habitats.

10.4.2 Chikungunya Risk

Chikungunya viruses with A226V mutation in the glycoprotein envelope 1 (E1) gene were isolated in 2007 from Kerala (Kumar et al. 2008). This mutation had already been suggested to be directly responsible for a significant increase in CHIKV infectivity in *A. albopictus*. The new strain of virus has almost replaced the older strain in Southeast Asian region (Tsetsarkin et al. 2011). In addition to this biological change affecting the virus, populational changes affecting its vector probably play a role also. Regular outbreaks of chikungunya in the major rubber-cultivating districts in the Kerala state (India) support this hypothesis.

The simple increase of *A. albopictus* abundance could be the main cause of such association, and our data show that the abundance of the vector is significantly increased in RPs. Rubber plantations create an artificial microenvironment made of cups for rubber milk that can act as ovitraps for mosquitoes. It is safe to say that heavy downpour during the rainy season transforms a major percentage of RP ecosystems into mosquito-borne disease-transmitting systems. The obvious cause for such abundance is the tremendous number of additional breeding sites represented by the latex containers: in the Kerala state of India, the potential breeding habitats (latex collection cups) were estimated to be approximately 240 million. However, one cannot rule out the possibility of a special attractiveness of the milk itself modifying the ovipositing behavior of some species or helping their development. Rubber latex contains nutrients belonging to sugars and proteins. Qualitative analysis of latex for sugar has shown the presence of reducing monosaccharides, most likely glucose. Besides, rubber latex is a good medium for the growth of bacteria (Taysum 1956), also forming one of the important diets of mosquito larvae. Since dry latex is present in the containers, it is likely to provide sufficient nutrition to the growing mosquito larvae. Comparison of larvae in the containers with latex and without latex showed that the larvae in the former were healthier and also the density was much higher (Sumodan, unpublished data).

The multiplier effect of RP on vector abundance increases the risk for human-vector contact and enhances the possibility of access to chikungunya viruses. In India as well as in central Thailand, the source of human blood was available in all the plantations surveyed as human dwellings were present well within the flight range of *A. albopictus* (Rosen et al. 1976).

10.4.3 Other Risks

A significant feature of the RP fauna was the abundance of important filarial vectors, especially the *Aedes desmotes* (7 %), *Mansonia dives* (5 %) (Gould et al. 1982; Apiwathnasorn et al. 2006), and some others from the *Aedes* genus (7 %). The abovementioned species were not recorded from the northern RP, but other filariasis vectors were found in both northern and central Thailand: *C. quinquefasciatus* at Khon Kaen in the RP (6 %) and in the forest (19 %), while at very low frequency at Kanchanaburi (0.4 %), and *Ar. subalbatus*, frequent in both areas. *Ar. subalbatus* has been incriminated not only as a vector of *W. bancrofti* (Tanaka et al. 1979) but also as a vector of the dog heartworm *Dirofilaria immitis* (Cheong et al. 1981). Together, the filarial vectors represented 37 % of the total captures in Kanchanaburi and about 20 % in Khon Kaen. In the RP of Kanchanaburi where a huge collection was available, a special mention has to be given to the presence also of malaria vectors such as *Anopheles minimus* (6 %) or *An. barbirostris* (1 %). In the RP of Khon Kaen, in spite of few specimens collected (107), some *An. minimus* were captured by the BG traps. There is probably a special malaria risk for daily workers in RP of Thailand (Satitvipawee et al. 2012).

Acknowledgments The research at Kanchanaburi station received the kind help of Rapee Boonplueang (Department of Biology), Wilai Noonpakdee (Department of Biochemistry, Faculty of Science, Mahidol University, Bangkok 10400, Thailand), Wirat Soysaeng (Vector-Borne Disease Control Center 4.1.7 Kanchanaburi, MOPH, Thailand), and Theeraphap Chareonviriyaphap (Department of Entomology, Faculty of Agriculture, Kasetsart University, Bangkok 10900, Thailand). The research in the northern part of Thailand was helped by Waraporn Putalun (Department of Pharmacognosy and Toxicology, Faculty of Pharmaceutical Sciences, Khon Kaen University) and Noppawan Phumala Morales (Department of Pharmacology, Faculty of Sciences, Mahidol University). The study in the Kerala state of India was funded by the University Grants Commission (India). Funding for the research in the Center of Thailand came from the Senior Research Scholar Program (RTA5280007) and the TRF/BIOTEC Special Program for Biodiversity Research and Training Grant (BRT R 150011). The investigation work in northern Thailand was supported by the PHC-SIAM grant number 25646ZL, as well as by IRD grant numbers HC3165-3R165-GABI-ENT2 and HC3165-3R165-NV00- THA1.

References

Apiwathnasorn C, Samung Y, Prummongkol S, Asavanich A, Komalamisra N, Mccall P (2006) Bionomics studies of *Mansonia* mosquitoes inhabiting the peat swamp forest. Southeast Asian J Trop Med Public Health 37:272–278

Benedict MQ, Levine RS, Hawley WA, Lounibos LP (2007) Spread of the tiger: global risk of invasion by the mosquito *Aedes albopictus*. Vector Borne Zoonotic Dis 7:76–85

Charrel RN, de Lamballerie X, Raoult D (2007) Chikungunya outbreaks – the globalization of vector borne diseases. N Engl J Med 356:769–771

Cheong WH, Mak JW, Naidu S, Mahadevan S (1981) *Armigeres subalbatus* incriminated as an important vector of the dog heartworm *Dirofilaria immitis* and the bird *Cardiofilaria* in urban Kuala Lumpur. Southeast Asian J Trop Med Public Health 12:611–612

Delatte H, Bagny L, Brengue C, Bouetard A, Paupy C, Fontenille D (2011) The invaders: phylogeography of dengue and chikungunya viruses *Aedes* vectors, on the south west islands of the Indian Ocean. Infect Genet Evol. doi:10.1016/j.meegid.2011.07.016

Dujardin JP, Slice DE (2006) Contributions of morphometrics to medical entomology. Wiley, pp 435–447. 10.1002/9780470114209.ch25, http://dx.doi.org/10.1002/9780470114209.ch25

Dujardin JP, Thongsripong P, Henry AB (2012) The mosquito fauna: from metric disparity to species diversity. In: Wahl C (ed) Morphometrics. InTech, ISBN: 978-953-51-0172-7, Available from: http://www.intechopen.com/books/morphometrics/the-mosquito-fauna-from-metric-disparity-to-species-diversity

Gould DJ, Bailey CL, Vongpradist S (1982) Implication of forest mosquitoes in the transmission of *Wuchereria bancrofti* in Thailand. Mosq News 42:560–564

Gübler DJ (1996) The global resurgence of arboviral diseases. Trans R Soc Trop Med Hyg 90:449–451

Hapuarachchi HC, Bandara KB, Sumanadasa SD, Hapugoda MD, Lai YL, Lee KS, Tan LK, Lin RT, Ng LF, Bucht G, Abeyewickreme W, Ng LC (2010) Re-emergence of Chikungunya virus in South-east Asia: virological evidence from Sri Lanka and Singapore. J Gen Virol 4:1067–1076

Henry A, Thongsripong P, Fonseca-Gonzalez I, Jaramillo-Ocampo N, Dujardin JP (2010) Wing shape of dengue vectors from around the world. Infect Genet Evol. doi:10.1016/j.meegid.2009.12.001

Jirakanjanakit N, Leemingsawat S, Thongrungkiat S, Apiwathnasorn C, Singhaniyom S, Bellec C, Dujardin JP (2007) Influence of larval density or food variation on the geometry of the wing of *Aedes (Stegomyia) aegypti*. Trop Med Int Health 12:1354–1360

Kumar NP, Rajan J, Kamaraj T, Jambulingam P (2008) A226v mutation in virus during the 2007 chikungunya outbreak in Kerala, India. J Gen Virol 89:1945–1948

Manju GE, Sushamabai S (2009) Outbreak of Chikungunya disease in Kerala in 2007. Indian Pediatr 46:440

Morales Vargas RE, Phumala-Morales N, Tsunoda T, Apiwathnasorn C, Jean-Pierre D (2013) The phenetic structure of *Aedes albopictus*. Infect Genet Evol 13:242–251

Paupy C, Girod R, Salvan M, Rodhain F, Failloux AA (2001) Population structure of *Aedes albopictus* from La Reunion island (Indian Ocean) with respect to susceptibility to a dengue virus. Heredity 87:273–283

Paupy C, Delatte H, Bagny L, Corbel V, Fontenille D (2009) *Aedes albopictus*, an arbovirus vector: from the darkness to the light. Microbes Infect 11:1177–1185

Rattanarithikul R, Harbach R, Harrison B, Panthusiri P, Jones J, Coleman R (2005a) Illustrated keys to the mosquitoes of Thailand. II. Genera *Culex* and *Lutzia*. Southeast Asian J Trop Med Public Health 36:1–97

Rattanarithikul R, Harrison BA, Panthusiri P, Coleman RE (2005b) Illustrated keys to the mosquitoes of Thailand I. Background; geographic distribution; lists of genera, subgenera, and species; and a key to the genera. Southeast Asian J Trop Med Public Health 36:1–80

Rattanarithikul R, Harrison BA, Harbach RE, Panthusiri P, Coleman RE (2006a) Illustrated keys to the mosquitoes of Thailand IV. *Anopheles*. Southeast Asian J Trop Med Public Health 37:1–128

Rattanarithikul R, Harrison BA, Panthusiri P, Peyton EL, Coleman RE (2006b) Illustrated keys to the mosquitoes of Thailand III. Genera *Aedeomyia*, *Ficalbia*, *Mimomyia*, *Hodgesia*, *Coquillettidia*, *Mansonia*, and *Uranotaenia*. Southeast Asian J Trop Med Public Health 37:1–85

Rattanarithikul R, Harbach RE, Harrison BA, Panthurisi P, Coleman RE, Richardson J (2010) Illustrated keys to the mosquitoes of Thailand. VI. Tribe Aedini. Southeast Asian J Trop Med Public Health 41:1–225

Reiter P, Fontenille D, Paupy C (2006) *Aedes albopictus* as an epidemic vector of chikungunya virus: another emerging problem? Lancet Infect Dis 6:463–464

Rezza G, Nicoletti L, Angelini R, Romi R, Finarelli AC, Panning M, Cordioli P, Fortuna C, Boros S, Magurano F, Silvi G, Angelini P, Dottori M, Ciufolini MG, Majori GC, Cassone A (2007) Infection with chikungunya virus in Italy: an outbreak in a temperate region. Lancet 370:1840–1846

Rosen L, Rozeboom EL, Reeves WC, Saugrain J, Gubler DJ (1976) A field trial of competitive displacement of *Aedes polynesiensis* by *Aedes albopictus* on a Pacific atoll. Am J Trop Med Hyg 25:906–913

Satitvipawee P, Wongkhang W, Pattanasin S, Hoithong P, Bhumiratana A (2012) Predictors of malaria-association with rubber plantations in Thailand. BMC Public Health 12:1115

Sumodan PK (2003) Potential of rubber plantations as breeding source for *Aedes albopictus* in Kerala, India. Dengue Bull 27:197–199

Tanaka K, Mizusawa K, Saugstad E (1979) A revision of the adult and larval mosquitoes of Japan (including the Ryukyu archipelago and the Ogasawara islands) and Korea (Diptera: Culicidae). Contrib Am Entomol Inst (Ann Arbor) 16:1–987

Tawatsin A, Pengsakul T, Bhakdeenuan P, Chanama S, Anantgapreecha S, Molito C, Chompoosri J, Thammapalo S, Sawanpanyalert P, Siriyasatien P (2009) Outbreak of chikungunya fever in Thailand and virus detection in field population of vector mosquitoes *Ae. Aegypti* (L.) and *Ae. albopictus* Skuse (Diptera: Culicidae). Southeast Asian J Trop Med Public Health 40:951–962

Taysum DH (1956) A medium for the cultivation of bacteria from Hevea latex. Appl Microbiol 19:54–59

Triteeraprapab S, Kanjanopas K, Suwannadabba S, Sangprakarn S, Poovorawan Y, Scott AL (2000) Transmission of the nocturnal periodic strain of *Wuchereria bancrofti* by *Culex quinquefasciatus*: establishing the potential for urban filariasis in Thailand. Epidemiol Infect 125:207–212

Tsetsarkin KA, Chen R, Leal G, Forrester N, Higgs S, Huang J, Weaver SC (2011) Chikungunya virus emergence is constrained in Asia by lineage-specific adaptive landscapes. Proc Natl Acad Sci U S A 10819:7872–7877

Yergolkar PN, Tandale BV, Arankalle VA, Sathe PS, Sudeep A, Gandhe SS, Gokhle MD, Jacob GP, Hundekar SL, Mishra AC (2006) Chikungunya outbreaks caused by African genotype, India. Emerg Infect Dis 12:1580–1583

Part IV
Monitoring and Data Acquisition

Chapter 11
Rescuing Public Health Data

Marc Choisy, Philavanh Sitboulang, Malyvanh Vongpanhya, Chantalay Saiyavong, Bouaphanh Khamphaphongphanh, Bounlay Phommasack, Fabrice Quet, Yves Buisson, Jean-Daniel Zucker, and Wilbert van Pahuis

Abstract Modeling approaches in science can be dichotomized between the statistical versus the mathematical models. The former are strongly data oriented (experimental or field data) and can be used for quantitative predictions. The latter are more qualitative and conceptual and focus more on explaining the mechanisms ruling the phenomena under study. A powerful approach that has been developed recently aims at combining the advantages of both methods by fitting mathematical models to real data. Modern computers allow to simulate models that are more and more complex. Furthermore, recent statistical developments and algorithms allow to fit models to data that are importantly noisy and generated from natural systems that can be strongly nonlinear. A requirement is to have numerous enough data containing enough information. These technical advances bring new opportunities

---

M. Choisy (✉)
MIVEGEC (UMR IRD, CNRS, Universités Montpellier 1 & 2), Montpellier, France
e-mail: mchoisy@gmail.com

P. Sitboulang • M. Vongpanhya • F. Quet • Y. Buisson
Institut de la Francophonie pour la Médecine Tropicale (AUF-IFMT), Vientiane, Laos

C. Saiyavong
Epidemiology Unit, Vientiane Capital Department of Health, Vientiane, Laos

B. Khamphaphongphanh
Epidemiology Division, National Center for Laboratory and Epidemiology (NCLE), Ministry of Health, Vientiane, Laos

B. Phommasack
National Emergent Infectious Disease Coordination Office (NEIDCO), Ministry of Health, Vientiane, Laos

J.-D. Zucker
IRD, UMI 209, UMMISCO, IRD France Nord, F-93143 Bondy, France

Sorbonne Universités, Univ Paris 06, UMI 209, UMMISCO, F-75005 Paris, France

ICAN, AP-HP, Pitié-Salpêtrière hospital, F-75013 Paris, France

USTH, MSI-ICT Lab, 18 Hoang Quoc Viet, Cau Giay, Hanoi, Vietnam

W. van Pahuis
Graduate School of Public Health, University of Pittsburgh, Pittsburgh, PA, USA

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_11

to the scientific method. From a practical point of view, this method extends the possibilities of prediction by extrapolation. We here present how such methodology can be applied in epidemiology. Human infectious diseases have been routinely monitored by health authorities for a long time in a number of countries around the world. Yet, until recently, such data have rarely been exploited neither for scientific nor for public health purposes, the main reason being a quality of data often judged too poor (bias, missing values, etc.). On the other hand, these data are impressively abundant and offer unique opportunity to study infectious diseases over broad spatial and temporal ranges. We show how the abundance of data can partially compensate their quality issues and how biases can be dealt with in an efficient manner. Such public health data have been extensively collected in many parts of the world but have rarely been exploited so far. Furthermore, most of these data are currently in paper forms without any copy and thus prone to destruction. One aim of the Bill & Melinda Gates Foundation-funded Vaccine Modeling Initiative is to collect these data and convert them to electronic databases that are both safe and open for the whole scientific community for thorough exploitation. We present the achievement of this initiative on dengue fever in Southeast Asia.

11.1 Introduction

Tycho Brahe (1546–1601) was born 3 years after Nicolaus Copernicus (1473–1543)'s death and 18 years before Galileo Galilei (1564–1642)'s birth. One of his major occupations was astronomy, and he spent a substantial part of his life laboriously recording the positions of celestial objects. It is by using this enormous amount of data – of exceptional quality for that time – that Johannes Kepler (1571–1630), one of his very last assistants (he had more than 100 during his career), derived his laws of planetary motion between 1609 and 1619. These laws largely influenced Isaac Newton (1642–1727) in the elaboration of his theory of universal gravitation a century after Tycho Brahe started collecting data (1687).

This famous example, from the time when modern science really emerged (notably with Galileo Galilei and his controversial defense of heliocentrism), illustrates perfectly the constant dialog between data analyses and theoretical developments that has been at the basis of the scientific method since then. Astronomy has this in common with epidemiology that experimentation is impossible. Data come uniquely from observations of the natural system. This has both advantages and disadvantages. The disadvantages are obvious and pertain to the issues of data quality and control of potential confounding effects. But observation data are also strong assets that are rarely recognized as they should: they are the real data of the natural system and not data of an artificial experimental system.

Epidemiology is the science studying the distribution of diseases in space and time. Modern epidemiology is considered to have emerged with the pioneering investigation of John Snow (1813–1858) on the causes of cholera in London during the third pandemic (1846–1861). By carefully mapping the addresses of all recorded cholera cases, John Snow could identify clusters of cases and thus hypothesize on the role of one water distribution pump in the infection of the inhabitants of the neighbor. By removing the handle of the pump, he famously ended the epidemic. This event remains today as a classical example of successful public health intervention. More than that, these observations and his intervention proved the role of water in the transmission of the disease, which was eagerly debated at the time, 30 years before the identification of the etiologic agent by Robert Koch (1843–1910).

This chapter is about the key role that public health surveillance data play in the science of epidemiology. For long, the purpose of surveillance data collection was limited to the purpose of local or national public health monitoring only, and epidemiological investigations could be envisaged only in the context of well-defined cohort studies. The recent recognition that unique and extremely valuable information could also be drawn from surveillance data, despite their inherent quality issues, opens totally new avenues of investigation. But at the same time that the value of such data is recognized, their persistence is more than ever threatened, and it is likely that if no action is taken, a large proportion of it will be lost before having the opportunity to be analyzed by scientists. That would constitute an important loss for science but also for global and public health. In this chapter, we review the pros and cons of surveillance data and show how these can be efficiently analyzed to get an understanding of epidemiological systems that could have not be reached by any other classical epidemiological study. After a review of the major surveillance data-based results obtained over the last decade, we will present the challenges we are faced with concerning preservation and sharing of public health data and the initiatives that are currently undertaken to preserve this global source of historical information and improve its quality for the future. The end of the chapter will be illustrated by the initiative carried out for dengue syndromic data in Southeast Asia.

11.2 The Scientific Method

The scientific reasoning grounds on the hypothetico-deductive method in which theoretical hypotheses are formulated and empirically tested for possible refutation. The experimental approach has long been and still holds as the gold standard for hypothesis testing. A well-designed experimental setup allows, first, to control for effects that are of no interest to the study but still can affect the results (confounding variables) and, second, to produce data amenable to proper and efficient statistical treatments. The control of confounding variables addresses the "everything else being equal" prerogative by ensuring that individuals of the sample are as homogeneous as possible for the factors that are not the focus of the analysis. The classical statistical theory and scientific controlled experiments developed hand in hand in the field of agronomy during the first half of the twentieth century, during which most of the classical tests and models (t-test, F-test, χ^2-test, analysis of variance, linear regression, etc.) were developed by researchers such as Karl Pearson (1857–1936), Ronald Fisher (1890–1962), and Jerzy Neyman (1894–1981), to cite only the most famous of them. This statistical framework is extremely powerful but has the inconvenience of being also extremely restrictive. The famous three assumptions of the linear regression (normality, independence, and homoscedasticity of data) illustrate such strong constraints of the statistical theory, and researchers strive hard to comply with them. Experimental design is the most appropriate way to do so. Out of despair, others sometimes resort to ad hoc data transformation.

If experimental designs allow to efficiently control for confounding effects to statistically test for effects under study, they also have major drawbacks that tend, too often, to be eluded. Indeed, one should not lose sight of the fact that his/her experimentally controlled results, however statistically strong they may be, are true for the specific system under study, in that case the experimental setup, which is generally far from a real natural system. What is true in the laboratory may not be true in nature, and vice versa. This is all too much known by pharmacologists who design new medicines. A new engineered molecule has to go through a series of successive tests and filters before being granted for release in the general population. One of the final of such steps – clinical trial – aims at verifying that the effects of the molecule in the general population is not different from those observed in the laboratory. A number of molecules have failed this last stage, with excellent results in the laboratory and highly detrimental effect in real field situations. Some antimalaria molecules are thus extremely efficient in controlled laboratory situations and yet totally inefficient in natural for reasons not always understood (Nacher 2001, 2006). The experimental method, despite its rigor and powerfulness, has thus a major drawback, which is that the system under study is not exactly the real natural system.

As reminded in the introduction, experimentation is impossible in epidemiology for obvious ethical reasons. Thus, the abovementioned problem of representativity of nature does not hold in epidemiology. However, other problems naturally arise, related to the ability of analyzing data that are highly variable, biased, incomplete, and complex. Mathematical modeling is of great use to this.

11.3 Mathematical and Computational Resources

Modeling is more and more used in biology in general and in health sciences in particular, as attested by the growing number of scientific publications including modeling work (Levin et al. 1999; Cohen 2004). However, behind the word of modeling are a large number of different practices that differ in their approaches and their aims and that are quite often mixed up (Hilborn and Mangel 1997). For example, a major distinction stands between mathematical modeling and statistical modeling. Statistical modeling is basically what has been treated in the previous paragraph. Such modeling is by essence data oriented and is interested in the relationships between variables. Its purposes include hypotheses testing and predictions. As explained above, this modeling approach is efficient as long as the data in question comply with the underlying assumptions of the statistical theory at use. At the opposite of this approach is mathematical modeling, which is typically disconnected from data. Its fundamental aim is to understand the mechanics of the system that generate the observed relationships between variables. The major limitation of mathematical models, besides being disconnected from any form of real data, is that mathematical tractability often imposes oversimplifications of the system. Statistical and mathematical models oppose in many other respects: whereas statistical models are intrinsically quantitative, mathematical models are often qualitative; whereas statistical models are necessarily phenomenological, mathematical models can be mechanistic; whereas statistical models are by nature very precise and specific (to the sample or the population from which this sample is drawn), mathematical models are more general but also more vague.

More and more, statistical and mathematical models are considered as extremes of a same continuum, and the emerging trend in science is now to adopt a modeling approach that combines the advantages of both statistical and mathematical modeling (Fig. 11.1).

This is made possible by both the availability of ever more data and the raising computational ability to process them. With the development of the statistical theory of likelihood and, above all, its practical application to complex systems made possible by the availability of huge computer power, the idea now is to develop mathematical models both mechanistic and specific to a real system and to estimate its parameters by comparing its predicted variable values with real data. A model, be it mathematical or statistical, is made of two kinds of entities: the variables and the parameters (Fig. 11.2).

The variable, as its name indicates, is a quantity that varies and that can be measured directly. A number of diseased individuals is an typical example of a variable. A parameter is a quantity that is fixed by the modeler (or a program), which determines the fate of the variables' values and which cannot be measured directly. The major difference between phenomenological statistical and mechanistic mathematical models is that parameters do not necessarily – and most of the time they do not – have a biological meaning for statistical models, whereas they always have for mathematical models. The slope of a linear regression is a typical parameter for a statistical model: it does not mean much biologically besides giving an idea of

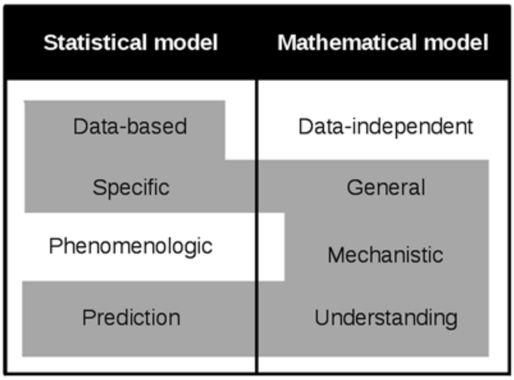


Fig. 11.1 Comparison of statistical and mathematical models as classically used. The trends today, thanks to the availability of enormous amount of data, but also to computer power, are to develop modeling approaches that combine the advantages of both statistical and mathematical models

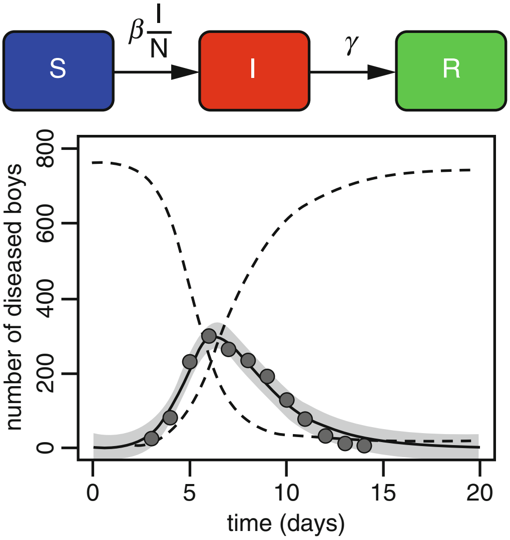


Fig. 11.2 The classical SIR compartment model and its fit to a local influenza epidemics. The total host population is partitioned into three compartments according to their clinical status, susceptibles (S), infected (I), and recovered I, the three state variables of the model. The two parameters are the contact rate (β) and the recovery rate (γ). The *dots* are the data, i.e., number of infected children in an English school board from day 3 to day 14. We use the information in this data set to fit the model-predicted prevalence (*full line curve*) as good as possible. This allows to make inference on the contact rate (1.67/day), the recovery rate (0.43/day), and the dynamics of the number of susceptibles and recovered (*dashed curves*, respectively), two parameters, and two variables that could not be measured directly (Source of data: 4th March edition of the British Medical Journal, 1978)

the association between two variables. A recovery rate is a typical example of a parameter for a mathematical model: the parameter necessarily has a biological meaning, by construction. These parameters always have a clear biological meaning, and hence they may be difficult or even impossible to measure in practice. It is here that the method of maximum likelihood plays its powerful role in allowing to estimate the values of the model's parameters.

A likelihood function depends on both data and parameters and expresses the probability that the data could have been generated by the model with specified parameters' values. For that, it compares the values of the model's variables for which data are available with their values that are actually measured. The comparison is made probabilistically. With such a likelihood function, the game is easy in principle: looking for the combination of parameters' values that yields the maximum likelihood. This combination gives the maximum-likelihood estimates of the parameters (Fig. 11.3).

All the powerfulness of the method lies here: by using information on a variable we can measure directly (such as the number of diseased individuals), we can

$$-LL(\beta,\gamma,\sigma) = -\sum_{t=3}^{14} \log(p[I_t^{pred}=I_t^{obs}|\beta,\gamma,\sigma]) = \frac{1}{2}\log(2\Pi\sigma^2) + \sum_{t=3}^{14} \frac{[I_t^{pred}(\beta,\gamma,\sigma)-I_t^{obs}]^2}{2\sigma^2}$$

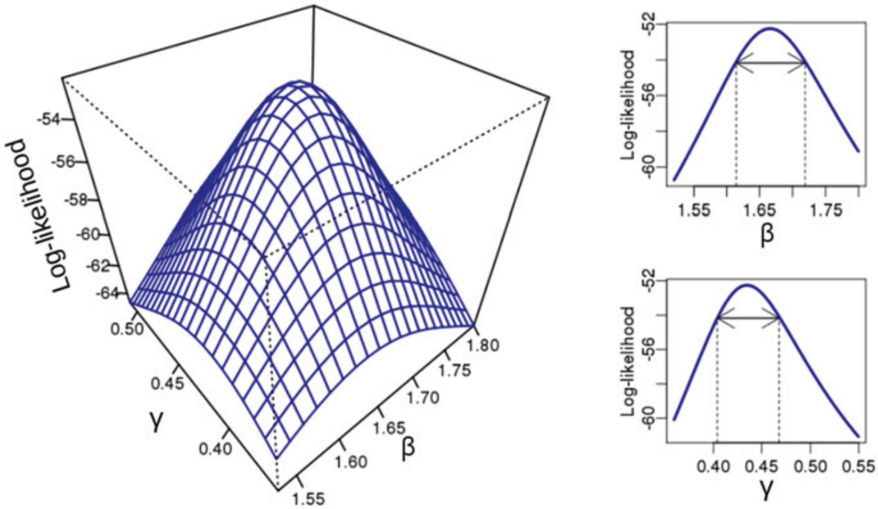


Fig. 11.3 The likelihood function applied to the model of Fig. 11.2. The *left* 3D plot shows the log-likelihood surface as a function of the value of the two parameters β (contact rate) and γ (recovery rate). The summit of this surface defines the maximum-likelihood estimates of the parameters (1.67 and 0.43, respectively). The two panels on the right show log-likelihood profiles and the use of the likelihood ratio test to estimate confidence intervals of the estimations

estimate the value of parameters of biological importance that can be out of reach by direct measure, such as a recovery rate. If simple in principle, the method can quickly become complicated in practice, especially for models with a large number of variables and parameters. More and more efficient searching algorithms and increasing computer power make such task more and more accessible. Thanks to their high flexibility, mathematical models allow to analyze complex data that would not be possible to analyze with classical statistical tools. They also allow one to analyze it in a powerful manner by using as much information from the data as possible. Given that data collection can be extremely expensive, these two points are of prime value.

The use of mathematical models and the fit of their parameters' values to data are a major shift in the scientific methodology. Instead of forcing the nature to comply with a predefined restrictive – though powerful – statistical theoretical framework, the effort is now made on the theoretical side in developing mathematical models that allow to analyze any form of data, however complicated and unorthodox they may be. By being able to draw valuable information from any form of data, we thus broaden the possibilities of scientific investigation by several orders of magnitude.

11.4 Surveillance Data and Their Quality

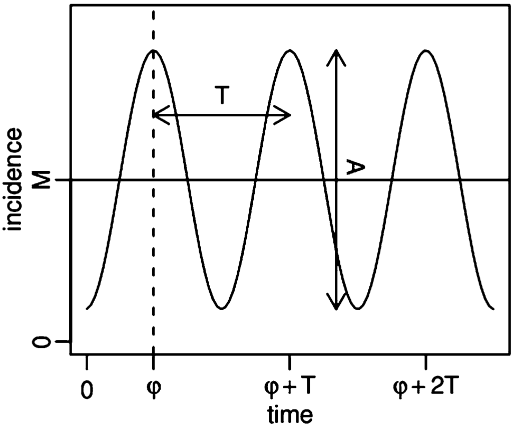
Any patient who enters a hospital is, at some stage, recorded with basic information regarding his gender, age, address, symptoms, and sometimes diagnosis. The aim of such records is to monitor the hospital activity. Sometimes, hospitals communicate with each other and can possibly share or exchange information from their records. It is through such practices that coincidental apparitions of rare diseases in the early 1980s on both coasts of the USA first alerted public health service about a new epidemic that soon after would be known all around the world as HIV/AIDS (Montagnier 2002).

Even long before the start of the first large-scale vaccination campaigns, infectious diseases, especially the most prevalent ones, have been the object of surveillance, through networks of health professionals and institutions, either on a voluntary or a compulsory basis (Rohani and King 2010). The primary aim of such surveillance was public health monitoring, and it became readily used after the start of the first vaccine policies in the 1940s and the 1950s in Europe and North America as a way of assessing the efficacy of disease prevention. However, the use of such data for scientific purpose remained very limited. Indeed, researchers have long refrained from using surveillance data arguing on their poor quality.

It is a fact that surveillance data such as the ones described above suffer from a number of quality issues. The first one is bias. Contrary to sentinel surveillance where a sample from the general population is chosen at random and actively tested for the disease under study (by serology or PCR), the surveillance data we are dealing with here are passively recorded from the people who do check for medical aid, and this is the source of a number of potential biases. First, people looking for medical assistance are clearly not representative of the general population, and this is strongly affected by socioeconomic factors. The high sex ratio bias in favor of males among tuberculosis-diagnosed patients is interpreted in some countries as the result of social pressures or habits where females seek for medical care less than males, especially in the case of stigmatizing diseases such as tuberculosis (Neyrolles and Quintana-Murci 2009). Second, asymptomatic carriers obviously do not seek for medical care, and yet they can play an important role in the epidemiological dynamics of the disease. Third is the problem of diagnostic: contrary to active sentinel studies where sample sizes are small enough to allow the use of sensitive and specific molecular diagnosis methods, the diagnosis carried out in case of passive surveillance systems mostly relies on symptoms, and the criteria are rarely consistent neither in space (despite WHO's efforts to homogenize it) nor in time, not speaking of the subjectivity of the examiner (HMN 2008). In addition to these biases, passive surveillance data also often suffer from frequent errors or missing values. There can be also underreporting for very small incidences (where the medical staff is not alert enough about the risk of a particular disease) or for very large incidences (where the medical staff get overwhelmed with too many patients).

Surveillance data thus suffer from a number of serious quality issues. However, they still remain the unique source of information over large spatial and temporal

Fig. 11.4 The anatomy of a periodic time series can be summarized by four statistics. Two of them are quantitative (the average M and the amplitude A) and are potentially affected by biases in the reporting rate. Two are qualitative (the period T and the phase φ) and robust to biases in the reporting rate



ranges. We thus have to find clever ways to use this valuable source of information. There are basically two ways to deal with biases. The first one is to use methods that are robust to biases; the second one is the correct for biases. For someone interested in the epidemiological dynamics of infectious diseases, in their seasonality of recurrence over multiyear periods, it is a fact that bias would largely affect the quantitative characteristics of such dynamics such as average incidences or amplitudes. However, it is as much a fact that biases will have only a very limited impact on qualitative features of the dynamics such as periodicity of epidemic peak recurrence (period) or the timing of these peaks (phase) (see Fig. 11.4).

There are a number of powerful statistical methods that allow to extract the qualitative statistics of the time series and to perform a number of scientific analyses which are robust to biases. The next section reviews some of them. The second method to deal with bias is to correct it or, more correctly, to account for it. This implies having some source of information on the potential biases. It can come from the surveillance recommendations, such as WHO's criteria for diagnosis, or from other complementary studies performed at much smaller scales such as sentinel surveillance. By taking advantage of the flexibility of mathematical models, as exposed in the previous section, one can incorporate these information into his/her model, thus explicitly accounting for possible major historical shift in diagnosis methods or any other source of bias. Even more powerful than that can be the situation where we suspect the specific bias to exist but we are not able to assess it by any means. In the previous section, we emphasized the powerfulness of mathematical modeling interfaced with real data within the maximum-likelihood framework. We indeed explained how parameters with clear biological meaning could be estimated by using the information that can be measured on variables. We can thus adopt this very approach here, and the bias, which would be one parameter of our model, could be estimated by maximum likelihood exactly the same way as any other parameter. This has been successfully applied recently on cholera in the state of Matlab in India. Since the pioneering work of John Snow (see introduction), it has been known that cholera can be transmitted either directly from person to person or indirectly through contaminated water. However, the respective weights of both routes of transmission remain lively debated, and a central topic of the debate has to do with the possibility of asymptomatic carriers who would not be counted in the incidence but yet who would play an important role in the incidence's dynamics. Using a mathematical model allowing the possibility of such asymptomatic carriers to analyze long-term cholera incidence time series within a maximum likelihood, Aaron King and his colleagues managed to demonstrate the existence of such asymptomatic carriers and to estimate their prevalence in the population (King et al. 2008). In the next section, we briefly review a number of studies that have been particularly influential to the scientific use of surveillance data, despite all the acknowledged quality issues.

11.5 Major Studies Based on Infectious Disease Surveillance Data

Surveillance records of major infectious diseases started at the end of the nineteenth century, but it is not before the early 2000s that their analysis with the approach exposed above really started. The work of Bryan Grenfell on measles and other childhood diseases in England and Wales was particularly influential. The extremely simple life cycle (high force of infection and permanent immunity after recovery) of childhood diseases makes them particularly amenable to analysis with mathematical models and parameter estimation with maximum likelihood. These diseases also often display specific symptoms (e.g., measles, pertussis, chicken pox), rendering their symptom-based diagnosis reliable, and they often display high incidences – at least in the pre-vaccine eras – and regular epidemics, easing the study of their dynamics. In addition to these surveillance data sets of exceptional quality and spatiotemporal coverage available in England and Wales, demographic information of similar quality and resolution are also available. Vaccine coverage is also available most of the time in the vaccine era. The study of more than six decades of such data allowed an unprecedented opportunity to investigate the role of demographic transitions and vaccination on the epidemiological dynamics of infectious diseases and to understand the laws that govern their diffusion in space. It has thus been shown that the recurrence of childhood diseases (annual, biannual, triannual, or any other multi-annual regimen), however complicated it may be, can be efficiently predicted simply from birth rate and vaccine coverage (Earn et al. 2000; Grenfell et al. 2002; Bjørnstad et al. 2002). The study of the timing of epidemics of measles in different localities of England and Wales, both before and after vaccine policies, revealed the mechanism of spatial diffusion where large cities lead the nationwide epidemiology according to a gravity-like process in which distances and population size are the main two predictors of spatial dynamics (Grenfell et al. 2001; Xia et al. 2004). This mechanism has been later on successfully verified on a variety of infectious diseases, childhood (pertussis), and others (influenza, Viboud et al. 2006).

Besides geography, demography, and vaccination, there have been investigations on the role of other mechanisms in driving infectious epidemiological dynamics. Among the most notable are climatic, socioeconomic, and immunological factors. Investigations on the putative impact of climatic conditions on the transmission of infectious diseases have been triggered by the general growing concern about global climate changes (IPCC, International Panel on Climate Change).

Climatic conditions are expected to affect disease transmission for different reasons. For diseases transmitted directly through aerial droplets, it is plausible that the survival of viral particles in these droplets and thus their infectiousness depend on climatic conditions such as humidity or temperature, as demonstrated for influenza virus both experimentally (Shaman and Kohn 2009) and empirically (Alonso et al. 2007; Shaman et al. 2010). The effect of climatic conditions is however expected to be even stronger on diseases that are either environmentally transmitted such as cholera or transmitted by vectors such as malaria or dengue fever. Cholera is a disease caused by the bacteria *Vibrio cholerae*. This bacterium naturally thrives on the surface of estuarine copepods with which it maintains a symbiotic interaction. Modifications in sea water temperature can stimulate the development of resources on which the cholera-carrying copepods feed, thus stimulating its development, which rises to several order of magnitude the probability of the copepods and the *V. cholerae* they carry to get into contact with human beings. Once such a contact has happened, an epidemic can start and spread in a human population at an incredible pace. In these conditions, we expect cholera epidemics from surveillance data to be synchronized with sea surface temperature that can be easily estimated from satellite images. This has been verified not only on the seasonal scale but also on the longer periods (3 to 7 years) of the El Niño Southern Oscillation (ENSO) (Pascual et al. 2000, 2002). Vector-borne diseases are the other group of diseases for which climatic factors are expected to influence the epidemiological dynamics. Indeed, most vector animal species, particularly the arthropod ones, have a population dynamics extremely dependent on climatic conditions for metabolic reasons (temperature) or for physical reason (rainfalls creating breeding niches). The role of temperature and rainfall on the development rate of dengue and malaria vectors has been demonstrated in the laboratory, and presence/absence field data tend to confirm this (Craig et al. 1999). However, this has never been precisely quantified in the field so far, for what concerns the timing of epidemics in one season and its severity.

The long underestimated effects of behavioral and socioeconomic factor effects on the epidemiological dynamics of major infectious diseases become more and more documented. Soper in 1929 (Soper 1929) was one of the very first to recognize the strong forcing that the alternation of vacations and school terms could have on the seasonality of measles among English children. This has been largely confirmed in recent studies where the precise school calendar can be included in the model (Keeling and Grenfell 1997). The structure of social contact is also a strong determinant of disease dynamics (Keeling and Eames 2005). Age structure is the most obvious one (Mossong et al. 2008) and has been recently put forward to explain the mysterious reemergence of pertussis in high-coverage vaccinated countries such as

Denmark (Rohani et al. 2010). Sexually transmitted diseases are the class of diseases where such social structure is intuitively expected to play the most important role. It is a well-known fact now that diseases such as HIV/AIDS have a totally different epidemiology in the homosexual and the heterosexual populations, among other factors (Keeling and Rohani 2008). The precise nature of the contact network here plays a key role (Eames and Keeling 2002). On the more economic side, it is only recently that links between economic welfare and infectious disease epidemiology have started to be investigated, with very promising possibilities (Bonds and Rohani 2009; Bonds et al. 2009).

The picture would not be complete without mentioning the immunological factors. This concerns diseases caused by pathogens that alternate (e.g., dengue serotypes) or succeed to each other (e.g., influenza strains) in time. A number of organisms causing infectious diseases have this particularity that the time scales of their molecular evolution and of their epidemiological dynamics are of the same order (Earn et al. 2002), allowing to study the interactions between these two sorts of mechanisms (Grenfell et al. 2004; Bedford et al. 2010).

The studies briefly reviewed above revealed the richness of mechanisms that can explain the epidemiological dynamics of infectious diseases. These can be immunological, climatic, environmental, behavioral, socio-economical, demographic, etc. Interestingly, it has also been proposed that infectious diseases can affect each others' dynamics, and this has been shown on childhood measles and whooping cough which infect the same cohort of children. Any child having one of these diseases is usually kept at home, which makes him/her unavailable for infection by the other disease, thus leading to some interference between the two diseases' dynamics (Rohani et al. 1998, 2003). All these studies that we presented in this section have thus contributed to some of the major changes in the history of infectious disease epidemiology. None of them would have been possible without the availability of long-term time series of surveillance notifications. The qualities of these data are unequal, but their strength resides in their huge quantity, allowing comparative and long-term studies that unravel singular mechanism that could not be detected otherwise. The availability of such data opens totally unexplored fields in epidemiology, and this is a paradigm shift that can be compared to the one that happened in astronomy with the use of the very first telescopes, which were of terrible quality too! It is likely that the transmission of diseases is multifactorial. One of the major challenges in the future would be to quantify the respective weights of the different factors that can affect infectious disease transmission. Indeed, a number of debates currently revolve around the major drivers of infectious disease dynamics. This is the case, for example, for dengue in Thailand where demographic factors have been put forward by some researchers (Cummings et al. 2004), whereas climatic factors have been claimed to play the most important role (Cazelles et al. 2005) and immunological interactions between the four serotypes by other groups (Adams et al. 2006; Wearing and Rohani 2006). Similarly, the respective importance of demographic (Viboud et al. 2006), climatic (Shaman et al. 2010), and immunological factors (Bedford et al. 2010) on the epidemiological dynamics of seasonal human influenza is still largely unresolved. Even measles, the paradigmatic model on the influence of demographic factors on epidemiological dynamics, seems also to be affected, to some extent, by climatic factors (Ferrari et al. 2008). Model confrontations in the maximum-likelihood framework and comparative analyses will be the ways to resolve these debates. Hence, there is a need for more and more historical surveillance data.

11.6 The Value of and Threats on Public Health Data

It is a fact that infectious disease data suffer from a number of quality issues. However, they also contain a unique source of valuable information that could not be generated by any other means. We hope that the above paragraph has convinced the reader that despite their limitations, surveillance data, when analyzed with appropriate mathematical and statistical tools, can lead to results of major significance, both from the basic scientific and the applied public health perspectives.

Scientific data are expensive to generate. Look at any research project and you will see that the largest chunk of its budget is devoted to data collection. And yet, most of the time, these data are analyzed only once, in the very study that did collect them. These data are stored for a while, and soon, the location of their repository is forgotten, and eventually the data are just lost. A foundation of modern science is repeatability, including repeatability of data analysis. This latter clearly cannot be ensured any more if the data disappear. Furthermore, there is often much more information in a data set than the information used for the purpose of their collection. But this information cannot be used if the data are not made available to other researchers with other research inquiries (Bolker 2005).

The recognition of these issues has recently encouraged researchers to make their data more available. It has been now 30 years that publication of study based on the analysis of molecular sequences requires the publication of original data on the open-access electronic database GenBank (www.ncbi.nlm.nih.gov/genbank). Scientific research founders now more and more require the produced original data to be made freely available to the rest of the scientific community. It also becomes common practice for international scientific journals to require that the data should be made available from electronic repositories such as Dryad (datadryad.org).

These changes in the way to communicate and share scientific data and results are timely and will certainly improve the situation in the future. Historical data that have been collected over long time periods, such as public health surveillance data, all share the same characteristics: (1) they are unique and cannot be collected again (contrary to experimental data for which the experiments can always be rerun); (2) they represent an enormous amount of valuable information that have been rarely really analyzed; (3) they most of the time exist only in paper format, and their number of copies is often low. The studies that have been presented in the previous paragraph were carried out on a very small number of data sets: measles and whooping cough in England and Wales, dengue in Thailand, measles in Niger, and influenza in the USA. This is only the tip of the iceberg of such existing data. This is also the very tiny proportion of such data are currently available in electronic format. Much

Fig. 11.5 Data collection on the field in Laos. (**a**) Particularly unordered public health data threatened by destruction. (**b**) A typical communal health center in rural Laos (Savannakhet province). (**c**) Public health record scanning. (**d**) An exceptionally well-ordered and well-preserved ensemble of public health data (Photos: Marc Choisy)

more of such data exist all around the world in a number of different health centers, hospitals, or ministries. The vast majority of them unfortunately exist only on paper format, in one unique copy, stored in some highly vulnerable place (Fig. 11.5).

These data are historical data spanning several decades, which means that if these data were to disappear, there would be no mean to regenerate them as we could do for classic experimental data. That would thus represent a huge loss for the scientific community, as well as for the public and international health. There is thus an urgent need to secure such data from destruction that can happen at any time by office relocation, flooding, fire, etc.

11.7 Data Rescuing Programs in Southeast Asia and Challenges

The Vaccine Modeling Initiative (VMI, www.vaccinemodeling.org) is a Bill & Melinda Gates Foundation-funded international project, the aim of which is to strengthen the links between mathematical and computational models and public health data. To this purpose, one of its activities consists in creating open-access electronic infectious disease surveillance databases, in the very same spirit as what has been done for molecular sequences with GenBank since the early 1980s. The first such database that has been created is the Tycho database (www.tycho.pitt.edu), named after Tycho Brahe (see introduction). This open-access electronic database is the result of digitization and manual double-blinded entering of the US weekly reports on infectious diseases. It represents a total of 6300 weekly reports for 55 infectious diseases from 1888 to present with data spatially aggregated by states (50) and cities and towns (1,500). In total, this database contains 100 million cases and 4 million deaths, and it took 90-man-year full-time employment to manually enter this database (Van Panhuis et al. 2013).

A similar program of the VMI is currently undertaken in Southeast Asia, focusing primarily on gathering dengue syndromic monthly surveillance notifications. As of today, it contains monthly data (since 1997) aggregated by provinces (189) for Malaysia, Thailand, Vietnam, Cambodia, and Laos, covering a population of 209 million people on 1.6 million km^2 (see Fig. 11.6).

The buildup of such an international database was eased by the fact that these province-aggregated data were already centralized at the level of each country

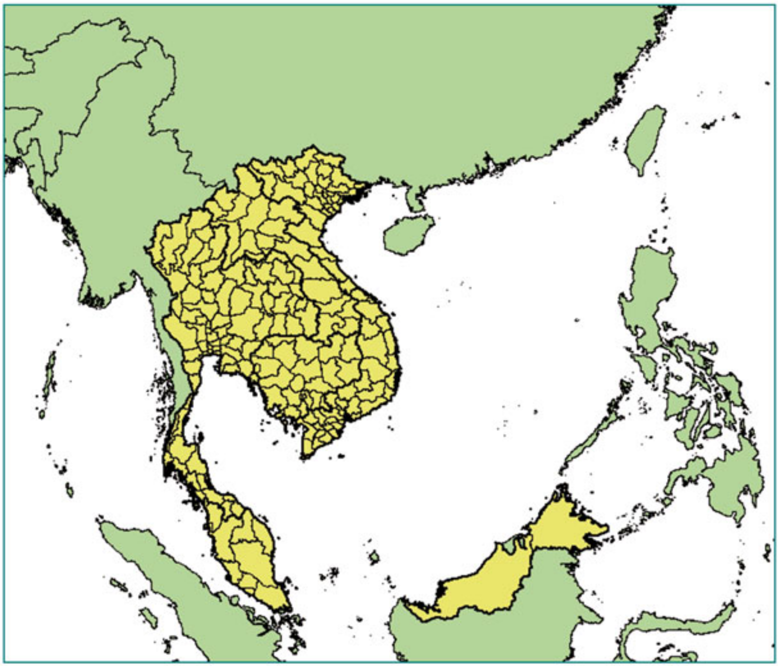


Fig. 11.6 Dengue database in Southeast Asia. Syndromic surveillance notifications have been collected and aggregated by month and province (189) for Malaysia, Thailand, Vietnam, Cambodia, and Laos for the last 15 years. This represents a total population size of 208 million individuals on an area of 1.6 million km^2

(usually the ministries of health). Disaggregated raw data are unfortunately not centralized, and their collection thus demands an important amount of field work.

In most of the countries of the region, public health surveillance networks are hierarchically organized from communal health centers to upper levels, districts, and provinces, up to the ministry of health (Fig. 11.7).

Being able to collect data from each of these levels will allow to assess the quality of data transfer along the national surveillance network, identify major weaknesses, and propose solutions of improvement. A first limitation is related to the lack of homogeneity in notification criteria and human resources, not only between countries but also within countries. The World Health Organization have developed electronic-based surveillance systems that are consistent between countries (HMN 2008), but the lack of equipment, internet access, and computer training for the medical staff unfortunately makes the use of such systems anecdotal in practice. The second major limitation pertains to the quality of information flow along the surveillance network. At each level of the network, information is received from the level below, processed and aggregated by time and space before being transferred to the next level. All this necessarily implies loss of information.

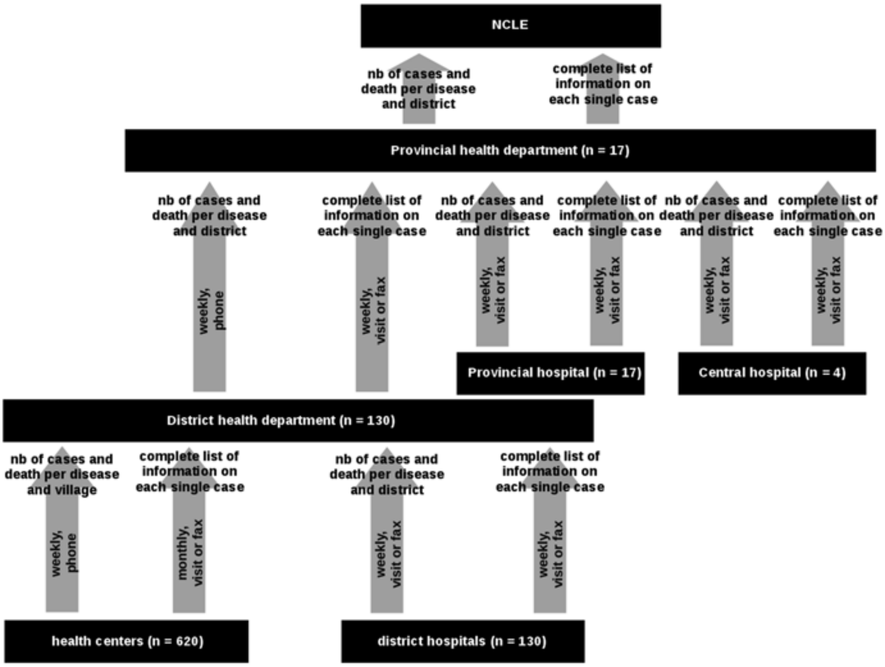


Fig. 11.7 A typical infectious disease surveillance network as implemented in Laos. Numbers in brackets refer to the numbers of health offices at each level. *Arrows* show the flow of information from the lower levels to the higher ones, up to the ministry of health (NCLE, National Center for Laboratory and Epidemiology) (note that all intermediate levels both gather data directly and aggregate data from lower levels before transmitting the total to the upper level)

Moreover, this data processing and aggregation is mostly performed by hand with all the error sources that this involves. In the absence of quality check, errors accumulate and propagate along the network. In the most remote areas, it may also happen that communication between levels is interrupted for various hazard sources.

Collecting disaggregated data at all the levels of the surveillance network will thus allow to identify the major bottleneck in information transfers and the major sources of data quality corruption. Only data aggregated by the province is maintained over a long term at the highest national level (ministry of health). At all other levels, after having processed the data from lower levels and transferred it to the higher level, the recommendation is to keep it for a minimum of 5 years. There are naturally no incentives to destroy the data after 5 years, but, in practice, because of storage space shortage, it is very rare to find disaggregated data older than 5 years. This represents an enormous loss of scientific and public health information. Only an electronic surveillance system would allow to cope with most of the issues raised in this section. By automating aggregation calculation and data transfer, it would reduce errors due to these two processes to its minimum. Furthermore, backup drives at each level would ensure the long-term preservation of raw data without requiring too much physical space. Backup in each health center of the network would also ensure that data are constantly saved in several different places. If one of the centers were to disappear, the data would be preserved in any upper level or could be reconstructed from any lower level.

11.8 Conclusion

Dengue is the first human arbovirus in the world in terms of affected population and population at risk (3.5 billion people, 55 % of the world population is estimated to be at risk by WHO, Beatty et al. 2007). It is primarily affecting the intertropical regions of the world, with a special high and ancient burden in Southeast Asia, and it has become a major international public health issue due to an increase in its worldwide distribution (Gibbons and Vaughn 2002; Guzman and Kouri 2002). In the absence of vaccine, the sole mean of dengue prevention is through vector control. A live-attenuated, tetravalent, chimeric yellow fever dengue vaccine has been in development for many years, and its commercial availability is announced for 2016 (phase III trials started in December 2010) (Guy et al. 2011). Yet, the public health services still have no clue of how to implement the best vaccine policy. It thus becomes timely to start thinking about efficient strategies that will involve both vaccine use and vector control (WHO-VMI Dengue Vaccine Modeling Group 2012). As reminded earlier, experimentation is impossible in epidemiology for obvious ethical reasons. Mathematical and computational modeling thus constitutes the only means we have to explore the efficiency of various vaccine policy scenarios (Ferguson et al. 2005). However, such prospective explorations are possible only with realistic enough models, and this depends strongly on the data available for parameter fitting. In the context of applying a vaccine policy to the Southeast Asia region, a number of questions arise respective to the spatial dynamics of the disease at between-country level. Since the spatial dynamics of a disease at local scales largely determine its persistence at larger scales (Grenfell and Harwood 1997; Earn et al. 1998), it appears most important to understand its major drivers among demographic (population size and birth rate), climatic (affecting vector population dynamics), administrative (contact networks), and immunological (serotype interaction) factors (Racloz et al. 2012). Only historical surveillance data would allow to develop and fit realistic enough models of practical use for the design of an optimal vaccine policy.

References

Adams B, Holmes EC, Zhang C, Mammen MPM Jr, Nimmannitya S, Kalayanarooj S et al (2006) Cross-protective immunity can account for the alternating epidemic pattern of dengue virus serotypes circulating in Bangkok. Proc Natl Acad Sci U S A 103:14234–14239

Alonso WJ, Viboud C, Simonsen L, Hirano EW, Daufenbach LZ, Miller MA (2007) Seasonality of influenza in Brazil: a traveling wave from the Amazon to the subtropics. Am J Epidemiol 165:1434–1442

Beatty M, Letson W, Edgil D, Margolis H (2007) Estimating the total world population at risk for locally acquired dengue infection. Am J Trop Med Hyg 77(Suppl 5):170–257

Bedford T, Cobey S, Beerli P, Pascual M (2010) Global migration dynamics underlie evolution and persistence of human influenza A (H3N2). PLoS Pathog 6:e1000918

Bjørnstad ON, Finkenstädt BF, Grenfell BT (2002) Dynamics of measles epidemics: estimating scaling of transmission rates using a time series SIR model. Ecol Monogr 72:169–184

Bolker B (2005) Other people's data. BioScience 55:550–551

Bonds MH, Rohani P (2009) Herd immunity acquired indirectly from interactions between the ecology of infectious diseases, demography and economics. J R Soc Interface 7:541–547

Bonds MH, Keenan DC, Rohani P, Sachs JD (2009) Poverty trap formed by the ecology of infectious diseases. Proc R Soc Lond B 277:1185–1192

Cazelles B, Chavez M, McMichael AJ, Hales S (2005) Nonstationary influence of El Niño on the synchronous dengue epidemics in Thailand. PLoS Med 2:e106

Cohen JE (2004) Mathematics is biology's next microscope, only better; biology is mathematics' next physics, only better. PLoS Biol 2:e439

Craig MH, Snow RW, le Sueur DA (1999) Climate-based distribution model of malaria transmission in sub-Saharan Africa. Parasitol Today 15:105–111

Cummings DAT, Irizarry RA, Huang NE, Endy TP, Nisalak A, Ungchusak K, Burke DS (2004) Travelling waves in the occurrence of dengue haemorrhagic fever in Thailand. Nature 427:344–347

Eames KTD, Keeling MJ (2002) Modeling dynamic and network heterogeneities in the spread of sexually transmitted diseases. Proc Natl Acad Sci U S A 99:13330–13335

Earn DJ, Rohani P, Grenfell BT (1998) Persistence, chaos and synchrony in ecology and epidemiology. Proc R Soc Lond B 265:7–10

Earn DJ, Rohani P, Bolker BM, Grenfell BT (2000) A simple model for complex dynamical transitions in epidemics. Science 287:667–670

Earn DJD, Dushoff J, Levin SA (2002) Ecology and evolution of the flu. Trends Ecol Evol 17:334–340

Ferguson NM, Cummings DAT, Cauchemez S, Fraser C, Riley S, Meeyai A et al (2005) Strategies for containing an emerging influenza pandemic in Southeast Asia. Nature 437:209–214

Ferrari MJ, Grais RF, Bharti N, Conlan AJK, Bjørnstad ON, Wolfson LJ et al (2008) The dynamics of measles in sub-Saharan Africa. Nature 451:679–684

Gibbons RV, Vaughn DW (2002) Dengue: an escalating problem. Br Med J 324:1563–1566

Grenfell BT, Harwood J (1997) (Meta)population dynamics of infectious diseases. Trends Ecol Evol 12:395–399

Grenfell BT, Bjørnstad ON, Kappey J (2001) Travelling waves and spatial hierarchies in measles epidemics. Nature 414:716–723

Grenfell BT, Bjørnstad ON, Finkenstädt BF (2002) Dynamics of measles epidemics: scaling noise, determinism, and predictability with the TSIR model. Ecol Monogr 72:185–202

Grenfell BT, Pybus OG, Gog JR, Wood JLN, Daly JM, Mumford JA et al (2004) Unifying the epidemiological and evolutionary dynamics of pathogens. Science 303:327–332

Guy B, Almond J, Lang J (2011) Dengue vaccine prospects: a step forward. Lancet 377:381–382

Guzman MG, Kouri G (2002) Dengue: an update. Lancet Infect Dis 2:33–42

Hilborn R, Mangel M (1997) The ecological detective. Confronting models with data. Princeton University Press, Princeton

HMN (2008) Framework and standards for country health information systems. WHO, Geneva

Keeling MJ, Eames KTD (2005) Networks and epidemic models. J R Soc Interface 2:295–307

Keeling MJ, Grenfell BT (1997) Disease extinction and community size: modeling the persistence of measles. Science 275:65–67

Keeling MJ, Rohani P (2008) Modelling infectious diseases in humans and animals. Princeton University Press, Princeton

King AA, Ionides EL, Pascual M, Bouma MJ (2008) Inapparent infections and cholera dynamics. Nature 454:877–880

Levin BR, Lipsitch M, Bonhoeffer S (1999) Population biology, evolution, and infectious disease: convergence and synthesis. Science 283:806–809

Montagnier L (2002) Historical essay. A history of HIV discovery. Science 298:1727–1728

Mossong J, Hens N, Jit M, Beutels P, Auranen K, Mikolajczyk R et al (2008) Social contacts and mixing patterns relevant to the spread of infectious diseases. PLoS Med 5:e74

Nacher M (2001) Malaria vaccine trials in a wormy world. Trends Parasitol 17:563–565

Nacher M (2006) Worms and malaria: resisting the temptation to generalize. Trends Parasitol 22:350–351

Neyrolles O, Quintana-Murci L (2009) Sexual inequality in tuberculosis. PLoS Med 6:e1000199

Pascual M, Rodó X, Ellner SP, Colwell R, Bouma MJ (2000) Cholera dynamics and El Niño-Southern Oscillation. Science 289:1766–1769

Pascual M, Bouma MJ, Dobson AP (2002) Cholera and climate: revisiting the quantitative evidence. Microbes Infect 4:237–245

Racloz V, Ramsey R, Tong S, Hu W (2012) Surveillance of dengue fever virus: a review of epidemiological models and early warning systems. PLoS Negl Trop Dis 6:e1648

Rohani P, King AA (2010) Never mind the length, feel the quality: the impact of long-term epidemiological data sets on theory, application and policy. Trends Ecol Evol 25:611–618

Rohani P, Earn DJ, Finkenstädt B, Grenfell BT (1998) Population dynamic interference among childhood diseases. Proc R Soc Lond B 265:2033–2041

Rohani P, Green CJ, Mantilla-Beniers NB, Grenfell BT (2003) Ecological interference between fatal diseases. Nature 422:885–888

Rohani P, Zhong X, King AA (2010) Contact network structure explains the changing epidemiology of pertussis. Science 330:982–985

Shaman J, Kohn M (2009) Absolute humidity modulates influenza survival, transmission, and seasonality. Proc Natl Acad Sci U S A 2009(106):3243–3248

Shaman J, Pitzer VE, Viboud C, Grenfell BT, Lipsitch M (2010) Absolute humidity and the seasonal onset of influenza in the continental United States. PLoS Biol 8:e1000316

Soper HE (1929) The interpretation of periodicity in disease prevalence. J R Stat Soc A 92:34–61

Van Panhuis WG, Grefenstette J, Jung SY, Chok NS, Cross A, Eng H et al (2013) Contagious diseases in the United States from 1888 to the present. N Engl J Med 369:2152–2158

Viboud C, Bjørnstad ON, Smith DL, Simonsen L, Miller MA, Grenfell BT (2006) Synchrony, waves, and spatial hierarchies in the spread of influenza. Science 312:447–451

Wearing HJ, Rohani P (2006) Ecological and immunological determinants of dengue epidemics. Proc Natl Acad Sci U S A 103:11802–11807

WHO-VMI Dengue Vaccine Modeling Group (2012) Assessing the potential of a candidate dengue vaccine with mathematical modeling. PLoS Negl Trop Dis 6(3):e1450

Xia Y, Bjørnstad ON, Grenfell BT (2004) Measles metapopulation dynamics: a gravity model for epidemiological coupling and dynamics. Am Nat 164:267–281

Chapter 12
The New Science of Metagenomics and the Challenges of Its Use in Both Developed and Developing Countries

Edi Prifti and Jean-Daniel Zucker

Abstract Our view of the microbial world and its impact on human health is changing radically with the ability to sequence uncultured or unculturable microbes sampled directly from their habitats, ability made possible by fast and cheap next-generation sequencing (NGS) technologies. Such recent developments represent a paradigmatic shift in the analysis of habitat biodiversity, be it the human, soil, or ocean microbiome. We review here some research examples and results that indicate the importance of microbiomes in our lives and then discus some of the challenges faced by metagenomic experiments and the subsequent analysis of the generated data. We then analyze the economic and social impact on genomic medicine and research in both developing and developed countries. We support the idea that there are significant benefits in building capacities for developing high-level scientific research in metagenomics in developing countries. Indeed, the notion that developing countries should wait for developed countries to make advances in science and technology that they later import at great cost has recently been challenged.

E. Prifti (✉)
Institute of Cardiometabolism and Nutrition, ICAN, AP-HP, F-75013 Paris, France

Metagenopolis, Institut National de la Recherche Agronomique, 78350 Jouy en Josas, France
e-mail: e.prifti@ican-institute.org

J.-D. Zucker
IRD, UMI 209, UMMISCO, IRD France Nord, F-93143 Bondy, France

Sorbonne Universités, Univ Paris 06, UMI 209, UMMISCO, F-75005 Paris, France

ICAN, AP-HP, Pitié-Salpêtrière hospital, F-75013 Paris, France

USTH, MSI-ICT Lab, 18 Hoang Quoc Viet, Cau Giay, Hanoi, Vietnam
e-mail: jean-daniel.zucker@ird.fr

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_12

12.1 Introduction

Our view of the microbial world and its impact on our lives is changing very rapidly. Until recently we have considered ourselves as largely independent from the microbial ecosystem we live in (Blaser 2006; Ley et al. 2008; Davies 2009). The mainstream thinking that we would be healthier when staying away from microbes is now debated (Bloomfield et al. 2006); hygiene and antibiotics excess during childhood may be associated with allergies and asthma during adulthood (Hanski et al. 2012; Kawamoto et al. 2012; Russell et al. 2012).

Bacteria, one of the first organisms on Earth (present for more than three billion years), have been evolving and adapting to all sorts of environments ever since, elaborating a large genetic pool that codes for many biological pathways that perform a plethora of functions (Canganella and Wiegel 2011). In the interconnected web of life where microbes are most abundant (Whitman et al. 1998), humans, like other multicellular organisms, have evolved to live in equilibrium and in symbiosis with them. Indeed, our genome does not code for all the biological functions needed for our survival nor to take full advantage of the environment we live in. We interact very tightly with our microbiota, and as a consequence, the health of this ecosystem is closely linked to ours.

Most abundant in the intestine, the gut microbiota is now considered to be an organ reaching approximately 2 kg in mass (Baquero and Nombela 2012). With 150 times more genes than our own genome, the collective genome of our microbiome (also called “our other genome” or metagenome) codes for many different functions that are not undertaken by our cells. For instance, gut bacteria can protect us by producing anti-inflammatory factors, antioxidants, and vitamins but also harm us by producing toxins that mutate DNA or affecting the nervous and immune systems. The outcome of microbiome deregulation may take the form of various chronic diseases, including obesity, diabetes, and even cancers (Zhao 2010). The very nature of human identity is now being questioned, and an increasing number of scientists state that we are indeed a super-organism with a microbial majority: ten times more microbes than human cells, which should be taken into consideration as part of us (Blaser 2006; Gill et al. 2006; Davies 2009).

Gene therapy was developed at the beginning of the twenty-first century and came with the promise of revolutionizing medicine, but its implementation was more challenging than anticipated. Such difficulties were partially due to the multifactorial nature of most diseases but also to the complex implementation and success rate of such therapy. The gut microbiota opens new means of intervention in curing complex diseases linked to it, such as the use of probiotics, ecosystem restoration through transplantation, or other microbiome targeted approaches (Borody and Khoruts 2012; Lemon et al. 2012; Shanahan 2012). Such interventions are thought to be simpler than any human gene therapy and are of great economical potential for both the private and the public health sector.

Prokaryotes are some of the most diverse organisms on the planet bearing many known and unknown functions that affect nearly all aspects of life on Earth. For instance, the bacteria that populate the ocean affect key chemical balances in the atmosphere and ensure the very habitability of our planet. Also it is a known fact that soil microorganisms are fundamental for terrestrial processes as they play an important role in various biogeochemical cycles by contributing to plant nutrition and soil health (Mocali and Benedetti 2010). As such microorganisms are of great hope for scientific research and potential biotechnological applications. This increasing interest in understanding the role of the microbiome in our planet's ecology, health, and disease as well as other biotechnological applications promises important economic and societal benefits for those countries that are involved in such research. The holistic study of the human microbiome is a fairly new approach that necessitates still expensive cutting-edge technologies and above all multidisciplinary teams. Only big research institutions with large funding programs, usually from developed countries, are currently able to undertake such projects, leaving developing countries behind in this field.

This chapter introduces first the new science of metagenomics and its many challenges while reviewing some of the major discoveries up to date. We discuss next the benefits that developing countries might reap if they were to build the needed infrastructure and become involved in microbiome research.

12.2 The New Science of Metagenomics

Now that we have established the importance of the microorganisms that live inside and around us, let us focus on the available methods and tools used to study them. An estimated 99 % of the prokaryotes are difficult to study in isolation for several reasons (Streit and Schmitz 2004; Schloss and Handelsman 2005): (i) they depend on other organisms for critical processes, (ii) fail to grow in vitro, or (iii) have even become extinct in fossil records (Tringe and Rubin 2005). These obstacles can be bypassed by focusing on DNA, a very stable molecule that can be isolated directly either from living or dead cells. Usually DNA extracted from a given sample belongs to different microbial genomes constituting what is termed a metagenome. The study of metagenomes is a new emerging field, which is referred to as metagenomics (NRCC 2007). The continuous reduction in the cost of high-throughput sequencing made possible to sequence large quantities of DNA from mixtures of organisms (Shendure et al. 2004; Metzker 2010) while offering a very detailed insight into entire ecosystems previously thought to be inaccessible.

Quantitative metagenomics (QM) focuses on quantifying DNA molecules in a given sample as opposed to functional metagenomics which focuses on clone expression (Lakhdari et al. 2010). QM, on which we will mostly focus in this chapter, can be approached through different strategies (Gabor et al. 2007). The sequencing of the 16S ribosomal RNA gene is one of the most accessible and thus most frequently used approach. Prior studies of bacterial evolution and phylogenetics provided the foundation for subsequent applications of sequencing based on 16S rRNA genes for microbial identification (Winker and Woese 1991). Indeed the 16S rRNA genes consist of highly conserved region sequences that alternate with regions of variable nucleotide sequence, which are used for taxonomic classification. Although the16S rRNA gene is a good marker to explore the phylogenetic composition of a given sample and identify new species or even unknown phylogenetic groups, it can also be used to roughly quantify the abundance of the higher taxonomic representatives. The variable regions of bacterial 16S rRNA genes are usually amplified by PCR and then subjected to library construction followed by sequencing using NGS technologies. The pool of sequenced reads is then clustered, may be mapped onto a database of previously characterized sequences, and used for further analyses in the studied context. Microbial 16S rDNA sequencing is considered the gold standard for characterizing microbial communities, but this approach would fail to capture information about what the functions of different organisms are, knowing that organisms with identical 16S sequencing may perform very different functions. A good example is the difference between various strains of *Escherichiacoli*(*Enterohemorrhagic*,*EHEC*;*Enterotoxic*,*ETEC*;*Enteroaggregative*, *EAEC*) and related organisms such as *Shigella sonnei*, which have different clinical manifestations and different treatment modalities, yet are undistinguishable by 16S rRNA sequences (Harris and Hartley 2003).

To overcome the limitations of the 16S rRNA profiling approach, the sequencing of entire metagenomes (made possible by NGS technologies) constitutes a very attractive strategy for comprehensive metagenomic studies. The whole-metagenome (WMS) approach is increasingly used and has already produced many interesting results that we discuss in the next two sections. Figure 12.1 illustrates an overview of a WMS pipeline from sample collection to the generation of hypotheses and the testing of prediction models. Sample collection from a given environment is a crucial process since the microbial communities may be quite different between two

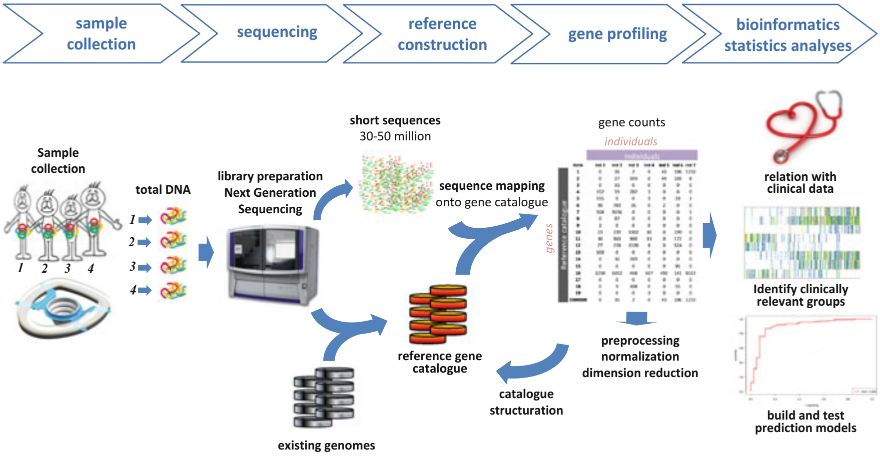


Fig. 12.1 Overview of a whole metagenome sequencing project from sample collection to hypotheses generation (After N. Pons & E. Le Chatelier)

very close locations (as is the case for soil) and should be determined according to the project needs. The DNA extraction protocols are also deciding factors and depend on the microbial composition of the sample. For example, Gram-positive bacteria, which are hard-to-lyse organisms, might be underrepresented or overrepresented in environmental DNA preparations depending on the DNA extraction protocol. Sequencing followed by mapping onto a selected reference gene catalogue and bioinformatics pretreatment analyses constitute yet another important part of this pipeline that will ensure that the biological signal is isolated while reducing the noise caused by the technical variability throughout the study. Finally, the use of the right statistical tools and datasets will be crucial in hypothesis generation and testing. We discuss later in this chapter the different issues and challenges faced at each stage of this process (cf. Fig. 12.1).

Another important and increasingly used application of WMS is the study of gene expression through RNA-Seq technology. The sequencing of cDNA, which corresponds to the whole RNA in a given sample, has brought many new application possibilities to scientists. This technology allows to bypass the limitations of cDNA microarray technology and gives a true holistic view of the transcriptome (Shendure 2008). Indeed with cDNA microarrays, a gene expression measuring technology, it is possible to focus only on those transcripts that have a corresponding probe on the chip and which are usually linked to coding sequences. Largely used in single genome transcriptomics, it is now starting to be applied in metatranscriptomics settings. The RNA-Seq approach offers an unprecedented resolution on both the activity of a given bacteria and the functional dynamics of the genes. On the other hand, it comes with a price to pay, that of the analytical challenge that underlies the complexity behind the very large number of variables in the data. Other "meta-omics" approaches such as metaproteomics or metabolomics are still in their infancy but just as promising as metagenomics is.

The precise bio-characterization of samples from different environments of interest is increasingly becoming a routine with the help of meta-omics technologies, and this new science is advancing very quickly. Many discoveries are being made in relation to human health but also to our environment as we discuss hereafter.

12.2.1 Metagenomics in Health and Disease

Many projects aiming to characterize the human microbiome and uncover its impact in human health and disease have been funded these past years. One of the first internationally coordinated efforts was the European-funded MetaHIT[1] project (Ehrlich and MetaHIT 2010), which started in early 2008. Its main objective was to establish associations between the genes of the human intestinal microbiota and disease, focusing on two main disorders of increasing importance in

---

[1] Acronym for "Metagenomics of the Human Intestinal Tract." URL: http://www.metahit.eu/

Europe: inflammatory bowel disease (IBD) and obesity. One of the first important achievements was the establishment of an extensive reference catalogue of microbial genes present in the human intestine. The results confirmed the immensity of the unknown. More than 85 % of gut bacteria were not known and around 80 % of them are considered unculturable (Eckburg et al. 2005; Qin et al. 2010). This study offered the first high-resolution picture of the diversity and complexity of the gut microbiota. The size of our intestinal metagenome is 150 times larger than that of our own genome and is composed of more than three million nonredundant microbial genes, which are largely shared among the individuals of the studied cohort. Over 99 % of them are bacterial genes, indicating that the entire cohort harbors more than 1,000 prevalent bacterial species and each individual at least 160 such species (Qin et al. 2010). An increasing number of gut microbial gene catalogues have been since published with the latest approximating ten million genes (Li et al. 2014).

The HMP[2] is another major project funded by the NIH. Its main goals are to characterize the microbial communities found at several different sites on the human body, including the nasal passages, oral cavities, skin, and gastrointestinal and urogenital tracts and to analyze the role of these microbes in human health and disease (Group et al. 2009). Researchers found that, in a cohort of healthy people, oral and stool communities were especially diverse in terms of community membership, while vaginal sites harbored particularly simple communities. Additionally, even though the diversity and abundance signature of each body site were found to vary among individuals, a niche specialization as well as the metagenomic carriage of metabolic pathways were observed to be stable among the subjects (Human Microbiome Project 2012b). Overall, in healthy humans, microbiota tends to occupy a range of distinct configurations from many of the disease-related perturbations studied to date (Sokol et al. 2008; Qin et al. 2010).

As a consequence of the complexity of metagenomic data and the relatively new age of this field, significant effort was needed in building the analytical framework as well as the associated bioinformatics tools and pipelines. Both of the aforementioned projects, among other more isolated initiatives, helped in developing such technologies that many of the current projects are now using in order to discover associations between the gut microbiome and clinical phenotypes and diseases (Ehrlich and MetaHIT 2010; Qin et al. 2010; Human Microbiome Project 2012a; Morgan and Huttenhower 2012).

One of the properties of a sampled ecosystem is species diversity, which when highly diverse is usually linked with good health. Indeed, it was discovered that low diversity in gut microbiota is associated with several human diseases such as obesity and inflammatory bowel disease (Turnbaugh et al. 2009; Qin et al. 2010; Cotillard et al. 2013; Le Chatelier et al. 2013). In some other cases, high diversity may be associated with disease such as bacterial vaginosis, for example (Srinivasan et al. 2012).

---

[2] Acronym for "Human Microbiome Project." URL: http://www.hmpdacc.org/

A recent study showed the involvement of intestinal flora in type 2 diabetes on a Chinese cohort. Approximately 60,000 microbial genes were found to be differentially abundant among type 2 diabetic patients who were also characterized by a moderate degree of gut microbial dysbiosis, a decrease in the abundance of some universal butyrate-producing bacteria, and an increase in various opportunistic pathogens. The authors also demonstrated that these gut microbial markers might be useful for classifying type 2 diabetic patients based only on their fecal samples (Qin et al. 2012).

Intestinal flora was also related to the inflammatory status of the host in symptomatic atherosclerosis patients, who were found to be enriched in the genus *Collinsella* as opposed to the controls enriched in *Eubacterium* and *Roseburia* (Karlsson et al. 2012). Even though this study cannot provide evidence for direct causal effects, these findings indicate that the gut microbes may play a role in the development of systematic atherosclerosis, knowing that inflammation is an important contributor to the pathogenesis of atherosclerosis (Hansson 2005).

Accumulating evidence now indicates that gut microbes also communicate with the central nervous system, possibly through neural, endocrine, and immune pathways, and thereby influences brain function and behavior (Grenham et al. 2011; Cryan and Dinan 2012). Studies in germ-free animals and in animals exposed to pathogenic bacterial infections, probiotic bacteria, or antibiotic drugs suggest a role for the gut microbiota in the regulation of anxiety, mood, cognition, and pain. Factors, including infection, disease, and antibiotics may alter the stability of the natural composition of the gut microbiota and thereby have a deleterious effect on the well-being of the host (Forsythe et al. 2010).

Another study demonstrated the key role of the gut microbiota in immunomodulatory mechanisms underlying multiple sclerosis. Mice genetically predisposed to spontaneously develop experimental autoimmune encephalomyelitis (EAE, an animal model for multiple sclerosis disease) were housed under germ-free conditions and, as a result, remained fully protected from EAE throughout their life until this protection dissipated upon colonization with conventional microbiota in adulthood (Berer et al. 2011). Several small studies have demonstrated links between altered intestinal microbiota in children with autism as compared with controls (Finegold et al. 2010, 2012; Adams et al. 2011). These relations may be explained however by different factors such as diet, and larger controlled clinical studies are needed for more evidence.

These are but a few studies among many others that have taken the first steps in demonstrating the existence associations between intestinal flora and different human diseases. Scientists haven't had enough time yet to gather evidence on causality, but this is the current and next step. Meanwhile there have already been some results indicating how we can use metagenomics and the microbiome to improve our health (Shanahan 2012). A first application area is personalized medicine. Information on the human microbial ecosystems may help stratify individuals and reduce the variability of the cohort so that a given treatment is more effective if adapted to any of the different sub-phenotypes. For instance, one discovery was the identification of enterotypes, three clusters, which remain consistent among different countries and cohorts and are quite stable over time (Arumugam et al. 2011). Even though the discrete nature of enterotypes is debated (Jeffery et al. 2012), they are found to be associated with long-term diet, particularly protein and animal fat (*Bacteroides*) versus carbohydrates (*Prevotella*) (Wu et al. 2011).

The potential of the human microbiome as an early detection biomarker for diagnostic and prognostic purposes is a very active area of research. Oral or fecal microbial samples can be obtained very easily and used immediately as diagnostic tools. As an example, 15 microbial genes are sufficient to discriminate with high accuracy (>90 %) liver cirrhosis patients from healthy controls. Liver cirrhosis is usually diagnosed based on biopsies, which are often proscribed in such patients due to possible complications. Patient-enriched gut microbial species originate from the oral cavity and can compose up to 40 % of the total bacterial abundance in the gut (Qin et al. 2014). In another example, microbial genes associated with type 2 diabetes (Qin et al. 2012) were used to construct prediction models that could correctly classify a sample with an accuracy of greater than 80 %. This is considerably better than model-based human genes discovered by GWAS (66 %) associated with type 2 diabetes (van Hoek et al. 2008). Most clinical indicators are not optimal such as the OGCT[3] for diabetes or BMI for obesity (Romero-Corral et al. 2008). Newer, more biologically relevant indicators are needed. The microbial biomarkers can help in this quest and could even be used to predict future occurrences of a disease.

The human microbiome and especially the gut flora offers a yet to-be-appreciated potential for interventional medicine and open unprecedented possibilities for curing human diseases. One area of intervention consists in modulating the disrupted microbial ecosystem and bringing it close to a normal state. This can be achieved through different ways such as by using prebiotics and probiotics (Sharp et al. 2009; Gareau et al. 2010). The use of probiotics has been already shown to be successful in animal studies where *Lactobacilli*- and *Bifidobacteria*-based probiotics can alleviate visceral pain induced by stress (Verdu et al. 2006); the role of probiotics in treating diseases such as IBS has also been shown (Aragon et al. 2010). Another way in achieving ecosystem modulation is through fecal transplantation, also known as fecal flora reconstitution (Baquero and Nombela 2012; Borody and Khoruts 2012). Different studies have already shown the success of this approach in treating extreme cases of *Clostridium difficile* infections that were resistant to antibiotics (van Nood et al. 2013). Despite the very high success rate (>90 % – far better than many drugs), there are still ethical issues that need to be addressed, and more clinical studies should be performed for this intervention approach to be more widely accepted and used in the medical field. Finally, therapeutic drugs can be designed to directly interact with the microbiome and modulate its different functions to change its state and thus transform the diseased phenotype into a healthy state (Jia et al. 2008; Haiser and Turnbaugh 2012).

---

[3] Acronym for “Oral Glucose Challenge Test” a score on which diabetes classification and diagnostics is based.

12.2.2 Environmental Metagenomics

Microorganisms represent the largest reservoir of genetic diversity on Earth, outnumbering all other organisms (NRCC 2007). As an example, bacteria are responsible for about half of the photosynthesis on Earth. In spite of their crucial role, prokaryotic diversity still suffers from one of the greatest knowledge gaps in the biological sciences and remains largely unexplored and unexploited (Rodriguez-Valera 2004). There is no universally agreed estimate about their real total number, their real diversity, or what principles govern their origin and evolution. Some researchers estimate the total number of prokaryotic cells on earth at 5×10^{30} including $10^6 - 10^8$ individual genomes belonging to different species (Sleator et al. 2008). For the soil, there are estimates ranging between 3,000 and 11,000 microbial genomes per gram of soil (Schmeisser et al. 2007), which makes it clear that current technologies could not support complete sequencing of such highly diverse environments (Kowalchuk et al. 2007). Beyond the interspecies diversity, there is also an intraspecies diversity that has been overlooked, but that has important consequences. For example, an easy-to-cultivate species such as *Escherichia coli* may lay a vast gene pool that is not accessible by studying one single strain. Indeed, the diversity of the genes within a bacterial species is another important facet of prokaryotic diversity (Boucher et al. 2001). Metagenomics as a culture-independent genomic analysis can help discover more about the microbial diversity of natural environments such as soil, water, and sediments (Lopez-Garcia and Moreira 2008) and has many applications in agriculture, sustainability, engineering, and environment.

12.2.3 Soil

It is a known fact that soil microorganisms are fundamental for terrestrial processes as they play an important role in various biogeochemical cycles by contributing to plant nutrition and soil health (Mocali and Benedetti 2010). This “hidden” biodiversity could be a great resource of natural products for agricultural and biotechnological applications (Steele and Streit 2005). It is thus crucial to assess and preserve the diversity of soil microorganisms. The most critical biotransformations at stake (degradation of pollutants, synthesis of biofuels, and production of novel drugs) require a whole microbial community to be performed. For instance, no single microbe is capable of converting ammonia to nitrate, but teams of microbes can do this very efficiently. These communities are likely to explain the farming mystery of “suppressive soil” in which a pathogen is known to persist but causes little damage to the crops. The activities of suppressive soil communities are quite beneficial to agriculture, ensuring the quality and provision of ecosystem services (NRCC 2007).

Sequencing the soil metagenome could bring large economic and environmental value but represents a task of unprecedented magnitude. A coordinated international effort was established to combine the skills of the global scientific community to focus on sequencing and annotating the soil metagenome: TerraGenome (Vogel et al. 2009). Launched in September 2011, the project relies on many existing bioinformatics resources, RDP (Ribosomal Database Project), QIIME (Quantitative Insights Into Microbial Ecology), Greengenes (a web application providing access to the current and comprehensive 16S rRNA gene sequence alignment for browsing, blasting, probing, and downloading), and IMG/M (Integrated Microbial Genomes/Microbiome) to name a few. The complete sequencing of a "reference" soil metagenome is aimed and the agroecology field experiment of Park Grass that has been running for more than 150 years at the UK agricultural sciences institute was chosen for investigation. There are several projects involved in soil sequencing, and a good review of soil metagenomic studies and their relevance for biotechnology and ecology is made by Van Elsas et al. (2008).

12.2.4 Marine Water

The marine environment is the largest contiguous ecosystem on Earth, occupying 71 % of the Earth's surface with an average depth of 4 km (Karl 2007). It is not surprising that the oceans represent one of the most significant yet least understood microbial-driven natural environments on the planet (Martin-Cuadrado et al. 2007). The bacteria that populate the oceans affect key chemical balances in the atmosphere and play an important role in maintaining the very habitability of our planet.

One of the first studies of marine environmental genomics was led by DeLong. This project was quite successful since the scientists involved in it discovered in archaea and bacteria the presence of a family of genes called rhodopsins. These genes were only known to exist before in plants where they play a role in collecting energy from the sun (Beja et al. 2000). Except for some species that use rhodopsins to capture energy, many others use them for communication or environmental awareness. The *Sargasso Sea Project* was another one who set a global expedition to gather microbes from the world's oceans and sequence their DNA. The authors found 1,800 species of microbes, including 150 new species of bacteria, and over 1.2 million new genes (Venter et al. 2004). Unfortunately, the Sargasso Sea Project unraveled only a small amount of the diversity. As Gilbert et al. noted, "with approximately 1 million bacteria per milliliter of seawater and an estimated average genome size of 2 million bp, the Sargasso Sea project sequenced only 0.05 % of the genomic information in a single milliliter – a proverbial drop in the ocean" (Gilbert and Dupont 2011). We are only at the beginning of a new vast domain of analyses of the biodiversity that needs to be achieved as soon as possible so that the loss of diversity that is foreseen in all habitats can be assessed as early as possible. Karl et al. review several case studies which illustrate the need for "comprehensive analyses – ranging from genomes to biomes, coupled to interdisciplinary physical and chemical observations of broad temporal – spatial scales – before a comprehensive understanding of the role of microorganisms in oceanic ecosystems can be achieved" (Karl 2007). There are many other projects related to metagenomics and marine environment. The Marine Microbiology Initiative (MMI) lunched a project aiming to sequence, assemble, and annotate approximately 200 diverse marine phage/virus genomes and to sequence approximately 50 viral metagenomes from an array of marine environments.

These studies, be it for health or environmental applications, are just the tip of the iceberg, and many are yet to come and bring fascinating and unimagined insight on the importance of the microbiome in our lives. This comes as a result of the evolution of genomics into metagenomics. The field is in its infancy and many challenges are yet to be addressed as discussed in the next section of this chapter.

12.3 Quantitative Metagenomics and Its Challenges

As for every new field, many tools and approaches need to be invented from scratch or adapted in order to answer questions and gain insight on the studied topic, and metagenomics is no exception. It is overwhelming to see the pace at which the whole experimental and analytical framework is being built as a consequence of international teamwork and different collaborations. Here we discuss some of the challenges that still need to be addressed in order to improve the efficacy of future investigations.

12.3.1 Experimental Challenges and Protocols

The classical whole-metagenome-sequencing pipeline as illustrated in Fig. 12.1 is composed of many steps, several of which are related to experimental biology. The first step after experimental design, which we will not discuss here, is sample collection. This component is crucial since samples contain the biology we are trying to study and understand. Protocols should be precise and applied similarly throughout the samples, but this is easier said than done since in some cases (such as in the study of human gut microbiome), fecal samples are extracted and stored by patients themselves. Storage is very important (Wallenius et al. 2010) and depends on the studied ecosystem but might be quite challenging when sampling, for instance, from deep sub-seafloor sediments (Alain et al. 2011) or other extreme environments. One key aspect specific to WMS strategies is the requirement for ever-greater amounts of input genomic DNA for comprehensive metagenomic studies (Petrosino et al. 2009). This is an important limitation when the starting material is limited, such as in paleogenomics (Tringe and Rubin 2005).

Another crucial issue is the process of DNA extraction. By definition, in a microbial community, there are many different species and phylogenetic groups, and as a consequence, the DNA is encapsulated in cells with different properties. The techniques that are used to lyse cells might also affect the composition of environmental DNA libraries, as the harsh lysis methods that are necessary to extract DNA from every organism will cause degradation of the DNA from some organisms (Tringe and Rubin 2005). Hard-to-lyse cells, such as Gram-positive bacteria, might therefore be underrepresented or overrepresented in environmental DNA preparations.

To coordinate the activities carried out within different programs, the International Human Microbiome Consortium (IHMC)[4] has been constituted and formally announced in October 2008. This has facilitated identification of a clear need to standardize[5] the procedures in the Human Microbiome research. The overall concept of IHMS is to promote the development and implementation of standard procedures and protocols in three separate but related fields: (i) collecting and processing of human samples, (ii) sequencing of the human-associated microbial genes and genomes, and (iii) organizing and analyzing the data gathered.

12.3.2 Bioinformatics/Biostatistics Challenges

Classical techniques in biology have been around for some time now; they are well tuned and have proved to be effective over the years. Solving some of the issues mentioned above and implementing standard protocols would greatly benefit in reducing experimental variability. The problem, however, is more complicated from an analytical point of view. Indeed, the amount of information generated by metagenomic studies is unprecedented and in addition to the informatics infrastructure needed to deal with the data deluge (Pennisi 2011), bioinformatics and biostatistics challenges need to be addressed promptly. One of the main challenging issues concerns the gene reference catalogue. The main difficulty is that the gene reference catalogue needs to be representative enough for each sample. Reducing the immense diversity of the microbial world to a single reference catalogue (similar to that of MetaHIT or the Human Genome Project) is still a challenge (Streit and Schmitz 2004). It would contain an astronomical number of genes that we would not be able to practically analyze. The solution for now is to focus on subsets of reference catalogues representative for a given ecosystem such as that of the human gut microbiota (Qin et al. 2010; Li et al. 2014). This might be population-dependent and meta-analyses studies can be difficult.

Gene profiling and data pretreatment constitute two major research points in the bioinformatics processing of metagenomic data. Gene profiling consists in mapping reads onto the reference catalogue and counting how many of them correspond to each gene. This is far from being a trivial task, and questions such as how to count those reads that map to more genes simultaneously are still a challenge. Similarly, existing preprocessing techniques, like the process that allows transforming the data in order to reduce the technical and experimental noise through normalization techniques, are not adapted to metagenomic data. Most of the genes differ in terms of abundance between different samples, in contrast to gene expression levels in

---

[4] http://www.humanmicrobiome.org/

[5] http://www.microbiome-standards.org/

microarray experiments where most of the normalization techniques were introduced (Smyth and Speed 2003). Finally, one of the biggest challenges that we face is the lack of an adapted statistical framework. The immense dimensionality of the data with millions of variables along with the very particular sparse nature of such data (due to the absence of species and thus genes among samples) make the use of classical statistics unsuitable. Even after log transforming, these data show particularly long-tailed distributions where the use of traditional parametric statistics is not possible. Some promising work in the context of 16S rRNA experiments is taking such distributions into account (Paulson et al. 2013), but its validity in WMS datasets is still to be demonstrated. Another major issue beside the difficulty of applying variable selection in such datasets is the strong interdependence that exists among genes (genes of the same genome show very similar abundance profiles) and even among species. Reducing dimensions is one way to tackle the problem, by clustering genes into groups of genes that would correspond to the core genomes using different techniques such as abundance profiles or gene assembly (Nielsen et al. 2014). By identifying bags of genes, a single abundance profile can be calculated, and thus the data can be reduced by more than three orders of magnitude and classical statistics could then be applied. Another issue with metagenomic data is that microorganisms very actively exchange parts of their genomes helped sometimes by other smaller genomic entities such as bacteriophages, which render the picture even more complex. This is still the beginning, and an increasing number of computational biologists and statisticians are working on these issues and proposing solutions.

12.4 The Importance of Expanding Metagenomics in Both Developed and Developing Countries

12.4.1 The Economic, Industrial, and Technical Promises of Metagenomics

The previous sections of this chapter demonstrate how metagenomics is prefiguring a paradigmatic change in many scientific fields. In fact, this very recent technology is already challenging the very basis of scientific practice in molecular biology. Some authors have even stated that "the hypothesis-driven science may find it hard to keep up" (Gilbert and Dupont 2011). There is already a vast number of "habitats" that have been sampled in the past ten years: marine viral community, human feces viral community, drinking water, Sargasso sea, Eel river sediments, farm soil (Minnesota), human gut microbiome (various countries), mammoth fossil, Mediterranean sea, coral reef, etc. (Hugenholtz and Tyson 2008). As indicated earlier, besides for purely environmental studies, metagenomics is becoming more and more important in health and medicine. There are yet unseen limitations to its potential applications ranging from medicine, farming, and energy to more generally everything that affects our planet (Lorenz and Eck 2005; Tripathi et al. 2007; Ehrlich and MetaHIT 2010).

In spite of the scientific and industrial excitement about the new possibilities of unraveling microbial diversity, a remaining challenge is to develop technologies at competitive prices and to turn metagenomics into commercial successes. As Lorenz and Eck put it, “Metagenomics, together with in vitro evolution and high-throughput screening technologies, provides industry with an unprecedented chance to bring biomolecules into industrial application” (Lorenz and Eck 2005). Both the cost per sequenced base and the limitation in human and computational resources to analyze metagenomic data constitute clear bottlenecks. With the appearance of new next-generation sequencers, the dye-terminator technology is becoming obsolete, and the price per base has dropped by three orders of magnitude (Liu et al. 2012). Moreover, the reduction of sequencing costs comes along with an increase in data quantity, which, without concerted efforts, will quickly outpace the ability of scientists to analyze it (Editorial 2009). As for the resources and costs for microbial sequence analysis, they are still extremely expensive, although cost-efficient bioinformatics alternatives to local computing centers exist (Angiuoli et al. 2011).

12.4.2 Developing Countries Investing in Metagenomics: From an Apparent Paradox to a Long-Term Necessity?

The aforementioned technology and experiments have given to wealthy nations a vast library of data and tools to analyze them, with a great potential for applications and discoveries. Since the beginning of genomics, many developing countries did not participate in the global initiatives for sequencing organisms and, more generally, in genomic research because of the cost of sequencers and lack of qualified staff. At first glance, it might not be so obvious that developing countries should now massively invest in metagenomics given these same reasons and the fact that many other key investments for health and economic development are more urgent. Moreover, for those developing countries who did manage to sequence new organisms, it was in most cases with little economic value to them (Coloma and Harris 2009). Several authors have thus argued that developing countries are the ones that can least afford to waste their limited health resources on ineffective diagnostics and therapies, knowing the urgent needs they have to fight infectious diseases and malnutrition (Auffray et al. 2009). Nevertheless some authors like Séguin et al. (Seguin et al. 2008) who even recently argued against such costly investments now challenge the very notion “that developing countries should wait for developed countries to make advances in science and technology that they later import at great cost.” Because of a slow progress in the areas of scientific research, along with low levels of available funding and investment in sciences in most developing countries, there has been very little scientific contribution toward solving major problems that hinder their global development.

There is no doubt that there is a need for a strong involvement of the scientific community from the developed world, but without taking into account microbial ecosystems from developing countries, any scientific program started at the world scale could not be complete. In other words, developed countries have a great interest in accessing the biodiversity of developing countries from both scientific and application perspectives. In turn, developing countries that cannot afford expensive next-generation sequencers may provide some limited and controlled access to their microbiome diversity because they possess unique ecosystems from which valuable knowledge can be learned (Coloma and Harris 2009). In the past, there have been bad experiences with "safari research" in which biological samples were taken out of the country for research and did not benefit local populations at all. This kind of behavior has raised concerns in several developing countries and prompted them to pass legislation regarding "sovereignty over genomic material and data."[6] Three countries – Mexico, India, and Thailand – have used this concept to express their wish "to capture the value of their investments" in large-scale genotyping projects (Virgin and Todd 2011). The positive benefit of legislation associated to this issue is that it can support setting rules for "trading" access to biodiversity with an access to genomics research capabilities. This may be critical for poor countries that do not have yet their own genomic initiatives.

12.4.3 Setting Priorities for Developing Countries?

There are several promising directions of research related to metagenomics in and with developing countries that are worth investigating. We list here a few of them inspired by Djikeng et al.'s seminal paper on this subject (2011):

(a) *Global surveillance of emerging and reemerging infectious diseases*. Infectious outbreaks in the human population occur regularly in the developing world (Africa, Southeast Asia, and South America), and thus the development of better control measures is crucially important. Early detection and genetic identification of known and unknown pathogens are among the main challenges. Human microbiome studies with the use of metagenomic technology may contribute significantly to discovering emerging pathogens and thus preventing epidemic outbreaks in the developing world.

(b) *Understanding sexually transmitted diseases (STDs)*. There are a growing number of studies (Atashili et al. 2008) aimed at analyzing the microbial populations in the vaginal ecosystem and how they vary under health and disease conditions. Metagenomics can help identify new clinical biomarkers based on the increasing knowledge on vaginal flora and open new ways of diagnosing

---

[6] A historic protocol was recently initiated at the Nagoya conference on the Convention for biological diversity, called the *Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity*. (http://www.cbd.int/abs/)

and treating STDs such as HIV, which is one of the biggest killers in the developing world.

(c) *Enhancing malaria treatment.* Malaria, as one of the most devastating diseases known, mostly impacts developing countries (90 % of all malaria deaths occur in sub-Saharan Africa). Metagenomics along with modeling approaches could help monitor the impact of the *Plasmodium* parasite on the microbial communities that reside on and in the human body. This would open new treatment perspectives such as bringing the protective microbiota ecosystem in a normal state with the help of new yet-to-be-developed probiotics (Djikeng et al. 2011).

(d) *Hunger and malnutrition.* Nutrigenomics focuses on identifying and understanding molecular-level interactions between nutrients and other dietary bioactives with the human genome (Kaput et al. 2005; Ahmed et al. 2009; Godard and Hurlimann 2009). Metagenomics in the context of nutrigenomics is a unique opportunity to assess the unacceptable consequences of hunger and malnutrition and to define research priorities that could benefit both developed and developing countries (Godard and Hurlimann 2009).

(e) *Developing new drugs.* Pharmacogenomics, which develops rational means to optimize drug therapy, with respect to the patients' genome and metagenome, to ensure maximum efficacy with minimal adverse effects is now becoming more and more critical to the development of drugs (Jia et al. 2008). Pharmacogenomics may help in the development of research and development capacities, which would, in turn, enable developing countries themselves to make meaningful contributions to the advancement of the field (Haiser and Turnbaugh 2012).

(f) *Food protection strategies.* Many developing countries are fragile in terms of food security, and any plant disease could devastate plantations and cause famine, bringing the country to its knees. Metagenomic research applied to agriculture and soils (Roossinck 2012) may help characterize their microbial diversity and propose new protection strategies.

This list is not exhaustive, but it contributes to our argument that it is critical for developing countries to participate in the metagenomics race (Auffray et al. 2009), in particular because of the applications to genomic medicine by implementing molecular diagnostics and molecular epidemiology. Science and technology, in particular the life sciences, are increasingly recognized as vital components for national progress in developing countries (Virgin and Todd 2011). It is clear that breaking the cycle of dependence of emerging economies toward other developed countries is critical. The costs of healthcare are increasing at a very high rate, and relying on developed countries to perform all the molecular diagnostics is not only a financial burden but slows down the building of capacities and the ability to internalize new technologies. Investing in the field of metagenomics and building life sciences-based capacities in developing countries might contribute to improving local health but also potentially stimulate economic growth.

12.4.4 The Need to Increase Capacity Building in Developing Countries

It is not simple to assess the level of technology, resources, and capacity to participate in genomics research for both developing and developed counties. India, Thailand, South Africa, Indonesia, Brazil, and Mexico, for example, have devoted considerable resources to large-scale population genotyping projects that explore human genetic variation (Coloma and Harris 2009). However, the poorer countries still do not have the resources to develop their own genomic projects on a large scale. Figures 12.2, 12.3, and 12.4 give an indicator of the importance of metagenomics capacity worldwide. The numbers are self-reported and only give an estimation of the capacities, but it is clear that developing countries lag far behind in terms of equipment. For developing countries, building such centers and research facilities to perform metagenomic analysis of their populations is critical for future healthcare infrastructure, reducing the gap between the developed and underdeveloped nations.

Sequencing capacity and equipment is not the only key to the problem. Staff, core facilities, and project funding are of uttermost importance to the development of the research as well. Efforts must be made by developed countries to host and form more students from the South, so that they may turn and invest their knowledge in their countries. Unfortunately it does not always work this way as many students from developing countries choose not to go back and take advantage of more developed research infrastructure in the host countries where they will build their careers. China, for instance, has developed very attractive programs to make

Fig. 12.2 Estimated map of reported high-throughput sequencers in Western World. The *flags* represent the research centers and the *dots* a collection of centers. The *numbers* indicate the number of sequencers. (From http://omicsmaps.com)

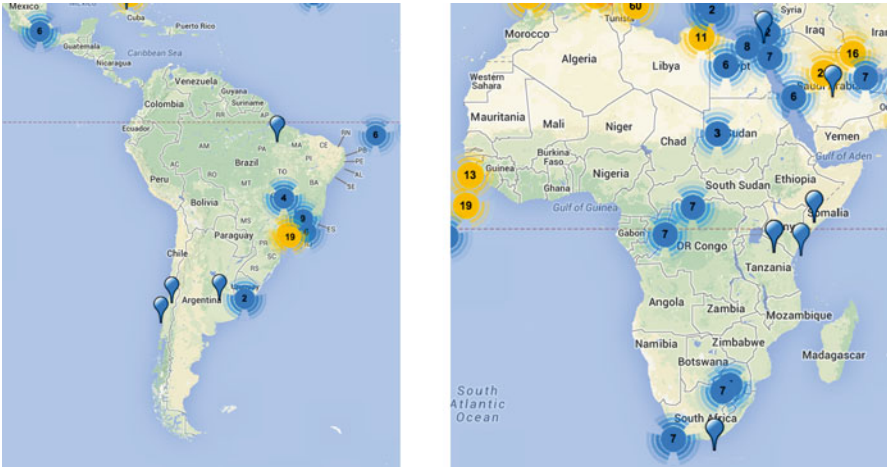


Fig. 12.3 Estimated map of reported high-throughput sequencers in South America and Africa (From http://omicsmaps.com)

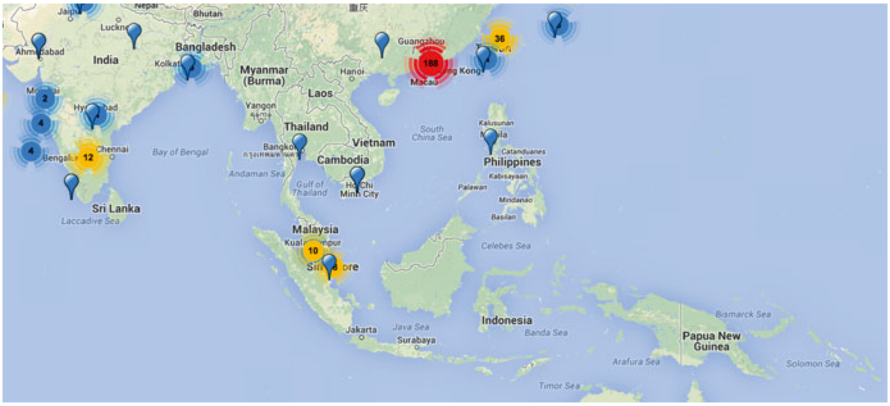


Fig. 12.4 Estimated map of reported high-throughput Southeast Asia (From http://omicsmaps.com)

sure its PhD students come back. Others like Vietnam fund PhD programs that require working for a few years in their universities after completion.

A second bottleneck for the development of metagenomic research in developing countries is the limited capacity of tool development for genomics and bioinformatics approaches (Djikeng et al. 2011). Although many computing grids exist, outsourcing analyses and computing is not always the best solution since data transfer requires significant bandwidth due to their size, constituting thus another bottleneck. Second of all, externalizing the analysis is not necessarily the best way to form local staff able to perform cutting-edge bioinformatics approaches, and it might prove more efficient to create partnerships and regional centers for technology and resources. Several success stories exist in building genomics initiatives in developing countries and could inspire also metagenomic projects as well (Seguin et al. 2008; Coloma and Harris 2009). Mexico has developed very effective translation of genomic findings into public health applications through a unique work plan called INMEGEN[7] (such as health promotion campaigns at Mexican subpopulations that might be at higher risk of certain chronic diseases). Another successful genomics comes from Brazil, where the Foundation for Research Support invested in projects relevant to the country and the rest of the developing world (e.g., sequencing the genes of the parasite that causes schistosomiasis that afflicts millions of people in Brazil). These problems are low on the list of priorities of the United States and Europe. Previous successful examples of collaborations in genomics program could initiate new ones in the context of human microbiome studies (Djikeng et al. 2011).

12.4.5 Several Metagenomics Challenges for Developing Countries and Pitfalls

In spite of the success stories above, researchers in most developing countries do not have access to resources nor the capacity to fully participate in genomics research (Coloma and Harris 2009). The ones that have access to local facilities are mostly those who were involved in the past decade in genome sequencing when they could build some sequencing capacities. An example of a successful collaboration is the joint effort of the International Livestock Research Institute (ILRI) in Nairobi and The Institute for Genome Research (Craig Venter Institute) to sequence and annotate the genome of a cattle parasite that causes important economic loss to small farmers in Africa and elsewhere. Beyond such "North–South" collaborations mainly aiming at capacity building, there is also a need for "South–South" collaborations. Access to training and capacity building of human resources ought to be shared between developing countries fostering joint projects and mutualization of platforms.

Thanks to several funds, trusts, and banks, there is increasing funding for research on diseases that affect the world's poor, such as the Bill & Melinda Gates Foundation (BMGF)[8], the United States National Institutes of Health[9], the United Kingdom Welcome Trust[10], the Asian Development Bank[11], etc. However, as mentioned by different authors, the success of the funded project depends on successful engagement with the intended beneficiaries and support from the local government: "Recent research in developing countries, such as the abandoned trials in Cameroon and Cambodia of tenofovir as pre-exposure prophylaxis against HIV infection has shown that even in studies where ethical issues have been addressed, challenges

---

[7] Acronym for "Mexican National Institute of Genomic Medicine"

[8] http://www.grandchallengesgh.org

[9] http://grants1.nih.gov/grants/index.cfm

[10] http://www.wellcome.ac.uk/funding

[11] http://www.adb.org

related to community engagement (CE) can still undermine the research" (Djikeng et al. 2011). Aside from the absence of community engagement and initiatives, corruption, and nonreturning of PhD students, there are still many pitfalls that may slow down the access of developing countries to technology, resources, and capacity that would allow their scientists to participate in metagenomics research.

12.5 Conclusion

The very young field of metagenomics is encountering a great success and is offering the possibility to explore in very high-resolution places whose landscapes we could only have imagined before. Seeing the outstanding diversity of the microbial world at the gene level is not enough to understand the functions and dynamics of the constituting parts. Ultimately, integrated analysis of metagenomes, metatranscriptomes, metaproteomes, and metabolomes will be needed to understand the microbial systems biology (Sleator et al. 2008). Achieving such integration necessitates interdisciplinary efforts and continuous development of appropriate bioinformatic tools to decipher the complex biological networks underlying molecular, functional, and community structure. The in silico investigation of biological networks could be quite effective in identifying central connected components that could bring, at a later time, more insight on their functionality and dynamics within the system.

International projects such as MetaHIT and HMP have already released a wealth of data on ecosystems along with the corresponding reference catalogues and their available functional and phylogenetic annotations. Making data public as well as bioinformatics/biostatistics tools is crucial in helping scientists from developing countries to engage in the field. Being part of the metagenomic race is of uttermost economical importance for developed but also for developing countries. Being able to improve human health as a result of metagenomic studies would not only help taking an important medical burden away from society but also preserve active individuals that would participate to the economy. Many biotechnological applications still to be imagined could improve people's lives and reduce their impact on the environment. It is important for developing countries to "hop-on" the metagenomics train and join the international effort. North–South or South–South collaborations, legislation modification, sample trading, etc., are some of the strategies that could buy them the ticket. It is never too early to think big and invest in developing the needed resources and start this very exciting and promising journey.

References

Adams JB, Johansen LJ, Powell LD, Quig D, Rubin RA (2011) Gastrointestinal flora and gastrointestinal status in children with autism–comparisons to typical children and correlation with autism severity. BMC Gastroenterol 11:22

Ahmed T, Haque R, Shamsir Ahmed AM, Petri J, William A, Cravioto A (2009) Use of metagenomics to understand the genetic basis of malnutrition. Nutr Rev 67:S201–S206

Alain K, Callac N, Ciobanu MC, Reynaud Y, Duthoit F, Jebbar M (2011) DNA extractions from deep subseafloor sediments: novel cryogenic-mill-based procedure and comparison to existing protocols. J Microbiol Methods 87(3):355–362

Angiuoli SV, White JR, Matalka M, White O, Fricke WF (2011) Resources and costs for microbial sequence analysis evaluated using virtual machines and cloud computing. PLoS One 6(10):e26624

Aragon G, Graham DB, Borum M, Doman DB (2010) Probiotic therapy for irritable bowel syndrome. Gastroenterol Hepatol (NY) 6(1):39–44

Arumugam M, Raes J, Pelletier E, Le Paslier D, Yamada T, Mende DR, Fernandes GR, Tap J, Bruls T, Batto JM, Bertalan M, Borruel N, Casellas F, Fernandez L, Gautier L, Hansen T, Hattori M, Hayashi T, Kleerebezem M, Kurokawa K, Leclerc M, Levenez F, Manichanh C, Nielsen HB, Nielsen T, Pons N, Poulain J, Qin J, Sicheritz-Ponten T, Tims S, Torrents D, Ugarte E, Zoetendal EG, Wang J, Guarner F, Pedersen O, de Vos WM, Brunak S, Dore J, H. I. T. C. Meta, Antolin M, Artiguenave F, Blottiere HM, Almeida M, Brechot C, Cara C, Chervaux C, Cultrone A, Delorme C, Denariaz G, Dervyn R, Foerstner KU, Friss C, van de Guchte M, Guedon E, Haimet F, Huber W, van Hylckama-Vlieg J, Jamet A, Juste C, Kaci G, Knol J, Lakhdari O, Layec S, Le Roux K, Maguin E, Merieux A, Melo Minardi R, M'Rini C, Muller J, Oozeer R, Parkhill J, Renault P, Rescigno M, Sanchez N, Sunagawa S, Torrejon A, Turner K, Vandemeulebrouck G, Varela E, Winogradsky Y, Zeller G, Weissenbach J, Ehrlich SD, Bork P (2011) Enterotypes of the human gut microbiome. Nature 473(7346):174–180

Atashili J, Poole C, Ndumbe PM, Adimora AA, Smith JS (2008) Bacterial vaginosis and HIV acquisition: a meta-analysis of published studies. AIDS 22(12):1493–1501

Auffray C, Chen Z, Hood L (2009) Systems medicine: the future of medical genomics and healthcare. Genome Med 1(1):2

Baquero F, Nombela C (2012) The microbiome as a human organ. Clin Microbiol Infect 18(Suppl 4):2–4

Beja O, Aravind L, Koonin EV, Suzuki MT, Hadd A, Nguyen LP, Jovanovich SB, Gates CM, Feldman RA, Spudich JL, Spudich EN, DeLong EF (2000) Bacterial rhodopsin: evidence for a new type of phototrophy in the sea. Science 289(5486):1902–1906

Berer K, Mues M, Koutrolos M, Rasbi ZA, Boziki M, Johner C, Wekerle H, Krishnamoorthy G (2011) Commensal microbiota and myelin autoantigen cooperate to trigger autoimmune demyelination. Nature 479(7374):538–541

Blaser MJ (2006) Who are we? Indigenous microbes and the ecology of human diseases. EMBO Rep 7(10):956–960

Bloomfield SF, Stanwell-Smith R, Crevel RW, Pickup J (2006) Too clean, or not too clean: the hygiene hypothesis and home hygiene. Clin Exp Allergy 36(4):402–425

Borody TJ, Khoruts A (2012) Fecal microbiota transplantation and emerging applications. Nat Rev Gastroenterol Hepatol 9(2):88–96

Boucher Y, Nesbo CL, Doolittle WF (2001) Microbial genomes: dealing with diversity. Curr Opin Microbiol 4(3):285–289

Canganella F, Wiegel J (2011) Extremophiles: from abyssal to terrestrial ecosystems and possibly beyond. Naturwissenschaften 98(4):253–279

Coloma J, Harris E (2009) Molecular genomic approaches to infectious diseases in resource-limited settings. PLoS Med 6(10):e1000142

Cotillard A, Kennedy SP, Kong LC, Prifti E, Pons N, Le Chatelier E, Almeida M, Quinquis B, Levenez F, Galleron N, Gougis S, Rizkalla S, Batto JM, Renault P, ANRM Consortium, Dore J, Zucker JD, Clement K, Ehrlich SD (2013) Dietary intervention impact on gut microbial gene richness. Nature 500(7464):585–588

Cryan JF, Dinan TG (2012) Mind-altering microorganisms: the impact of the gut microbiota on brain and behaviour. Nat Rev Neurosci 13(10):701–712

Davies J (2009) Darwin and microbiomes. EMBO Rep 10(8):805

Djikeng A, Nelson BJ, Nelson K (2011) Implications of human microbiome research for the developing world. In: Nelson KE (ed) Metagenomics of the human body. Springer, New York, pp 317–336

Eckburg PB, Bik EM, Bernstein CN, Purdom E, Dethlefsen L, Sargent M, Gill SR, Nelson KE, Relman DA (2005) Diversity of the human intestinal microbial flora. Science 308(5728):1635–1638

Editorial (2009) Metagenomics versus Moore's law. Nat Methods 6(9):623–623

Ehrlich D, MetaHIT Consortium (2010) Metagenomics of the intestinal microbiota: potential applications. Gastroenterol Clin Biol 34:S23–S28

Finegold SM, Dowd SE, Gontcharova V, Liu C, Henley KE, Wolcott RD, Youn E, Summanen PH, Granpeesheh D, Dixon D, Liu M, Molitoris DR, Green JA 3rd (2010) Pyrosequencing study of fecal microflora of autistic and control children. Anaerobe 16(4):444–453

Finegold SM, Downes J, Summanen PH (2012) Microbiology of regressive autism. Anaerobe 18(2):260–262

Forsythe P, Sudo N, Dinan T, Taylor VH, Bienenstock J (2010) Mood and gut feelings. Brain Behav Immun 24(1):9–16

Gabor E, Liebeton K, Niehaus F, Eck J, Lorenz P (2007) Updating the metagenomics toolbox. Biotechnol J 2(2):201–206

Gareau MG, Sherman PM, Walker WA (2010) Probiotics and the gut microbiota in intestinal health and disease. Nat Rev Gastroenterol Hepatol 7(9):503–514

Gilbert JA, Dupont CL (2011) Microbial metagenomics: beyond the genome. Ann Rev Mar Sci 3(1):347–371

Gill SR, Pop M, Deboy RT, Eckburg PB, Turnbaugh PJ, Samuel BS, Gordon JI, Relman DA, Fraser-Liggett CM, Nelson KE (2006) Metagenomic analysis of the human distal gut microbiome. Science 312(5778):1355–1359

Godard B, Hurlimann T (2009) Nutrigenomics for global health: ethical challenges for underserved populations. Curr Pharm Pers Med 7(3):205–214

Grenham S, Clarke G, Cryan JF, Dinan TG (2011) Brain-gut-microbe communication in health and disease. Front Physiol 2:94

Group NHW, Peterson J, Garges S, Giovanni M, McInnes P, Wang L, Schloss JA, Bonazzi V, McEwen JE, Wetterstrand KA, Deal C, Baker CC, Di Francesco V, Howcroft TK, Karp RW, Lunsford RD, Wellington CR, Belachew T, Wright M, Giblin C, David H, Mills M, Salomon R, Mullins C, Akolkar B, Begg L, Davis C, Grandison L, Humble M, Khalsa J, Little AR, Peavy H, Pontzer C, Portnoy M, Sayre MH, Starke-Reed P, Zakhari S, Read J, Watson B, Guyer M (2009) The NIH human microbiome project. Genome Res 19(12):2317–2323

Haiser HJ, Turnbaugh PJ (2012) Is it time for a metagenomic basis of therapeutics? Science 336(6086):1253–1255

Hanski I, von Hertzen L, Fyhrquist N, Koskinen K, Torppa K, Laatikainen T, Karisola P, Auvinen P, Paulin L, Makela MJ, Vartiainen E, Kosunen TU, Alenius H, Haahtela T (2012) Environmental biodiversity, human microbiota, and allergy are interrelated. Proc Natl Acad Sci U S A 109(21):8334–8339

Hansson GK (2005) Inflammation, atherosclerosis, and coronary artery disease. N Engl J Med 352(16):1685–1695

Harris KA, Hartley JC (2003) Development of broad-range 16S rDNA PCR for use in the routine diagnostic clinical microbiology service. J Med Microbiol 52(Pt 8):685–691

Hugenholtz P, Tyson G (2008) Microbiology: metagenomics. Nature 455(7212):481–483

Human Microbiome Project, C (2012a) A framework for human microbiome research. Nature 486(7402):215–221

Human Microbiome Project, C (2012b) Structure, function and diversity of the healthy human microbiome. Nature 486(7402):207–214

Jeffery IB, Claesson MJ, O'Toole PW, Shanahan F (2012) Categorization of the gut microbiota: enterotypes or gradients? Nat Rev Microbiol 10(9):591–592

Jia W, Li H, Zhao L, Nicholson JK (2008) Gut microbiota: a potential new territory for drug targeting. Nat Rev Drug Discov 7(2):123–129

Kaput J, Ordovas J, Ferguson L, van Ommen B, Rodriguez R, Allen L, Ames B, Dawson K, German B, Krauss R, Malyj W, Archer M, Barnes S, Bartholomew A, Birk R, van Bladeren P, Bradford K, Brown K, Caetano R, Castle D, Chadwick R, Clarke S, Clement K, Cooney C, Corella D, Da Cruz I, Daniel H, Duster T, Ebbesson S, Elliott R, Fairweather-Tait S, Felton J, Fenech M, Finley J, Fogg-Johnson N, Gill-Garrison R, Gibney M, Gillies P, Gustafsson J, Hartmann J, He L, Hwang J, Jais J, Jang Y, Joost H, Junien C, Kanter M, Kibbe W, Koletzko B, Korf B, Kornman K, Krempin D, Langin D, Lauren D, Lee J, Leveille G, Lin S, Mathers J, Mayne M, McNabb W, Milner J, Morgan P, Muller M, Nikolsky Y, van der Ouderaa F, Park T, Pensel N, Perez-Jimenez F, Poutanen K, Roberts M, Saris W, Schuster G, Shelling A, Simopoulos A, Southon S, Tai E, Towne B, Trayhurn P, Uauy R, Visek W, Warden C, Weiss R, Wiencke J, Winkler J, Wolff G, Xi Z, Zucker J-D (2005) The case for strategic international alliances to harness nutritional genomics for public and personal health. Br J Nutr 94(5):623–632

Karl DM (2007) Microbial oceanography: paradigms, processes and promise. Nat Rev Microbiol 5(10):759–769

Karlsson FH, Fak F, Nookaew I, Tremaroli V, Fagerberg B, Petranovic D, Backhed F, Nielsen J (2012) Symptomatic atherosclerosis is associated with an altered gut metagenome. Nat Commun 3:1245

Kawamoto S, Tran TH, Maruya M, Suzuki K, Doi Y, Tsutsui Y, Kato LM, Fagarasan S (2012) The inhibitory receptor PD-1 regulates IgA selection and bacterial composition in the gut. Science 336(6080):485–489

Kowalchuk GA, Speksnijder AG, Zhang K, Goodman RM, van Veen JA (2007) Finding the needles in the metagenome haystack. Microb Ecol 53(3):475–485

Lakhdari O, Cultrone A, Tap J, Gloux K, Bernard F, Ehrlich SD, Lefèvre F, Doré J, Blottière HM (2010) PLoS One. 5(9). pii: e13092. doi: 10.1371/journal.pone.0013092. Erratum in: PLoS One. 2010;5(10). doi: 10.1371/annotation/9f1b7f00-bcc0-4442-9775-491ebdafc7bc. PLoS One. 2010;5(10). doi: 10.1371/annotation/4ea12169-7c97-497c-a45f-52203543065f

Le Chatelier E, Nielsen T, Qin J, Prifti E, Hildebrand F, Falony G, Almeida M, Arumugam M, Batto JM, Kennedy S, Leonard P, Li J, Burgdorf K, Grarup N, Jorgensen T, Brandslund I, Nielsen HB, Juncker AS, Bertalan M, Levenez F, Pons N, Rasmussen S, Sunagawa S, Tap J, Tims S, Zoetendal EG, Brunak S, Clement K, Dore J, Kleerebezem M, Kristiansen K, Renault P, Sicheritz-Ponten T, de Vos WM, Zucker JD, Raes J, Hansen T, MetaHIT Consortium, Bork P, Wang J, Ehrlich SD, Pedersen O (2013) Richness of human gut microbiome correlates with metabolic markers. Nature 500(7464):541–546

Lemon KP, Armitage GC, Relman DA, Fischbach MA (2012) Microbiota-targeted therapies: an ecological perspective. Sci Transl Med 4(137):137rv135

Ley RE, Lozupone CA, Hamady M, Knight R, Gordon JI (2008) Worlds within worlds: evolution of the vertebrate gut microbiota. Nat Rev Microbiol 6(10):776–788

Li J, Jia H, Cai X, Zhong H, Feng Q, Sunagawa S, Arumugam M, Kultima JR, Prifti E, Nielsen T, Juncker AS, Manichanh C, Chen B, Zhang W, Levenez F, Wang J, Xu X, Xiao L, Liang S, Zhang D, Zhang Z, Chen W, Zhao H, Al-Aama JY, Edris S, Yang H, Wang J, Hansen T, Nielsen HB, Brunak S, Kristiansen K, Guarner F, Pedersen O, Dore J, Ehrlich SD, H. I. T. C. Meta, Bork P, Wang J (2014) An integrated catalog of reference genes in the human gut microbiome. Nat Biotechnol 32:834–841

Liu L, Li Y, Li S, Hu N, He Y, Pong R, Lin D, Lu L, Law M (2012) Comparison of next-generation sequencing systems. J Biomed Biotechnol 2012(7):1–11

Lopez-Garcia P, Moreira D (2008) Tracking microbial biodiversity through molecular and genomic ecology. Res Microbiol 159(1):67–73

Lorenz P, Eck J (2005) Metagenomics and industrial applications. Nat Rev Microbiol 3(6):510–516

Martin-Cuadrado AB, Lopez-Garcia P, Alba JC, Moreira D, Monticelli L, Strittmatter A, Gottschalk G, Rodriguez-Valera F (2007) Metagenomics of the deep Mediterranean, a warm bathypelagic habitat. PLoS One 2(9):e914

Metzker ML (2010) Sequencing technologies – the next generation. Nat Rev Genet 11(1):31–46

Mocali S, Benedetti A (2010) Exploring research frontiers in microbiology: the challenge of metagenomics in soil microbiology. Res Microbiol 161(6):497–505

Morgan XC, Huttenhower C (2012) Chapter 12: human microbiome analysis. PLoS Comput Biol 8(12):e1002808

Nielsen HB, Almeida M, Juncker AS, Rasmussen S, Li J, Sunagawa S, Plichta DR, Gautier L, Pedersen AG, Le Chatelier E, Pelletier E, Bonde I, Nielsen T, Manichanh C, Arumugam M, Batto JM, Quintanilha Dos Santos MB, Blom N, Borruel N, Burgdorf KS, Boumezbeur F, Casellas F, Dore J, Dworzynski P, Guarner F, Hansen T, Hildebrand F, Kaas RS, Kennedy S, Kristiansen K, Kultima JR, Leonard P, Levenez F, Lund O, Moumen B, Le Paslier D, Pons N, Pedersen O, Prifti E, Qin J, Raes J, Sorensen S, Tap J, Tims S, Ussery DW, Yamada T, H. I. T. C. Meta, Renault P, Sicheritz-Ponten T, Bork P, Wang J, Brunak S, Ehrlich SD (2014) Identification and assembly of genomes and genetic elements in complex metagenomic samples without using reference genomes. Nat Biotechnol 32:822–828

NRCC (2007) The new science of metagenomics: revealing the secrets of our microbial planet. National Research Council Committee on Metagenomics, Challenges, Washington, DC

Paulson JN, Stine OC, Bravo HC, Pop M (2013) Differential abundance analysis for microbial marker-gene surveys. Nat Methods 10(12):1200–1202

Pennisi E (2011) Human genome 10th anniversary. Will computers crash genomics? Science 331(6018):666–668

Petrosino JF, Highlander S, Luna RA, Gibbs RA, Versalovic J (2009) Metagenomic pyrosequencing and microbial identification. Clin Chem 55(5):856–866

Qin J, Li R, Raes J, Arumugam M, Burgdorf KS, Manichanh C, Nielsen T, Pons N, Levenez F, Yamada T, Mende DR, Li J, Xu J, Li S, Li D, Cao J, Wang B, Liang H, Zheng H, Xie Y, Tap J, Lepage P, Bertalan M, Batto JM, Hansen T, Le Paslier D, Linneberg A, Nielsen HB, Pelletier E, Renault P, Sicheritz-Ponten T, Turner K, Zhu H, Yu C, Jian M, Zhou Y, Li Y, Zhang X, Qin N, Yang H, Wang J, Brunak S, Dore J, Guarner F, Kristiansen K, Pedersen O, Parkhill J, Weissenbach J, H. I. T. C. Meta, Bork P, Ehrlich SD (2010) A human gut microbial gene catalogue established by metagenomic sequencing. Nature 464(7285):59–65

Qin J, Li Y, Cai Z, Li S, Zhu J, Zhang F, Liang S, Zhang W, Guan Y, Shen D, Peng Y, Zhang D, Jie Z, Wu W, Qin Y, Xue W, Li J, Han L, Lu D, Wu P, Dai Y, Sun X, Li Z, Tang A, Zhong S, Li X, Chen W, Xu R, Wang M, Feng Q, Gong M, Yu J, Zhang Y, Zhang M, Hansen T, Sanchez G, Raes J, Falony G, Okuda S, Almeida M, LeChatelier E, Renault P, Pons N, Batto JM, Zhang Z, Chen H, Yang R, Zheng W, Yang H, Wang J, Ehrlich SD, Nielsen R, Pedersen O, Kristiansen K (2012) A metagenome-wide association study of gut microbiota in type 2 diabetes. Nature 490(7418):55–60

Qin N, Yang F, Li A, Prifti E, Chen Y, Shao L, Guo J, Le Chatelier E, Yao J, Wu L, Zhou J, Ni S, Liu L, Pons N, Batto JM, Kennedy SP, Leonard P, Yuan C, Ding W, Chen Y, Hu X, Zheng B, Qian G, Xu W, Ehrlich SD, Zheng S, Li L (2014) Alterations of the human gut microbiome in liver cirrhosis. Nature 513:59–64

Rodriguez-Valera F (2004) Environmental genomics, the big picture? FEMS Microbiol Lett 231(2):153–158

Romero-Corral A, Somers VK, Sierra-Johnson J, Thomas RJ, Collazo-Clavell ML, Korinek J, Allison TG, Batsis JA, Sert-Kuniyoshi FH, Lopez-Jimenez F (2008) Accuracy of body mass index in diagnosing obesity in the adult general population. Int J Obes (Lond) 32(6):959–966

Roossinck MJ (2012) Plant virus metagenomics: biodiversity and ecology. Annu Rev Genet 46:359–369

Russell SL, Gold MJ, Hartmann M, Willing BP, Thorson L, Wlodarska M, Gill N, Blanchet MR, Mohn WW, McNagny KM, Finlay BB (2012) Early life antibiotic-driven changes in microbiota enhance susceptibility to allergic asthma. EMBO Rep 13(5):440–447

Schloss PD, Handelsman J (2005) Metagenomics for studying unculturable microorganisms: cutting the Gordian knot. Genome Biol 6(8):229

Schmeisser C, Steele H, Streit WR (2007) Metagenomics, biotechnology with non-culturable microbes. Appl Microbiol Biotechnol 75(5):955–962

Seguin B, Hardy BJ, Singer PA, Daar AS (2008) Universal health care, genomic medicine and Thailand: investing in today and tomorrow. Nat Rev Genet 9(Suppl 1):S14–S19

Shanahan F (2012) The gut microbiota in 2011: translating the microbiota to medicine. Nat Rev Gastroenterol Hepatol 9(2):72–74

Sharp RR, Achkar JP, Brinich MA, Farrell RM (2009) Helping patients make informed choices about probiotics: a need for research. Am J Gastroenterol 104(4):809–813

Shendure J (2008) The beginning of the end for microarrays? Nat Methods 5(7):585–587

Shendure J, Mitra RD, Varma C, Church GM (2004) Advanced sequencing technologies: methods and goals. Nat Rev Genet 5(5):335–344

Sleator RD, Shortall C, Hill C (2008) Metagenomics. Lett Appl Microbiol 47(5):361–366

Smyth GK, Speed T (2003) Normalization of cDNA microarray data. Methods 31(4):265–273

Sokol H, Pigneur B, Watterlot L, Lakhdari O, Bermudez-Humaran LG, Gratadoux JJ, Blugeon S, Bridonneau C, Furet JP, Corthier G, Grangette C, Vasquez N, Pochart P, Trugnan G, Thomas G, Blottiere HM, Dore J, Marteau P, Seksik P, Langella P (2008) *Faecalibacterium prausnitzii* is an anti-inflammatory commensal bacterium identified by gut microbiota analysis of Crohn disease patients. Proc Natl Acad Sci U S A 105(43):16731–16736

Srinivasan S, Hoffman NG, Morgan MT, Matsen FA, Fiedler TL, Hall RW, Ross FJ, McCoy CO, Bumgarner R, Marrazzo JM, Fredricks DN (2012) Bacterial communities in women with bacterial vaginosis: high resolution phylogenetic analyses reveal relationships of microbiota to clinical criteria. PLoS One 7(6):e37818

Steele HL, Streit WR (2005) Metagenomics: advances in ecology and biotechnology. FEMS Microbiol Lett 247(2):105–111

Streit WR, Schmitz RA (2004) Metagenomics–the key to the uncultured microbes. Curr Opin Microbiol 7(5):492–498

Tringe SG, Rubin EM (2005) Metagenomics: DNA sequencing of environmental samples. Nat Rev Genet 6(11):805–814

Tripathi CKM, Tripathi D, Praveen V, Bihari V (2007) Microbial diversity–biotechnological and industrial perspectives. Indian J Exp Biol 45(4):326–332

Turnbaugh PJ, Hamady M, Yatsunenko T, Cantarel BL, Duncan A, Ley RE, Sogin ML, Jones WJ, Roe BA, Affourtit JP, Egholm M, Henrissat B, Heath AC, Knight R, Gordon JI (2009) A core gut microbiome in obese and lean twins. Nature 457(7228):480–484

van Elsas JD, Costa R, Jansson J, Sjoling S, Bailey M, Nalin R, Vogel TM, van Overbeek L (2008) The metagenomics of disease-suppressive soils – experiences from the METACONTROL project. Trends Biotechnol 26(11):591–601

van Hoek M, Dehghan A, Witteman JC, van Duijn CM, Uitterlinden AG, Oostra BA, Hofman A, Sijbrands EJ, Janssens AC (2008) Predicting type 2 diabetes based on polymorphisms from genome-wide association studies: a population-based study. Diabetes 57(11):3122–3128

van Nood E, Vrieze A, Nieuwdorp M, Fuentes S, Zoetendal EG, de Vos WM, Visser CE, Kuijper EJ, Bartelsman JF, Tijssen JG, Speelman P, Dijkgraaf MG, Keller JJ (2013) Duodenal infusion of donor feces for recurrent clostridium difficile. N Engl J Med 368:407

Venter JC, Remington K, Heidelberg JF, Halpern AL, Rusch D, Eisen JA, Wu D, Paulsen I, Nelson KE, Nelson W, Fouts DE, Levy S, Knap AH, Lomas MW, Nealson K, White O, Peterson J, Hoffman J, Parsons R, Baden-Tillson H, Pfannkoch C, Rogers YH, Smith HO (2004) Environmental genome shotgun sequencing of the Sargasso Sea. Science 304(5667):66–74

Verdu EF, Bercik P, Verma-Gandhu M, Huang XX, Blennerhassett P, Jackson W, Mao Y, Wang L, Rochat F, Collins SM (2006) Specific probiotic therapy attenuates antibiotic induced visceral hypersensitivity in mice. Gut 55(2):182–190

Virgin HW, Todd JA (2011) Metagenomics and personalized medicine. Cell 147(1):44–56

Vogel TM, Simonet P, Jansson JK, Hirsch PR, Tiedje JM, van Elsas JD, Bailey MJ, Nalin R, Philippot L (2009) TerraGenome: a consortium for the sequencing of a soil metagenome. Nat Rev Microbiol 7(4):252–252

Wallenius K, Rita H, Simpanen S, Mikkonen A, Niemi RM (2010) Sample storage for soil enzyme activity and bacterial community profiles. J Microbiol Methods 81(1):48–55

Whitman WB, Coleman DC, Wiebe WJ (1998) Prokaryotes: the unseen majority. Proc Natl Acad Sci U S A 95(12):6578–6583

Winker S, Woese CR (1991) A definition of the domains Archaea, Bacteria and Eucarya in terms of small subunit ribosomal RNA characteristics. Syst Appl Microbiol 14(4):305–310

Wu GD, Chen J, Hoffmann C, Bittinger K, Chen YY, Keilbaugh SA, Bewtra M, Knights D, Walters WA, Knight R, Sinha R, Gilroy E, Gupta K, Baldassano R, Nessel L, Li H, Bushman FD, Lewis JD (2011) Linking long-term dietary patterns with gut microbial enterotypes. Science 334(6052):105–108

Zhao L (2010) Genomics: the tale of our other genome. Nature 465(7300):879–880

Chapter 13
Barcoding, Biobanking, e-Banking: From Ecological to Ethical and Legal Aspects. Insights from the PathoDivSEA Project

Claire Lajaunie and Serge Morand

Abstract The project Pathogen Diversity in Southeast Asia (PathoDivSEA) supported by the Agence Française de Développement (AFD) and the Centre National de la Recherche Scientifique (CNRS – French National Centre for Scientific Research) aimed to investigate and share information through a research network on the diversity of zoonotic pathogens and parasites that can inflict public health hazards on the indigenous human populations in the SEA environments. The project had the ambition to develop and apply new tools to study the diversity of zoonotic pathogens and their transmission within the fast-changing environments of the region. The applications are crucial not only for the diagnosis of human infectious diseases but also for the identification of pathogens in animals and as means of conservation. Our aim is to acknowledge the results and advancements, in barcoding, biobanking and e-banking, as well as to underline the challenges that remain to be tackled within the PathoDivSEA network or with the help of other partners.

13.1 Introduction

The project Pathogen Diversity in Southeast Asia (PathoDivSEA) supported by the Agence Française de Développement (AFD) and the Centre National de la Recherche Scientifique (CNRS – French National Centre for Scientific Research) aimed to investigate and share information through a research network on the diversity of zoonotic pathogens and parasites that can inflict public health hazards on the populations in the Southeast Asian environments. Southeast Asia is an area prone to

---

C. Lajaunie (✉)
Institut National de la Santé et de la Recherche Médicale, UMR 1095 URMITE,
Faculty of Medicine, Aix Marseille University, Marseille, France
e-mail: claire.lajaunie@inserm.fr

S. Morand
CNRS-CIRAD AGIRs, Centre d'Infectiologie Christophe Mérieux du Laos,
Vientiane, Lao PDR

© Springer Science+Business Media Singapore 2015
S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_13

emerging and re-emerging infectious diseases due to the rapid environmental changes and threats regarding the local biodiversity richness (Morand et al. 2014).

The project had the ambition to develop and apply new tools to study the diversity of zoonotic pathogens and their transmission within the fast-changing environments of the region. The applications are crucial not only for the diagnosis of human infectious diseases but also for domestic fauna and wildlife.

This chapter intends to present insights from the PathoDivSEA project regarding the issues linked to barcoding, biobanking and e-banking. The first findings that resulted from a first workshop held in Singapore in August 2013, which addressed the ‘One Health’ concept, have been enriched since then, notably during a symposium on ‘Health and Biodiversity’ which gathered the partners of the PathoDivSEA projects and other researchers.

Our aim is to acknowledge the general results and advancements as well as to underline the challenges that remain to be tackled within the PathoDivSEA network or with the help of other partners.

The PathoDivSEA project has been launched based on the pivotal idea that the control of infectious diseases depended ultimately on the capacity of researchers to identify pathogens, parasites, vectors and reservoirs, especially in a region considered as a hotspot of biodiversity.

The identification from biological samples implies to preserve the samples and the information linked with those samples for checking information or for further research, in an appropriate place to allow material and data sharing among researchers.

In this regard, it appears that the collection, identification and storage of samples necessitate skilled manpower trained to standard handling techniques, storage infrastructure and equipments that could be expensive depending on the mode of preservation used and on the size of the collection and database gathering suitable information in a secure but accessible way. If important biobanks are already constituted in the western world and organised with standards regarding the preservation and storage of samples, biobanks in Southeast Asia are just starting to develop, and trainings and procedures have to be extended.

We will first present the identification, preservation and associated data sharing and then examine the ethical and legal challenges as well as the choices to be made by researchers for the development of biobanks and linked databases.

13.2 Identification, Preservation and Data Sharing

The identification of disease pathogens, vectors and reservoirs is a necessary step to achieve the Millennium Development Goal 6 ‘to combat diseases’ in helping to understand better the diseases and their evolution and to develop prevention strategies or treatments.

The identification should be coupled with a systematic operation of preservation of the samples identified for future research, as standards or baselines for other identifications in biobanks. The biobank should go along with an appropriate management information system containing information about the samples and all the necessary and various references about their original environment, geo-references or even images depending on the samples concerned.

The first step, the identification, is very challenging, and until very recently, it relied only on expert eyes: the technique of barcoding proposed in 2003 by Hebert et al. (2003) is very powerful in this respect.

13.2.1 Barcoding

Acknowledging the lack of taxonomists, the difficulty of morphologically based identification and the time needed to describe and name all the existing species (Fontaine et al. 2012), a technique using a short, standardised gene region to identify species (usually the mitochondrial COI gene) called DNA barcoding system has been developed.

In medicine, diagnosis relies on a gold standard test which constitutes the best available benchmark available in a given situation under reasonable conditions. This test thus constitutes a perpetual quest as it is constantly challenged (Versi 1992).

In the field of veterinary medicine, it belongs to the head of the OIE (World Organisation for Animal Health) to develop and validate diagnostic tools as well as to give label to national reference centres, specialised in one or several infectious diseases following the process used by the WHO (World Health Organization) with its collaborative centres.

It is estimated that in the field of biodiversity, less of 10 % of all the species have been described. In order to foster and promote molecular identification of living organisms, an international consortium called the Barcoding of Life (BoL) has been created to operate a rapid compilation of high-quality DNA barcode records in a public library of DNA sequences. It launched the International Barcode of Life (IBoL), a project aiming at barcoding 5 million specimens representing 500,000 species within the first phase of 2010–2015.

The purpose of the BoL is in accordance with Article 7 of the Convention on Biological Diversity which states that each contracting party should identify components of biological diversity important for its conservation and sustainable use; monitor, through sampling and other techniques, the components of biological diversity identified; identify processes and categories of activities which have or are likely to have significant adverse impacts on the conservation and sustainable use of biological diversity and monitor their effects through sampling and other techniques; and maintain and organise, by any mechanism, data derived from identification and monitoring activities.

Whether it is in human medicine, veterinary medicine or conservation, screening and identification use the same technologies but a different vocabulary (for instance, barcoding being rarely used in veterinary medicine or parasitology). If in medicine the main purpose of identification resides in the diagnosis, in the field of conservation, it relates more to the need of a systematic compilation of species in a context of increasing biodiversity loss and to the attempt to determine a baseline in order to quantify the number of species existing on Earth (Mora et al. 2011) and then evaluate the effects of conservation measures (Krishnamurthy and Francis 2012).

Consequently, the three fields presented above rely on different protocols and distinct systems of database.

13.2.2 Biobanking

The preservation of samples is realised in biobanks. The discrepancy already observed in screening and identification of pathogens, parasites, vectors and reservoirs is also found in various ways tissues, parasites and pathogens are preserved according to the different fields.

The terms used to designate the collections of samples preserved have thus been various even within a same field of study, 'human genetic research databases', 'biorepositories', 'tissue banks', 'conservation banks' and 'mitigation banks', but the most commonly used term nowadays is the overarching term biobank (European Commission 2012).

In the field of human medicine, the need to cryopreserve human tissues and pathogens manifested early. It became clear that preservation of materials was necessary for the improvement of screening, genetic studies and treatments.

Regarding wildlife, the storage of voucher specimens is usually led by internationally recognised institutions such as national natural history museums (Hajibabaei et al. 2007): it can include parasites but rarely microbes which are conserved within medical institutions when they relate to zoonotic concerns.

An equivalent systematic storage of parasites and pathogens of domestic animals does not seem to exist in official and recognised institutions apart from OIE collaborative centres (although their primary missions are diagnosis and control). Nevertheless, we should mention that the Istituto Superiore di Sanità, in Rome, Italy, has been appointed European Union Reference Laboratory for Parasites to operate in the areas of feed and food safety and animal health in coordination with the National Reference Laboratories in Europe and with international organisations such as FAO, OIE and WHO. That European Laboratory is hosting biobanks of parasites of domestic animals as its role is to control parasites, circulating in Europe and those at risk of being imported into the European Union by the animal and food trade. Other European Union Reference Laboratories in the area of food security work on antimicrobial resistance, animal proteins in feeding stuffs and pesticide residues, for instance (Commission Regulation 2006).

As we have seen, there is a multiplicity of definitions of biobanks as biobanks are very heterogeneous regarding their finality or the material they contain. We can refer to the broad definition given by a group of experts of the European Commission:

biobank collections mean ‘the biological samples themselves, plus the related databases, allowing a certain level of accessibility, availability and exchange for scientific studies’ (European Commission 2004).

13.2.3 e-Banking and Open Databases

The construction of databases related to biobanks is sometimes referred to as e-banking. Numerous international and national databases are available (WHO, OIE, FAO, GIDEON database, etc.) with some geo-referencing. Most of them concern reports of disease outbreaks, and few give access to information on tissues/pathogens/parasites preserved in specific institutions. This is again particularly true for veterinary medicine and conservation medicine. On the other hand, information on genetics is provided in international database such as International Nucleotide Sequence Databases (http://www.insdc.org/) or GenBank (http://www.ncbi.nlm.nih.gov/genbank/) with no or few information on geographic origins (i.e. geo-referencing) or voucher collection.

In the field of biodiversity, an informatics workbench, the Barcode of Life Data System (BOLD), has been developed to aid in the acquisition, storage, analysis and publication of DNA barcode records (Ratnasingham and Hebert 2007). The BOLD is now a partner of the Global Biodiversity Information Facility (GBIF), an international open data infrastructure funded by governments which aims to make the world’s primary data on biodiversity freely and universally available via the Internet. That partnership allows the use of a ‘taxonomy browser’ displaying a map of GBIF-served occurrences alongside the distribution of barcoded specimens for more than 170,000 species.

The project CERoPath (‘Community Ecology of Rodents and Their Pathogens in Southeast Asia’, www.ceropath.org) for reservoirs of rodent-borne diseases in Southeast Asia is one example of open database assembling molecular, morphological and distributional data, thus bridging a traditional bioinformatics chasm (Morand and Claironm 2014).

If the databases are a necessary element linked to biobanks, we will now examine the ethical and legal aspects to be taken into consideration by researchers developing biobanking and e-banking and the norms that can frame this activity.

13.3 The Normative Framework: Focus on Ethical and Legal Aspects

Barcoding, biobanking and e-banking are influenced by different kinds of norms that we have to present briefly in order to understand the complexity of the issues encountered.

The activities mentioned are simultaneously shaped by ethical norms, legal norms and industrial and economic standards that could overlap.

As we have seen, there is no general definition of biobanking, and the content and size of biobanks depend on the type of research conducted, on the research field and ultimately on fundings. Nevertheless, as biobanking is implying sharing of information between researchers, it appeared crucial to define quality standards for sampling, handling, and preservation and for data attached to the samples in order to ensure the efficiency and the interoperability of databases.

If international standards are already applying to informatics in the health sector or to quality management, for instance, there is a call for the definition of international standards regarding biobanking (Enright 2014) more specifically. A technical committee on biotechnology has been created in 2013 to work on standardisation in the field of biotechnology processes. It is in charge of the development of standards for biobanks, bioresources, bioprocessing and data resources. This committee works notably in liaison with the International Society for Biological and Environmental Repositories (ISBER) and the European, Middle Eastern and African Society for Biopreservation and Biobanking (ESBB).

This need for standardisation even if it is more reflected by large private biobanks tends to a global harmonisation of the procedures even though obstacles might remain in emerging countries due to a lack of appropriate infrastructure.

The polysemy of the term biobank used variably for several types of collections of undetermined size creates uncertainty among researchers and leads to ethical and legal issues.

13.3.1 Ethical Issues

International networks are working on different aspects of those issues. For instance, HUGO (Human Genome Organisation) sponsors factually grounded dialogues on the social, legal and ethical issues related to genetic and genomic information. The Global Alliance for Genomics and Health aims to create a common framework of harmonised approaches to enable the responsible, voluntary and secure sharing of genomic and clinical data.

Regarding human health, the global network of WHO collaborating centres for bioethics encourages connections and synergies among those centres to facilitate resource mobilisation and strengthen institutional capacity notably at a regional level. The collaborating centre for Southeast Asia is based in the National University of Singapore.

For veterinary medicine, the OIE has a Collaborating Centre for Animal Welfare Science and Bioethical Analysis that is hosted by the Ministry for Primary Industries of New Zealand.

At the regional level, we can mention the existence of the FERCAP (Forum for Ethical Review Committees in Asia and the Western Pacific) based in Thammasat University in Bangkok: it gathers bioethics specialists and medical experts with the objective of fostering an improved understanding and better implementation of ethical review of behavioural and biomedical research in the region and defining standard operating procedures.

The UNESCO Asia-Pacific School of Ethics hosted by UNESCO in Bangkok is a regional network of individuals, institutions and associations working on projects and meetings together with the Regional Unit for Social and Human Sciences in Asia and the Pacific.

Regarding biobanking, a multiplicity of ethical guidelines have been drafted depending on the content and purpose concerned (personalised medicine, treatments for the most common genetic disorders, health surveys or study of environmental factors, etc.), the field of activities (human health, veterinary, conservation) and the specific focus.

The Helsinki Declaration of 1964 has been developed by the World Medical Association as a statement of ethical principles for medical research involving human subjects, including research on identifiable human material and data[1]: that declaration is regularly amended to take account of new elements in medical research.[2]

Ethical controversies about researches conducted on the human genome led to the Universal Declaration on the Human Genome and Human Rights of 1997 endorsed by the United Nations General Assembly. It is not a legally binding document, but nevertheless it has been cited among the relevant international texts together with the Council of Europe Convention on Human Rights and Biomedicine of 1997 by the European Court of Human Rights in the case *Evans v United Kingdom* (European Court of Human Rights Grand Chamber 2007). This Declaration under the auspices of UNESCO and the two subsequent ones, the International Declaration on Human Genetic Data (UNESCO 2003) and the Universal Declaration on Bioethics and Human Rights (UNESCO 2005) linking explicitly bioethics and human rights, 'may well evolve, like the Universal Declaration of Human Rights, into a component of international customary law, or be the precursor to an International Convention on Bioethics' (Faunce 2005; see also Nys 2005).

Along the same line, in 2002, the Council for International Organizations of Medical Sciences (CIOMS) in collaboration with the World Health Organization (WHO) presented *Guidelines for Biomedical Research Involving Human Subjects*. If all those texts can apply to the constitution of human biobanks, the OECD proposed *specific Guidelines on Human Biobanks and Genetic Research Databases in 2009 in order to* aid policymakers and practitioners who are establishing new HBGRDs. The Guideline acknowledges the existence of previous enacted principles and best practices that could also helpfully apply.

All those texts represent ethical norms that can guide researchers but that are not currently legally binding. We can underline the fact that they all concern biomedical research on humans.

---

[1] Following the Nuremberg Code of 1947 constituting the basic text of modern medical ethics

[2] The latest revision dates back to 2013 right before the 50th anniversary of the Declaration.

There are numerous ethical issues regarding research on infectious diseases, and they depend on the source of material studied (animal, human), the purpose of the storage of samples (dedicated to a project or undetermined future uses) and the way to conduct research activities.

As stated in a report of 2003 by the French and German National Ethics Committee, ‘the ethical and legal challenges connected to biobanks are legion and demand the creation of a framework where by new and coherent regulations, on a national or international scale, can be implemented’ (French National Consultative Ethics Committee 2003).

One of the major ethical questions in the constitution of biobanks resides in the notion of consent of the persons concerned. As stated in the Universal Declaration on Bioethics and Human Rights (2005), ‘scientific research should only be carried out with the prior, free, express and informed consent of the person concerned’. The need of prior informed consent for a future storage and use of any removed part of a human body challenged the idea of the absence of proprietary rights over our body or body parts (Beyleveld and Brownsword 2008).

The notion of consent is assumed in material transfer agreements (MTAs) signed in the case of transfer of research material in order to precise the use of the material and to define the rights over material and any derivatives.

The UK biobank, a wide and long-term research resource, concerning various samples and epidemiological information of more than 500,000 people, is giving an emblematic example of the numerous ethical concerns attached to the constitution of such a biobank. The different aspects regarding the ethics, the governance and the protocols have been deeply scrutinised and reviewed leading to the establishment of an Ethics and Governance Framework to set up standards for a scientifically and ethically approved research.

It became clear that the consent encompasses many aspects including the use of sensitive information, a possible link to the medical record and the confidentiality with anonymisation but giving a possibility to recontact the participant in the future. It illustrates the necessity to clearly inform the participant about the actual or potential uses of samples and to give him the right to withdraw.

The need to submit an experimental protocol to an independent committee for comment and guidance was stated in the amendment of the Helsinki Declaration in 1975, and it led to the creation of many ad hoc committees in the USA, Canada or different countries of Western Europe. France was the first country to create a permanent National Consultative Ethics Committee for Health and Life Sciences in 1983 quickly followed by many other countries over the world. The necessity to create such committees has been reaffirmed by the different texts notably the Universal Declaration on Bioethics and Human Rights of 2005 fostering the establishment of national ethics committees in many countries.

If the documents about ethics are numerous regarding human health and are used as basis for national law, there is no single international text about animal welfare even though a Universal Declaration on Animal Welfare is debated and supported by the OIE (2007).

Regarding animal health, ethics concerns should comprehend animal welfare and take into consideration animal suffering by enacting good laboratory practices and ultimately addressing the legal issues of animal rights. The consideration for animal welfare should encompass ethical concerns regarding the killing of wildlife for disease control and environmental reasons (Littin and Mellor 2005).

In addition, the activity of research itself should respond to the ethical concern of solidarity and mutual assistance (Prainsack and Buyx 2011) and include the necessity for researchers to return benefits to providers.

13.3.2 Legal Aspects

The ethical and legal aspects relating to biobanks, human genome or medical samples are sometimes overlapping which has raised questions among lawyers when the Universal Declaration on Bioethics and Human Rights has been adopted, medical ethics and international human rights belonging to distinct normative systems (Nys 2005).

The absence of consensus towards the definition of biobank can lead to legal issues: a recent study conducted by Shaw, Elger and Colledge (2014) among 36 biobanking stakeholders with an international experience has shown that the core concepts constituting biobanks are biological samples and associated data with one key criterion, ‘the planned use of samples including sharing’.

The study underlines the fact that researchers are not aware that their collections should be considered as biobanks and thus ignore the obligations attached to them. The lack of precise definition of biobank could also give the opportunity to some researchers not to qualify their collections as biobanks on purpose, to escape their legal obligations such as the formal prior informed consent (Shaw et al. 2014).

The use of genetic resources itself is not regulated by an international legal text in the health domain: that aspect is encompassed by international environmental law and more specifically by the Convention on Biological Diversity in 1992.

The Convention contains general provisions on the use of biotechnology regarding genetic resources. It belongs to the national states to take the appropriate measures as stated in Article 19 of the Convention:

> Each Contracting Party shall take legislative, administrative or policy measures to provide for the effective participation in biotechnological research activities by those Contracting Parties, especially developing countries, which provide the genetic resources for such research (…).

Some ethical issues such as the prior informed consent or mutual agreement are integrated into the Convention giving them legal value.

The Convention regulates the issue of benefit sharing and solidarity with a particular concern for the respect of traditional knowledge. The legally binding principles to be implemented into national laws on access to genetic resources and benefit sharing are detailed by the Nagoya Protocol (2010) entered into force in October 2014, to ensure legal certainty and transparency for both providers and users.

It details the access obligations to be implemented at the national level insisting on the need to promote and encourage research contributing to biodiversity conservation and sustainable use. Concerning the benefit sharing obligations, the nonmonetary part relates to the sharing of research results, transfer of technology or training and education. ASEAN urges the states to adopt national measures regarding the access to genetic resources and benefit sharing and to ensure its enforcement through institutionalised arrangements (Asean Biodiversity Centre 2013).

The monetary benefits should be shared with the provider, and there should be a necessary trade-off between the legal protection of intellectual property rights and the respect of benefit sharing, traditional knowledge and cultural biodiversity.

The multiplicity of legal issues relating to biobanks for the research on infectious diseases is vast. It concerns human health, veterinary and conservation matters and relates to many different law fields such as trade law, data protection or intellectual property. It also depends on the type of research conducted: it could go on a gradient from private-funded research for industrial purpose to public-funded research aiming to share widely scientific results.

13.4 Conclusion and Perspectives

The choices are crucial for scientific research on infectious diseases within the ASEAN economic community of 2015 and a debate among the scientific community and with policymakers in order to answer questions such as:

- How to integrate collections gathered at the regional level by a variety of scientists into a reliable biobank respecting standard conditions of efficiency, safety and interoperability?
- How to allow an effective sharing for actual and future projects?

It is necessary to have a reflection about the required standards, the sharing conditions and the potential issues of all kind and ultimately on the potential ethical and legal issues of the choices made at the regional level.

The growing exchanges of samples among researchers should lead to the definition of a coherent corpus of ethical and legal norms, so researchers could be informed about their rights and duties at the national, regional and international level as the samples can be sent to research teams all over the world. Even though the legal obligations or custom procedures are not specific to biobanks, as, for instance, obligations regarding data used for e-banking, policymakers could help researchers to find their way through the maze of ethical and legal obligations in domestic and foreign law in that specific area.

A dialogue between researchers, policymakers and legal practitioners could help to check for the different countries of ASEAN the existence of a national ethics committee, its organisation and the existing procedures. It could be completed by an assessment of the existing links and involvement of the different countries with the WHO collaborating centre on bioethics in Singapore and networks such as

The UNESCO Asia-Pacific School on bioethics and the links between the national focal points on access to genetic resources and benefit sharing.

The aim of such a platform of dialogue would be to invite researchers to participate into the elaboration of regulations and then to ensure a legal monitoring to inform researchers about the evolution of law (national and regional) and its implementation in the different fields studied.

References

Asean Biodiversity Centre (2013) An urgent need: institutionalizing access to genetic resources and benefit sharing in Southeast Asia. Policy brief series, ABS issue 1 June 2013, 2 pp

Beyleveld D, Brownsword R (2008) My body, my body parts, my property*?* Health Care Anal 8:87–99

Commission Regulation (2006) No 776/2006 of 23 May 2006, European Community, OJEU, 24 May 2006, 136/3

Enright K (2014) It's time for an ISO for biobanks and CCB is helping lead the way. Blog "inside biobanking" on http://acceleratingscience.com

European Commission (2004) Expert group, 25 recommendations on the ethical, legal and social implications of genetic testing, European communities, p 22

European Commission (2012) Expert group on dealing with ethical and regulatory challenges of international biobank research. Biobanks for Europe – a challenge for governance. Directorate-General for research and innovation, p 13

European Court of Human Rights Grand Chamber (2007) *Evans v/ United Kingdom*, application no. 6339/05, §52

Faunce TA (2005) Will international human rights subsume medical ethics? Intersections in the UNESCO Universal Bioethics Declaration. J Med Ethics 31:173–178

Fontaine B et al (2012) New species in the old world: Europe as a frontier in biodiversity exploration, a test bed for 21st century taxonomy. PLoS One 7:e36881

French National Consultative Ethics Committee for Health and Life Sciences Opinion (2003) Ethical issues raised by collections of biological material and associated information data: "biobanks", "biolibraries", 77, 20 Mar 2003, pp 1–40

Hajibabaei M, Singer GA, Hebert P, Hickey DA (2007) DNA barcoding: how it complements taxonomy, molecular phylogenetics and population genetics. Trends Genet 23:167–172

Hebert P et al (2003) Biological identifications through DNA barcodes. Proc R Soc Lond B 270:313–321

Krishnamurthy PK, Francis RA (2012) A critical review on the utility of DNA barcoding in biodiversity conservation. Biodivers Conserv 21:1901–1919

Littin KE, Mellor DJ (2005) Strategic animal welfare issues: ethical and animal welfare issues arising from the killing of wildlife for disease control and environmental reasons. Rev Sci Tech 24:767–782, Revue scientifique et technique de l'Office international des epizooties

Mora C et al (2011) How many species are there on earth and in the ocean? PLoS Biol 9:e1001127

Morand S, Clairon N (2014) Projet BiodivHealthSEA. Biodiversité et santé en Asie du Sud-Est. Ingénierie des Systèmes d'Information 19(3):175–179

Morand S, Jittapalapong S, Supputamongkol Y, Abdullah MT, Huan TB (2014) Infectious diseases and their outbreaks in Asia-Pacific: biodiversity and its regulation loss matter. PLoS One 9:e90032

Nagoya Protocol (2010) Nagoya protocol on access to genetic resources and the fair and equitable sharing of benefits arising from their utilization to the convention on biological diversity. Adopted on 29 Oct 2010 in Nagoya, Japan

Nys H (2005) Towards an international treaty on human rights and biomedicine? Some reflections inspired by UNESCO's universal declaration on bioethics and human rights. Eur J Health Law 13:5–8

OIE (2007) Resolution No. XIV, Universal Declaration on Animal Welfare, 75 GS/FR – Paris, May 2007

Prainsack B, Buyx A (2011) Solidarity: reflections on an emerging concept in bioethics. Nuffield Council on Bioethics, London, 112 pp

Ratnasingham S, Hebert P (2007) BOLD: the barcode of life data system. Mol Ecol Notes 7:355–364

Shaw DM, Elger BS, Colledge F (2014) What is a biobank? Differing definitions among biobank stakeholders. Clin Genet 85:223–227

UNESCO (2003) International declaration on human genetic data. Adopted on 16 Oct 2003

UNESCO (2005) Universal declaration on bioethics and human rights. Adopted 19 Oct 2005

Versi E (1992) Gold standard is an appropriate term. Br Med J 305:187

Part V
Managing Health Risks

Chapter 14
Methods for Prioritisation of Diseases: Case Study of Zoonoses in Southeast Asia

Marion Bordier, Lucas Léger, Suwicha Kasemsuwan, Sirichai Wongnarkpet, and François Roger

Abstract Prioritisation of diseases is an essential tool for policy-makers in charge of allocating resources for surveillance and control programmes or for research projects, to target diseases that need to be addressed ahead of others. Nevertheless, methods for prioritisation need to be transparent, standardised and repeatable to be effective and objective in setting priorities. To date, various models have been developed, experimenting different approaches, but it remains some room for improvement in the design of such tools. The definition of the criteria – indicators used to assess diseases regarding the objective of the prioritisation exercise – is one of the cornerstones of the efficiency of the methodology. In previous developed methods, this step was usually poorly addressed and up to now, no standardised method has been developed and described to select relevant and accurate criteria. Through the use of an electronic-based questionnaire to collect data about criteria from a large population of respondents, this study, based on the analysis of zoonoses and their impact in Southeast Asia, aimed at investigating an innovative approach to identify criteria that ensure a good differentiation between the diseases. The findings of this study highlighted that refining an initial list of criteria using multivariate analysis was a reliable approach to select clear, accurate and relevant criteria that allow a differentiation between diseases for a further prioritisation exercise. Furthermore, this study indicated that using an electronic-based questionnaire, carefully designed,

---

M. Bordier (✉)
Animal Health Consultant, Les Dambruères, 71 190 La Chapelle sous Uchon, FRANCE
e-mail: marion.bordier@gmail.com

S. Kasemsuwan • F. Roger
CIRAD, AGIRs, Campus International Baillarguet, Montpellier Cedex 5 34398, France

Faculty of Veterinary Medicine, Kasetsart University,
50 Pahon Yothin Road, Bangkok 10900, Thailand

L. Léger
CIRAD, AGIRs, Campus International Baillarguet, Montpellier Cedex 5 34398, France

S. Wongnarkpet
Faculty of Veterinary Medicine, Kasetsart University,
50 Pahon Yothin Road, Bangkok 10900, Thailand

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_14

might be an interesting alternative of expert opinion elicitation, for the collection of data. Finally, the results of this study opened to other new perspectives to develop and improve methods for the prioritisation of infectious diseases.

14.1 Introduction

In light of the fact that financial and human resources are limited, there is nowadays a general agreement at national, regional and international level that policy for prevention, surveillance and control of infectious diseases must be made cost effective by focusing on the most relevant risks for both animal and human populations (WHO 2006; OIE 2008; Cardoen et al. 2009). Nevertheless, decision making in controlling infectious diseases is a complex, conflicting process, characterised by a mixture of epidemiological, economical and social-ethical value judgements, and priority setting becomes a multidimensional problem in which technical information is often intertwined with those value judgements (Kurowicka et al. 2010; Ng and Sargeant 2013). In this context, in order to make the best use of limited human and financial resources, prioritisation is an efficient tool that can be used as an aid in making decisions for resource allocation in different areas, such as surveillance and control strategies and the formulation of key research questions. However, methods for prioritisation need to be transparent, standardised and repeatable to be effective in setting priorities. To date, various models have been developed, experimenting with different approaches, but there still remains some room for improvement in the design of such tools.

The definition of criteria is one of the cornerstones of the efficiency of a prioritisation exercise as they will support the assessment of the diseases and so their relative ranking. In previously developed methods, this step is usually poorly described. Criteria are selected either through bibliographic study (Kemmeren et al. 2006; Fosse et al. 2008; Krause 2008b; Eger et al. 2009; Havelaar et al. 2010) or through expert opinion (Capek et al. 2006; Perry et al. 2002; Defra 2006; WHO 2006; McKenzie et al. 2007; OIE 2008; Cardoen et al. 2009; Eger et al. 2009), but up to now, no standardised method has been developed and described to select relevant and accurate criteria.

After presenting and discussing the different methods and models for prioritisation of diseases, we propose to investigate an innovative approach to improve the choice of the criteria. Based on the analysis of zoonoses and their impact in Southeast Asia, this study used a web-based questionnaire to collect data on selection criteria from a large population of respondents and applied multivariate analysis to identify criteria that would ensure a clear and standardised differentiation between diseases and that could be used further on for a prioritisation exercise.

14.2 Methods for Prioritisation of Diseases

Methods for the prioritisation of infectious diseases had mainly two objectives, either identifying those diseases, which should be a priority focus of surveillance and control programmes, or selecting diseases, which should be addressed first in specific research programmes. Prioritisation exercises can focus on diseases currently present in the region of the study or on the most relevant hazards for the future, regarding environmental, economical and sociological changes (Discontools 2009). Three different approaches, qualitative, semi-quantitative and quantitative, can be used to support the different methods, but for whatever approach, all the models follow the same step-by-step outline.

14.2.1 A Step-by-Step Approach

The different steps that need to be rigorously followed to ensure an effective prioritisation exercise are the following:

- Step 1. Setting a clear definition of the objective of the prioritisation exercise.
- Step 2. Establishing the list of diseases that need to be ranked.
- Step 3. Selecting the list of criteria against which the prioritisation is undergone (e.g. indicators that will be used to assess the importance of the disease regarding the objective of the prioritisation exercise).
- Step 4. Allocating a score to each criterion: qualitative values, as low/medium/high for qualitative methods, quantitative scale (3–5 classes) for the semi-quantitative methods and true numerical values for quantitative methods.
- Step 5. Applying a weighting system: allocate a weight to each criterion to take into account the relative importance of the criteria regarding each other and according to the objective of the prioritisation exercise.
- Step 6. Aggregating the values of all criteria to obtain a total score per disease (methods range from very simple ones, such as summing weighted score, to more complex ones, such as aggregating probabilistic distributions of the scores).
- Step 7. Ranking the disease from highest to lowest total score.

14.2.2 The Different Approaches for Prioritisation

Three approaches support the different methods for prioritisation.

14.2.2.1 Qualitative Approach

In this approach, criteria are assessed using qualitative value and data are then combined to obtain a total qualitative value per disease, regarding which the ranking is undergone.

Eger et al. (2009) use a qualitative approach for the prioritisation of diseases and target groups for integrated care measures at the national level of Austria. A catalogue of criteria is settled and assessed using literature review, grey literature and expert interviews. For each selected diseases, results are given in qualitative terms, such as average, clear, low, high, rising and existing. An expert workshop is then organised to value the criteria and the method, according to their experience and from the perspective of the national security. The final prioritisation process results in the summary of four weighted criteria for each of the selected disease. Diseases are then classified regarding three levels of priority.

Capek et al. (2006) use a qualitative method to prioritise non-food-borne zoonoses in order to allocate rationally resources for knowledge improvement, prevention and control, at the national scale of France. A preselected list of diseases is ranked regarding three criteria and using expert opinion. After discussion, a consensus is reached on the categorisation of diseases into three categories of different levels of priority.

14.2.2.2 Semi-quantitative Approach

The principle is quite similar to the one developed in quantitative approach but criteria are scored according to a scale: different classes are defined for each criterion and a numerical value is attributed to each class. Each criterion is classified into a class and so is allocated a numerical score. The sum of the scores leads to a total score per disease regarding which the diseases are ranked. The semi-quantitative approach has been largely used by organisations to settle a list of diseases on which surveillance and research programmes should focus on (Discontools 2009). Context and characteristics of the main semi-quantitative methods previously developed are presented in Table 14.1.

14.2.3 Quantitative Approach

In this approach, each criterion is associated with a true numerical value and then all the values are aggregated to give a total value regarding which the diseases are ranked. Methods based on a purely quantitative approach are still few.

Kemmeren et al. (2006) developed a quantitative model to help Dutch decision makers to establish the priority of pathogenic microorganisms that can be transmitted by food, as a basis for effective and efficient policy-making on control, prevention and surveillance. The hierarchic classification of diseases is based on the quantitative assessment of the burden of the disease and the cost of illness using an outcome tree for each pathogen. The estimation the disease burden and the cost of illness is proceeded using an incidence approach, i.e. calculating the present expected sum of current and future costs accruing to all incident cases of disease in a specific time period, taking into account age-specific disease risk and related illness costs.

Fosse et al. (2008) propose a quantitative method to prioritise food-borne zoonoses due to consumption of pork and beef meat, to support decision making in veterinary public health area. The method is based on the construction of a hazard typology and the calculation of a risk score for each selected hazards (combination of the incidence of human cases due to pork consumption and of the severity of the cases).

Table 14.1 Examples of semi-quantitative methods for disease prioritisation

References	Country/ organisation	Objectives	Number of disease	Number of criteria	Scoring system	Weighting system	Collecting opinion methodology	Number of participants	Type of participants
Doherty (2000)	Canada, Center for Diseases Control	Surveillance strategy for human diseases	43	10	3, 4 and 5 tiered	No	Subcommittee on communicable diseases	Nonavailable	Epidemiologists of the subcommittee
Perry et al. (2002)	ILRI[a]	Setting priorities for animal health research in developing countries		5	5 tiered	Yes (economic impact scale)	Workshop	Nonavailable	International experts
WHO[b] (2006)	WHO[b]	Diseases surveillance with changing needs	–	5–8	5 tiered	Ranking of the criteria	Workshop + 1 facilitator	–	–
McKenzie et al. (2007)	New Zealand, Massey University	Surveillance strategy of wildlife pathogens	82	3	4 tiered	No	Electronically	–	Wildlife disease expert project team members
OIE[c] (2008)	OIE, European Union	Risk management of animal-related threats	–	34	5 tiered	Yes	CVO[d] working party	11	CVOs
Krause (2008a)	Germany, RKI[e]	Epidemiological research and surveillance	85	12	3 tiered	Yes	Delphi	11	Epidemiologists and infectious disease specialists of RKI

(continued)

Table 14.1 (continued)

References	Country/ organisation	Objectives	Number of disease	Number of criteria	Scoring system	Weighting system	Collecting opinion methodology	Number of participants	Type of participants
Cardoen et al. (2009)	Belgium, Federal Agency for the Safety of Food Chain	Surveillance strategy for food and waterborne diseases	51	5	5 tiered	Yes (risk managers)	Working group	35	Scientific experts (animal and public health, food, clinical microbiology and epidemiology)

[a] *ILRI* International Livestock Research Institute
[b] *WHO* World Health Organization
[c] *OIE* World Organisation for Animal Health
[d] *CVO* Chief Veterinary Officer
[e] *RKI* Robert Koch Institute

Havelaar et al. (2010) work on a general method to prioritise pathogens in order to support the development of early warning and surveillance systems of emerging zoonoses in the Netherlands. The quantitative method is based on a multi-criteria method that allows the combination of objective information on the epidemiology and societal impact of zoonotic pathogens with subjective information on the relative weights of different criteria. The risk score is based on seven epidemiological and societal criteria that cover the complete pathway from introduction to societal impact of the diseases. Authors decided to restrict the number of criteria to avoid the challenge to develop complex validated databases.

Brookes et al. (2014) use a multi-criteria framework, combining disease information with pig producer values, in order to rank exotic diseases for the pig industry in Australia, as a decision aid to identify priority research topics. Thirty diseases, pathogens and syndromes were identified and evaluated by the research team, according to 9 criteria, using information from a literature review. Weights of importance for the criteria were elicited using a survey targeting the pig industry stakeholders. Finally, the diseases are ranked according to their final mean score after the aggregation of weights of importance for the criteria with criteria measurements for each disease.

Ng and Sargeant (2013) present a zoonoses prioritisation method, based on conjoint analysis, which is a well-established quantitative method in market research to explore consumer preferences. The research team selected 21 criteria, for which three or four levels were assigned, depending on the quantitative data available in the literature, which could be quantitatively measured with scientific data in the literature. Sixty-two diseases were included in the study. Participants of a survey were proposed different disease combinations containing varying levels of 5 of the 21 criteria and were asked to select one zoonosis to prioritise for control and prevention in the country. The analysis of the data allowed to identify the relative importance of the criteria for the prioritisation of zoonotic diseases and led to the development of a robust weighted point-scoring system to rank diseases in order of priority. This preference elicitation method overcomes the need to assign arbitrary scores and subjective weights as relative weighted scores for each characteristic are derived from the choice data.

14.2.4 Analysis of the Advantages and Disadvantages of Each Approach

The qualitative approach is a quick and simple tool, easy to communicate to decision makers. However, all the methods described previously are very subjective and show a lack of repeatability and transparency and so can lead to important bias in the ranking of the disease.

The semi-quantitative approach increases transparency and repeatability compared with the qualitative approach, but methods developed so far remain subjective and arbitrary (Krause 2008b; Kurowicka et al. 2010). There is no objective basis to combine highly divergent criteria on the same scale and then simply add up or multiply all scores (Kemmeren et al. 2006) and the linear relation between the different scales of a criterion or between criteria are often assumed but not supported by data (Havelaar et al. 2010). Some methods have attempted to improve the differentiation between the diseases by increasing the number of scales in the scoring system. However, the difficulty to generate clear definitions for each scale increases with the number of scale and there might not be sufficient detailed information available for many diseases and criteria to allow such a differentiated approach (Krause 2008b). Furthermore, not all the criteria have the same importance when undergoing a prioritisation exercise, and so a relative weight needs to be applied (Krause 2008a). For the approaches in which a weighting system is applied, there is a widespread lack of transparency and objectivity in the way the weightings are attributed to criteria. Finally, most of the methods require inputs from expert groups for the scoring of the criteria. There is a high risk that the answers of these experts are biassed by their individual professional focus, and there is thus an important part of subjectivity in the final result of disease ranking (Krause 2008b).

The quantitative approach is less arbitrary than the semi-quantitative approach as the criteria are scored using natural values or an associated numerical scale. Also, all criteria are weighted in proportion to their true values, instead of given arbitrary numbers, and so the final ranking result is expected to be more accurate and realistic (Kurowicka et al. 2010). A disadvantage is that the process is very resource intensive, requiring careful consideration of a large volume of data, and many data gaps may exist. Such data gaps result in uncertainties about the final results, but the quantitative approach also helps to prioritise between data needs and to identify key research questions. To avoid the complexity of gathering a large amount of data, quantitative methods use a restricted number of criteria. Even if the authors tried to reach a high level of integration in the choice of the criteria to cover the wider range of features, they may have missed some components of the diseases that could contribute to the objective of their study (Brookes et al. 2014; Ng and Sargeant 2013). Nevertheless, according to Cox et al. (2005), simple quantitative models will often be more accurate and useful than qualitative risk rating, while requiring no more information than would be needed to assess, justify and interpret qualitative rating.

The previous literature study illustrates the three main approaches which have been used to prioritise diseases, each with their limitations: the qualitative approach which is subjective and unable to support accurate models reliably, the semi-quantitative approach which leads to reproducible but still somewhat arbitrary models and the quantitative approach which is more transparent and objective but requires a large amount of data. A summary of principles, advantages and disadvantages of the three different approaches is presented in Table 14.2.

Table 14.2 Overview of the three main approaches for diseases prioritisation

	Qualitative approach	Semi-quantitative approach	Quantitative approach
Principles	Weighting and combining qualitative data about diseases	Scoring of criteria according to a scale, ± weighting of the criteria, summing score	Natural value associated to each criteria, ± weighting of the criteria, aggregation
Advantages	Quick and simple tool	Quick and easy tool	Transparent, objective
	Easy to communicate	Acceptable transparency and accuracy	Heavy to perform
Disadvantages	High subjectivity level	Subjectivity of scoring (expert opinion)	Requirement of large amount of data
	Lack of transparency and repeatability	Arbitrary scale of criteria and weighting system	
	High risk of bias in the ranking		

14.3 An Innovative Approach to the Selection of Criteria for the Prioritisation of Diseases, Based on the Case Study of Zoonoses in Southeast Asia

14.3.1 Selection of the Zoonotic Diseases

In light of the expected large amount of zoonoses present in Southeast Asia, the scope of the study was restricted to: (1) zoonotic diseases for which animals still represent the main reservoir and source of the pathogens (e.g. exclusion of HIV, which became effectively and essentially transmissible from human to human after a single species jump), (2) zoonotic diseases for which species other than non-human primate species are commonly involved in disease transmission (e.g. exclusion of dengue and malaria), (3) food-borne diseases for which transmission to humans is due to primary contamination of raw animal products and (4) zoonotic diseases that can be transmitted from animals to humans, excluding those transmitted exclusively from humans to animals (e.g. H1N1). The geographical area of interest was continental Southeast Asia, consisting of Cambodia, two Southeastern Chinese provinces (Yunnan and Guangxi), Lao PDR, Myanmar, Thailand and Vietnam. The aim of this selection was not to end with an exhaustive list of zoonotic diseases occurring in this geographical area but to identify the most commonly described diseases, to serve as a basis for the study.

Regarding this case definition, searches of peer-reviewed literature were conducted using the PubMed database from January 1990 to September 2011. The scan involved searches for terms such as ‘zoonoses or zoonosis or zoonotic diseases Southeast Asia’, ‘emerging diseases Southeast Asia’, ‘bacteriosis Southeast Asia’, ‘virosis Southeast Asia’, ‘protozoosis Southeast Asia’, ‘mycosis zoonotic Southeast

Asia', 'parasitosis Southeast Asia', 'unconventional agents Southeast Asia', 'food-borne Southeast Asia' and 'vector-borne Southeast Asia'.

14.3.2 Selection of the Criteria

The list of the criteria that were used as indicators to assess the different characteristics of the disease, as well as their different classes, was obtained through the study of a wide range of available prioritisation methods. In the context of prioritisation of zoonoses in Southeast Asia, a special focus was given to criteria that allow to assess diseases against a wide range of components at the human-animal-ecosystem interface (epidemiological features, animal and public health impact, socioeconomical impact) and take into account the cultural and economic issues of the region.

14.3.3 Web-Based Questionnaire

The questionnaire was a web-based survey, developed using the website SurveyMonkey©. Respondents entered it using an URL link. After providing details about their personal background and professional situation (position, organisation, disciplines, country of experience, specific expertise on zoonoses), respondents were asked to select a disease and, then, to choose the most appropriate class among the ones proposed for each criteria and to mention the level of confidence they had in their answer on a scale, ranging from 1 (low confidence in the answer) to 5 (very high confidence in their answer). The questionnaire was pretested on six experts to assess the explanation provided to recipients and the format of the questionnaire.

To define the population of recipients for the purpose of this study, a snowball sampling approach was used. The initial group of recipients was defined gathering different networks and sources, involving people working in the field of zoonoses in Southeast Asia. The questionnaire was sent to 204 people and they were asked to forward the questionnaire to people they might know with some expertise of zoonoses and working in Southeast Asia. The choice of this collection method was motivated by the need to collect as many answers as possible to support the study and by the fact that the identity of the respondents was not crucial (only their experience was taken into account for the interpretation of the results).

14.3.4 Data Analysis

Once the questionnaire was closed, all the surveys were downloaded from the website of SurveyMonkey© and the answers were displayed in an Excel© fact sheet. Only the complete questionnaires were taken into account for the study. A data matrix was obtained in which the respondents were identified with their IP address and criteria were considered as categorical variables (five modes per variable) and the levels of confidence as ordinal variables (ranging from 1 to 5).

Because of the large number of criteria (45), multivariate analysis (MA) was the most appropriate tool to describe the relationships between the diseases and to underline which criteria support their differentiation. MA encompasses several methods among which the multiple correspondence analysis (MCA) is specifically dedicated to investigating categorical variables. The main objective of MCA is to summarise the associations among a set of categorical variables in a small number of dimensions and to give a low-dimensional graphical representation of these associations. Basically, variables are summarised into factorial axis, which are characterised by their inertia, i.e. the variability of the data they represent. For each variable, a correlation ratio (CR) is computed, which measures the degree of representation of the variable by the factor, ranging from 0 (no representation of the variable by the factor) to 1 (complete representation of the variable by the factor) (Dohoo et al. 1997).

In order to investigate which criteria allow a differentiation between diseases without showing a wide variance in the respondents' answers for a same disease, two different types of MCA were applied. First, a between-class MCA was conducted to identify variables (criteria) differentiating groups (diseases). The principle of the between-class MCA is to calculate factors in order to maximise the intergroup variance and minimise the intragroup variance, and thus the inter-CR measures the degree of participation of the variable in the intergroup variance of the data set, explained by the factors. Second, a within-class MCA was applied on the data set to identify variables that showed a high variability for a same disease. In contrast to the between-class MCA, factors are constructed in order to maximise the intragroup variance and minimise the intergroup variance. Thus, when a variable shows a high intra-CR, that means that its distribution is characterised by a high variance of the modes of the variables obtained for a same disease (within a same group). Finally, by performing the ratio between these global inter- and intra-CR, we obtained an indicator that measures the ability of the variables (criteria) to optimise the inter-variability (discrimination between the diseases) and to minimise the intra-variability of the data (discrepancies between the answers of the respondents for a same disease).

In a classical MCA, all the individuals and variables have the same weight in the calculation. To take into account the level of expertise and the level of confidence of the respondents in the computation of the data for the same group of diseases, a weighting system was applied to the modes taken by the variables (Birol et al. 2010).

Hierarchical cluster analysis (HCA) was used to differentiate between diseases with similar profiles (epidemiological complexity and impacts on health and socioeconomy). HCA used a set of dissimilarities for the diseases being clustered. Initially, each disease is assigned to its own cluster and then the algorithm proceeds iteratively, at each stage joining the two most similar clusters, continuing until there is just a single cluster. HCA was conducted on the factorial coordinates of the diseases provided by the previous between-class MCA, using the Ward's minimum variance method of which the principle of aggregation is to minimise intracluster variance and to maximise intercluster variance (Costard et al. 2009). The distance matrix was computed based on the results of the first 14 factors (representing 90 % of the variance) from the previous MCA and using the Euclidean distance.

Multivariate analyses and classification were conducted with the statistical software R 2.11.1 (R Development Core Team 2014), using the package ade4 (Dray and Dufour 2007).

The way the classes of the criteria were encoded using a numerical scale that reflects the complexity and the burden of the disease allows to add the scores provided by the respondents to obtain a total score per disease or per category of variable, in order to quantify the impact of the disease in terms of five aspects:

- Epidemiology: the epidemiological profiling aims at determining the expected level of complexity of a disease, such as the distribution and the pattern of transmission of the disease, the variability of the pathogen, etc.
- Impact on public health: this step aims at determining the harm potential of the disease in terms of human health, taking into account two complementary notions, the strictly disease-related threat to human health and the possibility of controlling the disease in human; this will give the highest impact to diseases with a strong nuisance potential in humans and few possible means of control.
- Impact on animal health: same input but at the animal level.
- Impact on economy: the economic profiling of a disease aims at determining its nuisance potential for the economy and takes into account direct and indirect impact of the diseases at the animal and human scale.
- Impact on society: the impact of the disease on society indicators allows to assess the perception of the disease by the public based on its impact on economy, environment, health, control means, etc.

To do so, the sum of the overall scores and the score for each category of criteria, divided by the number of criteria taken into account, was computed. In case several respondents answered for the same disease, the weighted median of their scores (based on the level of confidence and the level of expertise) was used.

14.3.5 Selected Diseases and Criteria

Searches in literature led to a list of 25 diseases (Table 14.3).

Diseases caused by fungi were not included as the mycoses were poorly described. In addition, no cases due to unconventional agents, such as prions, have been reported in the area. 45 criteria were selected, classified into five categories: epidemiological trends (8 criteria), impact on animal health (9 criteria), impact on public health (11 criteria), economical impact (7 criteria) and social impact (10 criteria). The list of criteria is presented in Table 14.4.

Table 14.3 List of selected zoonotic diseases

Bacterioses/rickettsioses	Viroses	Parasitoses
Anthrax	Avian influenza (highly pathogenic)	Cryptosporidiosis
Bovine tuberculosis	Hantaviruses	Giardiasis
Brucellosis	Hepatitis E	Leishmaniasis
Campylobacteriosis	Japanese encephalitis	Lymphatic filariasis (*B. malayi*)
Leptospirosis	Nipah virus (infection due to)	Schistosomiasis
Plague	Rabies	Taeniasis/cysticercosis
Q fever		Toxoplasmosis
Salmonellosis		Trematodiases
Streptococcus suis (infection due to)		Trichinellosis
Scrub typhus		

Table 14.4 List of the selected criteria

Criteria name	
Epidemiological features	Presence of the disease in Southeast Asia
	Distribution of the disease in Southeast Asia
	Range of animal species commonly involved in the disease transmission in Southeast Asia
	Persistence of the agent in the environment including wildlife
	Zoonotic potential of the agent
	Speed of spread of the disease within human population
	Speed of spread of the disease within animal population
	Variability of the pathogen
Animal health	Prevalence of the disease in the main susceptible species in Southeast Asia impact
	Impact at herd scale
	Disease knowledge
	Effectiveness of existing prevention practices (movement control, biosecurity) at a global level
	Effectiveness of existing surveillance measures (clinical tests) at a global level (worldwide)
	Effectiveness of existing control measures at a global level (worldwide)
	Experience/success of prevention and control in other countries (outside Southeast Asia)
	Availability of vaccine and/or treatment in Southeast Asia
	Availability of diagnostic tools in Southeast Asia

(continued)

Table 14.4 (continued)

Criteria name	
Public health impact	Prevalence of the disease in the main susceptible species in Southeast Asia
	Impact at individual scale
	Impact at population scale
	Existence of risk groups (occupational, cultural, physiological)
	Disease knowledge
	Effectiveness of existing prevention measures (worldwide): public awareness, monitoring of food, biosecurity
	Effectiveness of existing surveillance measures (clinical tests) at a global level (worldwide)
	Effectiveness of existing control measures at a global level (worldwide)
	Experience/success of prevention and control in other countries (outside Southeast Asia)
	Availability of vaccine and/or treatment in Southeast Asia
	Availability of diagnostic tools in Southeast Asia
Economic impact	Global burden of the disease on public health based on DALYs value (disability adjusted years)
	Direct economic impact of human cases: cost of control measures (treatment, vaccination)
	Indirect economic impact of human cases: prevention measures, social trade
	Direct economic impact of animal disease: production losses, private and public control measures
	Indirect economic impact of animal disease: market distribution, prices of products, effect of consumption, social trade
	Impact on international trade regarding OIE standards and/or countries' regulations
	Poverty impact of the disease: high economic importance at household level
Social impact	Impact on animal welfare: disease and related control measures
	Impact on environment and biodiversity
	Threat to wildlife, pet species and animal species with a high social and cultural value
	Impact on security of food supply
	Potential impact on media: probability of media crisis
	Feasibility and acceptability of prevention and control measures
	Economic cost of the disease (individual and organisational levels)
	Perception of the disease
	Level of priority of the disease for stakeholders
	Bioterrorism potential of the agent

14.3.6 Descriptive Results of the Study Population

In total, 111 respondents entered the questionnaire in the website during the period of time of 45 days it was open. Fifty-nine people completed the questionnaire (53.2 %). Among the 111 respondents, the majority of respondents were veterinarians (56.8 %)

and/or epidemiologists (31.5 %), working mainly for international and governmental organisations (respectively, 32.4 % and 35.1 %) and for research institutes (26.1 %). The field of expertise of the respondents was mainly animal health for 47.7 %, epidemiology for 47.7 %, veterinary public health for 31.5 % and public health for 24.3 %. Among respondents who completed the questionnaire, people mainly mentioned a specific expertise in zoonoses (71.2 %) and usually filled the questionnaire choosing the disease they had experience for (59.3 %). On the contrary, people without any experience on zoonoses were more numerous (61.5 %) among respondents who dropped the questionnaire before the end.

For the further analysis of the data, only complete questionnaires were considered.

On the 25 diseases, complete questionnaires were obtained only for 17 of them, and for some diseases, several complete questionnaires were filled, such as for HPAI (21), rabies (11), anthrax (3), leptospirosis (4), salmonellosis (3), scrub typhus (2), bovine tuberculosis (2), filariasis (2) and *Streptococcus suis* infection (2).

It was observed that 62.7 % of the respondents answered the questionnaire with a high level of confidence (classes 4 and 5), 35.6 % with a medium level of confidence (class 3) and 1.7 % with a low level of confidence (classes 1 and 2). The distribution of the level of confidence for all the variables was the following: low for 10.4 % of the answers, medium for 29.1 % and high for 58.1 %. 2.4 % of data about level of confidence are missing.

14.3.7 Evaluation of the Criteria

The 12 first criteria that represented the most the intergroup variance (i.e. the variability of the respondents answers between the different diseases) mainly belonged to the category about the impact on animal health (n = 4) and the economic impact (n = 4), followed by those belonging to the category about the impact on society (n = 3). Only one criterion was found in the category about the impact on public health and none in the one about the epidemiological features. The 12 first criteria that influenced the intragroup variance (i.e. the variability in the answers of respondents for the same disease) were distributed homogeneously between the different categories of criteria: epidemiological trends (n = 2), animal health (n = 2), human health (n = 3), economy (n = 3) and society (n = 2).

The values of the inter-/intra-CR for all the criteria allowed the identification of criteria that supports the differentiation between diseases. Upon a ratio greater than two, there were, respectively, three, four, three, four and five criteria related to epidemiology, animal health, human health, economy and society. The criteria related to epidemiology were speed of spread of the disease within animal population (3.35), zoonotic potential of the pathogen (2.48) and the variability of the pathogen (2.2). The criteria related to animal health were effectiveness of existing surveillance measures (2.7), success of control in other countries (2.35), impact at herd scale (2.34) and prevalence of the disease (2.06). The criteria related to human health were effectiveness of existing surveillance measures (3.98), impact at individual scale (3.69) and effectiveness of existing prevention measures (2.7). The criteria related to economy were impact on international trade (3.95), direct economic impact of animal disease (3.22), indirect economic impact of animal diseases (2.59) and poverty impact of the disease (2.04). The criteria related to society were level of priority for stakeholders (3.54), economic cost of the disease (2.91), potential impact on media (2.87), impact on animal welfare (2.82) and threat to species with a social value (2.39).

14.3.8 Profile of the Diseases

For eight diseases (44 %), the epidemiological profile was quoted the highest: bartonellosis, Japanese encephalitis, leptospirosis, rabies, salmonellosis, scrub typhus, swine influenza and trematodiasis.

For the other diseases, the economic impact was quoted the highest for six (33 %) of them (anthrax, HPAI, bovine tuberculosis, brucellosis, filariasis, leishmaniasis) and the public health impact for four (22 %) of them (giardiasis, Nipah, *Streptococcus suis* and taeniasis). For one disease (6 %), the social impact was quoted the highest (anthrax). For any of the diseases, the impact on animal health was assessed as the main burden of the disease.

Respondents allocated the highest overall score to trematodiases (3.53), followed by HPAI (3.38) and bartonellosis (3.24). Bartonellosis and trematodiases were scored with the greatest epidemiological impact (4.38). Furthermore, according to the respondents, trematodiases obtained the greatest impact on animal health (4.33) and human health (4.18) and HPAI on economy (4.43) as well as on society (3.9).

The scores of each disease regarding the different category of criteria and the criteria altogether are displayed in Table 14.5.

14.3.9 Classification of the Diseases

The hierarchical cluster analysis performed on the results of the between-class MCA provided the dendrograms of the clusters of diseases regarding their profile. Simultaneously, the total score computed for each disease was displayed within the classification.

For the dendrogram representing the diseases (Fig. 14.1), aggregated by the MCA, regarding all the variables, four clusters were clearly identified: one gathering leishmaniasis and Nipah; one gathering seven diseases (salmonellosis, anthrax, HPAI and rabies grouped together, leptospirosis and scrub typhus grouped altogether, filariasis, Japanese encephalitis); one gathering bovine tuberculosis, swine influenza, brucellosis and *Streptococcus suis*; and the last one gathering bartonellosis, giardiasis and trematodiasis.

Table 14.5 Scores per disease for each category of variables and for all the variables

	n	Epidemiology	Animal health	Human health	Economy	Society	Total
Anthrax	3	2.75	2.89	2.73	3.14	3.30	2.96
HPAI	21	4.00	2.44	2.55	4.43	3.90	3.38
Bartonella infections	1	4.38	4.00	3.64	2.00	2.10	3.24
Bovine tuberculosis	2	3.25	2.56	2.64	3.86	3.20	3.04
Brucellosis	1	3.00	2.44	2.64	3.29	2.70	2.78
Giardiasis	1	3.13	3.11	3.64	3.14	2.50	3.11
Japanese encephalitis	1	3.13	2.56	2.55	2.43	1.90	2.49
Leishmaniasis	1	3.63	2.67	2.73	3.86	3.10	3.13
Leptospirosis	4	3.75	3.11	3.27	2.29	2.30	2.96
Filariasis	2	2.50	2.00	1.91	2.71	2.50	2.29
Nipah	1	3.38	3.00	3.55	2.43	3.10	3.13
Rabies	11	2.88	2.22	2.45	3.00	3.20	2.71
Salmonellosis	3	4.13	2.89	2.73	3.57	2.50	3.09
Scrub typhus	2	4.25	3.44	3.64	1.57	2.00	3.02
Streptococcus suis	2	2.63	2.89	3.73	3.14	2.50	3.00
Swine influenza	1	3.50	2.56	2.45	3.00	2.70	2.80
Taeniasis/ cysticercosis	1	2.88	2.67	3.09	2.29	2.60	2.73
Trematodiasis	1	4.38	4.33	4.18	1.86	2.60	3.53

14.4 Discussion

14.4.1 Data Collection

The findings of this study highlighted that data collection through a web survey may be an interesting alternative to expert opinion elicitation when collecting data about diseases.

Expert opinion is widely used in epidemiological surveys to collect data about diseases when data are scarce or too costly to collect through classical epidemiological studies (Gale et al. 2010; Mitchell et al. 2009; Birol et al. 2010; More et al. 2010). But it is challenging to select and involve experts with an enough good knowledge to give inputs about a broad range of zoonoses. In this study, the data collection method was designed to limit biases due to a lack of knowledge of experts for a broad range of zoonoses. Instead of asking a narrow list of participants to score various zoonotic diseases against a list of criteria, it was decided to ask numerous people involved with zoonotic diseases in Southeast Asia to fill out the questionnaire about a self-selected disease, expecting that they will pick the one they are the most

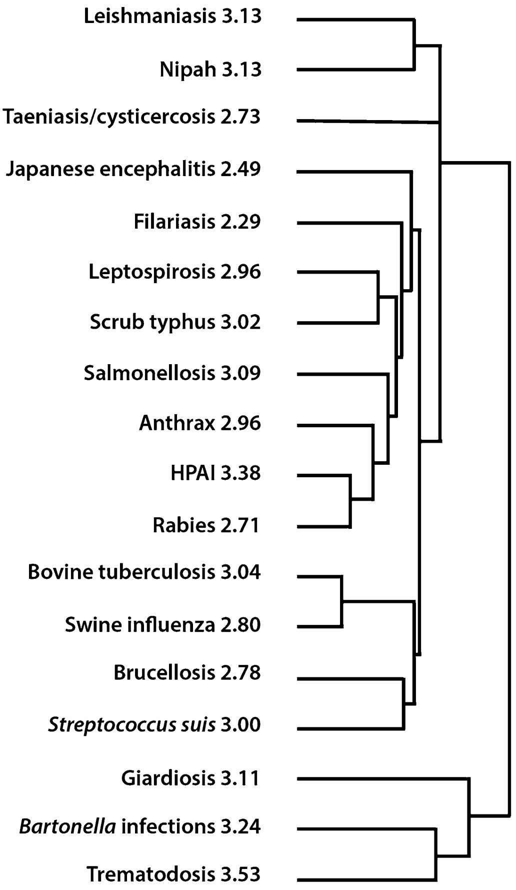


Fig. 14.1 Classification of the diseases regarding all the variables

familiar with. Even with the self-selection of the disease, varying levels of knowledge among respondents were also addressed by using a self-weighting assessment of respondents' confidence in their own answers.

The snowball sampling approach used to maximise the number of recipients did not allow to select respondents by specific criteria of expertise and location, but the length of the questionnaire and the high level of knowledge required by the questions likely played a role in selecting respondents. Indeed, among respondents who filled entirely the questionnaire, most of them mentioned a specific experience for a zoonotic disease (71.0 %) and were specifically working in countries of Southeast Asia (88.1 %). As a result, most respondents (98.3 %) answered with an overall level of confidence of medium or high. Furthermore, even if most of the respondents were veterinarians or epidemiologists (likely because of their predominance in the starting mailing list), the level of confidence was acceptable in the field of public health, economy and society for which the percentage of respondents who were highly confident in their answers was respectively 59.1 %, 54.5 % and 50.9 %. Nevertheless, this sampling approach might have led to an over-representation of some professional categories (veterinarians) and a discrimination against countries where there is a weak Internet connection. Indeed, in case the connection failed, the questionnaire quits without saving the answers.

14.4.2 Assessment of the Criteria

The correlation ratio calculated for each criterion regarding the different factorial axes of the multiple correspondence analysis allowed to compare criteria on their ability to discriminate diseases.

The results obtained from the MCA performed on all the variables indicated that the economic impact was the category that triggered the most important variability between the diseases. Criteria that supported the variability intragroup were equally allocated to the different categories. Regarding the inter-/intra-ratio of the criteria within each category, both for animal and public health, indicators related to the efficiency of prevention and surveillance measures appeared to be the most pertinent to discriminate diseases. For the economic category, the results indicated that the economic impact of the animal diseases ensured a greater differentiation than the economic impact of the human diseases. Five criteria related to the societal impact among the 10 evaluated presented a value of the inter-/intra-ratio greater than two, underlining that the impact on society was an important component to differentiate diseases.

The ratio between the intra-CR and the inter-CR, obtained by performing MCA, and the level of confidence of the respondents, obtained through the questionnaire, are two measures that can be combined to help in selecting accurate and relevant criteria for prioritisation. For instance, in this study, in the category of epidemiology, a particular attention should be paid to the criteria ‘speed of spread of the disease in animal population’, ‘zoonotic potential of the agent’, as well as ‘variability of the pathogen’, which combined a high inter-/intra-correlation ratio (respectively, 3.35, 2.48 and 2.20) and a large proportion of respondents which answered with a high level of confidence (respectively, 77.6 %, 82.8 % and 63.2 %). On the contrary, criteria with the lowest inter-/intra-CR do not ensure a good discrimination between diseases because of the high variability of the answers of respondents for a same disease and a low variability of the answers between diseases. Nevertheless, looking at the level of confidence self-assessed by the respondents and associated to criteria with a high intra-CR may give some interesting insights about the source of this variability. A high intra-CR associated with a high level of confidence of the respondents may suggest that the source of the variability is mainly due to a difference of understanding between the respondents or an inappropriate definition of the classes which did not allow an efficient differentiation between the diseases, while a high intra-CR associated with a low level of confidence may be due to knowledge gaps about the disease on this specific point. So in the first case, it emphasises the need to refine the definition of the criteria and their classes, to improve their understanding and their ability to differentiate diseases, and in the second case, it identifies some gaps in the knowledge of the disease that could support further key research questions. For example, in this study, the criterion 'presence of the disease in Southeast Asia', which combined a high intra-ratio (0.23) and an important proportion of respondents with a high confidence in their answers (77.6 %), should have been understood differently by the different respondents or was not associated with classes that allowed a good differentiation between the diseases. On the other hand, the criterion 'existence of risk groups' showed a high intra-ratio (0.18) as well as a large proportion of respondents with a low level of confidence in their answers (20.7 %). This result suggested that the high variability in the respondent answers was mainly due to a lack of knowledge on this particular point.

These findings must be interpreted in light of a main bias in the methodology, due to a variability of size of the groups (diseases), ranging from 21 for HPAI to one for bartonellosis, brucellosis, giardiasis, Japanese encephalitis, leishmaniasis, Nipah, swine influenza, taeniasis and trematodiasis. Indeed, for diseases selected by several individuals, the weighted mean corresponding to the level of confidence and the specific expertise of the respondents was much more accurate than the single values obtained for disease with only one respondent. Furthermore, calculations performed by the MCA take into account the size of the different group of individuals and a weight, proportional to the size of the group, is applied in the calculations.

14.4.3 Profile and Classification of Diseases

Displaying the classification of disease simultaneously with the scores provided by the respondents provides a good overview of how the disease clustered regarding their profile and how important their impacts were in terms of epidemiology, health, economy and society.

The way diseases were clustering was coherent with their epidemiological pattern and their burden on public and animal health. For instance, Nipah and leishmaniasis are two emerging/exotic diseases in the region grouped together. HPAI, salmonellosis, rabies and anthrax are main threats for both humans and animals and formed one cluster altogether. Finally, bovine tuberculosis, brucellosis and *Streptococcus suis* infection, gathered in a same group, are endemic in Southeast Asia and trigger some sporadic outbreaks in human and animal population.

But the results must be interpreted in light of biases in methodology at different levels. First, as explained previously, variable size of the groups was a main source of bias. When looking at the total score per disease, trematodiases obtained the highest score (score 3.53), followed by HPAI (score 3.38) and bartonellosis (score 3.24). This result is probably biassed by the fact that the sample size of the respondents is extremely different from one disease to another (1 for trematodiasis and bartonellosis and 21 for HPAI). It can be suspected than the high score obtained for trematodiasis and bartonellosis is influenced by the professional focus of the single respondent, contrary to HPAI for which the high number of respondents led to the dilution of the individual subjectivity and misinterpretation of the questions. For giardiasis, the level of confidence of the solitary respondent was very low (mode = 1) and this finding calls into question the reliability of the data collected from this participant. Then, the potential redundancy of some criteria might have also triggered some biases. Criteria related to animal health and economy are strongly interdependent as any disease with a great impact on animal health at the population scale (criterion belonging to animal health category) fatally triggers proportionate economic impact in terms of production losses and cost of control measures (criteria belonging to the economic category). Moreover, it is important to keep in mind that the economic impact is assessed regarding both the direct production losses due to the symptoms and the cost of the control measures. So, for a disease such as HPAI for which surveillance and control programmes have been carried out worldwide by international and national organisations, the cost of the prevention and control measures is very high and so a greater economic impact (score 4.43) is given to this disease compared with other economically important diseases such as brucellosis (score 3.29) or salmonellosis (3.57) for which no costly programme is applied. Finally the numerical scale applied to the different scales to allow to compute the scores is very arbitrary as there was no scientific evidence in applying a linear relation between the different classes.

14.4.4 Towards a New Approach to Prioritise Diseases

Prioritisation may be an efficient tool for policy-makers in charge of allocating resources for surveillance and control programmes or research projects, to target efficiently diseases that need to be addressed ahead of others. In developing countries, the importance to prioritise disease in an objective way is even more significant. In Southeast Asia, the occurrence of zoonoses and their spread is facilitated by the lack of public and animal health capacity on one hand and the exceptionally high population growth rate, the agricultural expansion and intensification, the human encroachment on game reserves, the globalisation of commerce and trade and more frequent contacts between humans, domestic animals and wildlife on the other hand (Cáceres and Otte 2009). Furthermore, the region is considered as a “hot spot” for future emergence and spread of zoonoses because of suitable environmental conditions (Jones et al. 2008): warm and humid climate, high biodiversity, high frequency of natural disasters (such as flooding), etc. So there is a strong need to address the prioritisation of zoonoses with objective tools, specifically adapted to the context of Southeast Asia.

The findings of the study opened new lines of work to improve prioritisation models or to develop new tools for prioritisation, based on the specific context of zoonoses in Southeast Asia. But this methodological framework could also be used in other contexts, depending on the objective of the prioritisation work.

Firstly, MCA can be a very useful tool to refine the list of criteria prior to performing the prioritisation exercise. The choice of the criteria against which the prioritisation is performed remains a weak point in most studies although it is determinant for the performance of the method (Krause 2008a). On one hand, their selection should be made with the objective of getting a well-balanced representation of the components of the disease to comply with the aim of the study – in the case study of zoonoses, public and animal health criteria, socioeconomic aspects in relation to public and animal health, environment impact and the perception by population. But on the other hand, to deal with the scarce availability of some data (Kemmeren et al. 2006; Fosse et al. 2008) and to ensure a clear differentiation between diseases (Cardoen et al. 2009), the list of criteria may be restricted as much as possible. The findings of this study indicate how MCA, combined with the analysis of the level of confidence of respondents in their answers, can help in identifying key criteria that ensure a good differentiation between diseases based on data collected through a web survey. According to the objective of the prioritisation exercise, an extended list of relevant criteria can be first set and followed by a preliminary analysis of the correlation ratio and the level of confidence, to determine those for which a reliable differentiation between diseases is obtained, those for which the definition needs to be improved and those which should be left. With a particular care to ensure that all the components of the diseases are taken into account to comply with the aim of the prioritisation, this approach allows to refine the list of criteria, in order to base the further scoring exercise on clear, relevant and accurate criteria. The clarity of the criteria and classes is a key point when using a web survey as participants answer on their own without any external help (such as a facilitator in a workshop) and there is no way to check for the correct understanding of the questions.

Secondly, the web-based questionnaire can be an interesting alternative to the scoring step by experts, commonly used in semi-quantitative models (Defra 2006). Despite the fact that there is no objective of prioritisation announced in first instance, the questionnaire was built following the example of those used for scoring diseases in semi-quantitative prioritisation methods. Once the objective of the prioritisation process is clearly defined, a numerical scale can be applied to the different classes in order to obtain a score for each criterion, which can be then aggregated to lead to an overall score per disease, which is then used as the base for the ranking. Contrary to the approach developed in previous methods, it is not a restricted panel of experts who are asked to rank a broad range of disease but a large population of stakeholders asked to give inputs about one disease that they have self-selected. So, this methodology circumvents the problem of the lack of knowledge and the subjectivity due to professional focus, encountered with expert opinion elicitation. In some methods, to manage the lack of ready knowledge of the experts for a wide range of diseases and to improve the objectivity and the accuracy of their responses, information data based on literature study are given to the experts to help them in scoring the criteria (WHO 2006; Cardoen et al. 2009). This approach presents different constraints and disadvantages. First, it is not always possible to gather from the literature all data about diseases, especially in developing countries, and it may be very resource intensive, which is why expert opinion elicitation is usually carried out to avoid these two constraints of data collection. Secondly, if this help aims to decrease the subjectivity of experts by making their scores evidence based, their own judgement are strongly biassed by the external information and the scoring is not based anymore on a purely expert opinion but on a mix of expert inputs and bibliographic data, in which the weight of each party cannot be assessed. Compared with expert opinion, the main advantages of such a questionnaire are that it is inexpensive and fast and makes a survey in a large population manageable. But possible disadvantages are related to the clarity of the questions, the validity of the responses and low response percentage (Ribbens et al. 2008). In this study, despite the pretesting step of the questionnaire, the high intragroup variability of the variables emphasised the fact that the criteria and the definition of the different classes associated were not clear enough to be understood the same way by all the respondents. Web-based questionnaires therefore appear to be a reliable alternative to expert opinion if the questionnaire is carefully designed in order to ensure that the discrepancies among respondent answers are due to a difference of opinion and not to a difference of understanding. The validity of data needs to be carefully analysed to be sure that all raters apply data collection method in a consistent manner. Different methods are currently available to evaluate the quality of collection method. Some are based on the inter-rater reliability assessment (probability), such as the kappa or the Fleiss's test (Gwet 2008), as some others calculate the sensitivity and specificity of data regarding a gold-standard method (Garabed et al. 2009) or geographic information system (Richardson et al. 2009). Furthermore, as previously mentioned, to improve the accuracy of the approach proposed in this study, the analysis of data should be performed on the same number of individuals for each disease. The consultation of a high number of experts results in the dilution of the effect of individual subjectivity and misinterpretation and will allow to work with the distribution of score instead of single-point values. As a result, the final ranking of diseases will take into account the uncertainty and the variability of the system and will be more accurate (Cardoen et al. 2009; Havelaar et al. 2010).

Some other lines of work should be also interesting to explore, in order to improve the accuracy and the relevancy of the data collection through a web survey. To enhance the representativeness of the respondents and to take into account the perception of the diseases by all the stakeholders involved with zoonoses, the questionnaire may be drawn up in different versions adapted to the different professions (veterinarians, medical doctors, economists, farmers, etc.). Furthermore to deal with the part of subjectivity which remains with respondents' answers, the definition of the criteria may focus on the identification of 'proxy criteria'. Those criteria do not present a great interest in themselves but they are not submitted to professional focus of respondents and they allow to assess other variables with which they are closely related to. Finally, the classification of disease based on the results of the MCA may provide clusters of diseases with similar profiles, which can be used as a start for the prioritisation exercise. Instead of ranking the diseases with regard to each other, they are first clustered together depending on their characteristics and then one in each cluster is selected as a priority. By focusing efficiently efforts on this disease to improve the surveillance and control systems, it can be expected that the future improvement obtained for this disease will spread to the other diseases of the same cluster (FAO 2008). This approach presupposes that the criteria are carefully selected to be sure that the clusters of diseases are accurate and relevant. An important advantage of this approach is that it avoids the risk of vertical programmes, which is always present when addressing the prioritisation task pathogen by pathogen (Krause 2008b). Indeed, when following a strict pathogen-focused approach, the original purpose of any health activity would be severely constrained and it would result in the competition of vertical programmes if decision makers do not keep in mind the operational commonalities among the high-priority diseases. To avoid this undesirable consequence of prioritisation, some research groups have therefore performed prioritisation exercises focused on general health issues rather than on individual pathogens (Eger et al. 2009), but the way diseases are grouped does not necessary lead to homogeneous clusters of diseases, which require the same individual methodological approach.

14.5 Conclusion

The findings of this study highlighted an innovative approach to improve objectivity and accuracy for some of the steps of prioritisation methodology. The use of a web-based questionnaire appeared to be an interesting alternative to expert opinion elicitation for the process of data collection and scoring, while the performance of multivariate analysis on a set of criteria prior to the prioritisation enhances the selection of clear, accurate and relevant criteria that allow a reliable differentiation between diseases. Nevertheless, the results of the study underlined several sources of bias in the methodology that need to be addressed to optimise the use of this new approach.

Dealing efficiently with zoonoses implies working on the human-animal-ecosystem interface. There is now an international consensus around the "One Health" approach (FAO 2008) that supports and legitimates the need of cooperation between animal, public and environmental health institutions to defeat emerging and re-emerging diseases that threaten both animal and human health. Since the emergence of the One Health concept, the management of several recent outbreaks (Q fever in the Netherlands in 2010, Hendra virus in Australia in 2009) underlined the importance of thinking about the animal-human-ecosystem interface to fight against old and emerging diseases (Leboeuf 2011).

This study underlined the need to address prioritisation within the One Health approach because criteria related to animal and human health, as well as those related to ecology and environment, contributed to a reliable and accurate differentiation of the diseases. Nevertheless, it also arose some difficulties in working within this framework, as it was challenging to gather reliable data about zoonoses from all the stakeholders involved with zoonotic diseases, both in the animal and health sectors. It is therefore important to continue the development of efficient tools for prioritisation in this context.

References

Birol E, Asare-Marfo D, Yakhshilikov Y (2010) Efficacy and adoption of strategies for avian flu control in developing countries (no 1023). International Food Policy Research Institute (IFPRI)

Brookes VJ, Hernández-Jover M, Cowled B, Holyoake PK, Ward MP (2014) Building a picture: prioritisation of exotic diseases for the pig industry in Australia using multi-criteria decision analysis. Prev Vet Med 113:103–117

Cáceres SB, Otte MJ (2009) Blame apportioning and the emergence of zoonoses over the last 25 years. Transbound Emerg Dis 56:375–379

Capek I, Vaillant V, Mailles A, De Valk H (2006) Définition de priorités et actions réalisées dans le domaine des zoonoses non alimentaires, 2000–2005. Buletin Epidémiologique Hebdomadaire 27–28:196

Cardoen S, Van Huffel X, Berkvens D, Quoilin S, Ducoffre G, Saegerman C, Speybroeck N, Imberechts H, Herman L, Ducatelle R, Dierick K (2009) Evidence-based semiquantitative methodology for prioritization of foodborne zoonoses. Foodborne Pathog Dis 6:1083–1096

Costard S, Porphyre V, Messad S, Rakotondrahanta S, Vidon H, Roger F, Pfeiffer DU (2009) Multivariate analysis of management and biosecurity practices in smallholder pig farms in Madagascar. Prev Vet Med 92:199–209

Cox LA, Babayev DB, Huber W (2005) Some limitations of qualitative risk rating systems. Risk Anal 25(3):651–662

DEFRA (2006) Approaches to the prioritisation of resources: a brief review of selected public sector organisations in the UK and abroad. http://archive.defra.gov.uk/foodfarm/farmanimal/diseases/vetsurveillance/documents/prioritisation-resources.pdf. Retrieved 3 Oct 2014

Discontools (2009) Approaches to the prioritization of diseases: a worldwide review of existing methodologies for health priority settings. www.discontools.eu/documents/1207_Draft%20Review%20of%20existing%20methodologies%20for%20priority%20settings.pdf. Retrieved 3 Oct 2014

Doherty JA (2000) Establishing priorities for national communicable disease surveillance. Can J Infect Dis 11:21

Dohoo IR, Ducrot C, Fourichon C, Donald A, Hurnik D (1997) An overview of techniques for dealing with large numbers of independent variables in epidemiologic studies. Prev Vet Med 29:221–239

Dray S, Dufour AB (2007) The ade4 package: implementing the duality diagram for ecologists. J Stat Softw 22:1–20

Eger K, Gleichweit S, Rieder A, Stein KV (2009) Prioritising integrated care initiatives on a national level. Experiences from Austria. Int J Integr Care 9:e91

FAO-OIE-WHO-UNSIC-UNICEF-WB (2008) Contributing to one world, one Health. A strategic framework for reducing risks of infectious diseases at the animal-human-ecosystems interface. ftp://ftp.fao.org/docrep/fao/011/aj137e/aj137e00.pdf. Retrieved 3 Oct 2014

Fosse J, Seegers H, Magras C (2008) Foodborne zoonoses due to meat: a quantitative approach for a comparative risk assessment applied to pig slaughtering in Europe. Vet Res 39:1–16

Gale P, Brouwer A, Ramnial V, Kelly L, Kosmider R, Fooks AR, Snary EL (2010) Assessing the impact of climate change on vector-borne viruses in the EU through the elicitation of expert opinion. Epidemiol Infect 138:214–225

Garabed RB, Perez AM, Johnson WO, Thurmond MC (2009) Use of expert opinion for animal disease decisions: an example of foot-and-mouth disease status designation. Prev Vet Med 92:20–30

Gwet KL (2008) Computing inter-rater reliability and its variance in the presence of high agreement. Br J Math Stat Psychol 61:29–48

Havelaar AH, van Rosse F, Bucura C, Toetenel MA, Haagsma JA, Kurowicka D, Heesterbeek JHAP, Speybroeck N, Langelaar MFM, van der Giessen JWB, Cooke RM, Braks MA (2010) Prioritizing emerging zoonoses in the Netherlands. PLoS One 5:e13965

Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, Daszak P (2008) Global trends in emerging infectious diseases. Nature 451:990–993

Kemmeren JM, Mangen M-JJ, van Duynhoven YTHP, Havelaar AH (2006) Priority setting of foodborne pathogens—disease burden and costs of selected enteric pathogens. National Institute for Public Health and the Environment, Bilthoven. http://rivm.openrepository.com/rivm/bitstream/10029/7316/1/330080001.pdf. Retrieved 3 Oct 2014

Krause G (2008a) How can infectious diseases be prioritized in public health? EMBO Rep 9: S22–S27

Krause G (2008b) Prioritisation of infectious diseases in public health – call for comments. Eurosurveillance 13(40):1–6

Kurowicka D, Bucura C, Cooke R, Havelaar A (2010) Probabilistic inversion in priority setting of emerging zoonoses. Risk Anal 30:715–723

Leboeuf A (2011) Making sense of one health: cooperating at the human-animal-ecosystem health interface. Health and Environment Reports 7. http://onehealthinitiative.com/publications/IFRI_ifrihereport7alineleboeuf.pdf. Retrieved 3 Oct 2014

McKenzie J, Simpson H, Langstaff I (2007) Development of methodology to prioritise wildlife pathogens for surveillance. Prev Vet Med 81:194–210

Mitchell RJ, Williamson AM, O'Connor R (2009) The development of an evaluation framework for injury surveillance systems. BMC Public Health 9:260

More SJ, McKenzie K, O'Flaherty J, Doherty ML, Cromie AR, Magan MJ (2010) Setting priorities for non-regulatory animal health in Ireland: results from an expert Policy Delphi study and a farmer priority identification survey. Prev Vet Med 95:198–207

Ng V, Sargeant JM (2013) A quantitative approach to the prioritization of zoonotic diseases in North America: a health professionals' perspective. PLoS One 8:e72172

Perry BD, Randolph TF, McDermott JJ, Sones KR, Thornton PK (2002) Investing in animal health research to alleviate poverty. International Livestock Research Institute (ILRI), Nairobi. http://mahider.ilri.org/handle/10568/2308. Accessed March 2012

R Development Core Team (2014) R tutorial. http://cran.r-project.org/doc/manuals/r-release/R-intro.pdf. Retrieved 3 Oct 2014

Ribbens S, Dewulf J, Koenen F, Mintiens K, De Sadeleer L, de Kruif A, Maes D (2008) A survey on biosecurity and management practices in Belgian pig herds. Prev Vet Med 83:228–241

Richardson E, Good M, McGrath G, More SJ (2009) The use of Geographic Information System (GIS) and non-GIS methods to assess the external validity of samples postcollection. J Vet Diagn Invest 21:633–640

World Health Organization (2006) Setting priorities in communicable disease surveillance. http://whqlibdoc.who.int/hq/2006/WHO_CDS_EPR_LYO_2006_3_eng.pdf. Retrieved 3 Oct 2014

World Organization for Animal Health (2008) Terms of reference and call for tender for a new OIE study: listing and categorisation of priority animal diseases, including those transmissible to humans. http://www.test.oie.int/fileadmin/Home/eng/Support_to_OIE_Members/docs/ppt/study_partnership_oie.pdf. Retrieved 3 Oct 2014

Chapter 15
Managing Global Risks: Vietnamese Poultry Farmers and Avian Flu

Muriel Figué and Stéphanie Desvaux

Abstract This chapter documents the logics underpinning farmers' management practices of an emerging disease. In the area of our survey, Vietnamese farmers, who are one of the front lines of the fight against H5N1, are called upon to collaborate to the international fight against the virus. Our study highlights that direct (poultry mortality) and indirect impacts (consequence of the measures imposed by the government to contain the virus, fluctuation of consumers' demand, etc.) tend to be relatively limited when compared to the permanent state of instability which characterises the context of poultry production in the surveyed village. This instability is mainly related to numerous and regular poultry infectious diseases and market fluctuations. If international community considers H5N1 as a zoonotic risk and a pandemic threat which asks for emergency tools, H5N1 is framed by the farmers of our study as an epizootic problem manageable through routinised measures. These measures aim at minimising the economic impact of the disease rather than preventing poultry and Human from the disease. Consequently, local management of the disease cannot fit with the precautionary approach promoted by the international community.

15.1 Introduction: Management of Emerging Infectious Risks by Poultry Farmers

The current context of emerging risks, and in particular emerging diseases, requires international and inter-sectorial cooperation (human health, animal health, etc.) as well as multi-scale cooperation (from local to international level). It is a question of encouraging very diverse operators to collaborate on what would be a common project, formalised by UN agencies in the "One Health" Initiative of the Food and Agriculture Organisation [FAO], the World Organisation for Animal Health [OIE],

M. Figué (✉)
CIRAD, UMR MOISA, Montpellier F-34398, France
e-mail: muriel.figuie@cirad.fr

S. Desvaux
CIRAD, UR AGIRS, Montpellier F-34398, France
e-mail: stephanie.desvaux@agriculture.gouv.fr

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_15

the International the World Health Organisation [WHO] and others international organisations (FAO et al. 2008).

Farmers are asked by international organisations to cooperate in this project of global health governance (OIE 2008) but are also often pointed at for their low compliance with the biosecurity measures that they are asked or recommended to apply in their farm. The gap between their behaviour and the recommendations addressed to them is often interpreted as a lack of knowledge or a problem of perception. On the contrary, we will focus in this chapter on the active role of farmers in risk management and on the constraints, opportunities, values and interests that underpin their behaviours. The purpose is to understand the logic of disease management at the local scale. We apply this approach to the case of poultry farmers facing H5N1 in a village in Vietnam.

15.2 The Context: Avian Flu in Vietnam

Vietnam is a rural country (70 % of the population lives in rural areas) where 90 % of households rear poultry. These birds, which are both consumed by the household and sold on the domestic market, account for 19 % of the incomes of agricultural households (Desvaux and Ton 2008). Vietnam was the first country to officially declare the re-emergence of the H5N1 avian flu virus to the OIE at the end of 2003. Vietnamese poultry farmers were affected not only by the virus itself but also by the preventive culling measure (in total, 17 % of all fowl died or were killed during the first months of 2004, GSO 2004), by the restrictions concerning the transport and commercialisation of poultry, by the regulations introduced to control the virus (and the related risk of a flu pandemic) and by the reactions of Vietnamese consumers.

Primarily in 2004 and 2005, poultry farmers were therefore required to deal with a context of high uncertainty linked to the epizootic situation [declarations of new outbreaks (see Pfeiffer et al. 2007 for the history of these outbreaks)], the market situation [strong fluctuations in demand and price (Figuié and Fournier 2008)] and the regulatory context [changing context depending on new outbreaks, international pressure, the development of scientific knowledge concerning the virus, etc. (Agrifood Consulting International 2007)].

In the Vietnamese Capital, Hanoi, the sale of poultry was entirely prohibited on two occasions from the beginning of the flu outbreak: in February 2004 and in November/December 2005 (periods during which Hanoi was officially declared to be infected by the virus), affecting greatly the poultry farmers supplying the area (like farmers of our zone of studies). Furthermore, to satisfy the resumption of consumer demand, the Vietnamese government reduced import taxes on poultry from 2006 onwards, generating a new situation of competition for locally produced poultry [taxes were reduced by between 20 % and 60 % depending on the product category (Tuong 2010). At the end of 2008, Vietnam increased these taxes again to protect domestic production].

Various sanitary control measures were implemented along the value chains following the emergence of the H5N1 virus. In addition to the preventive culling operations (the extent of which varied according to the intensity of the outbreaks and the policy of the different provinces within the country), these measures essentially relied on the traceability of the vaccination of the animals and their slaughter in certified abattoirs.[1] Our surveys enabled us to estimate that these measures lead to a surcharge of about 2,750 dongs per bird (i.e. almost 0.13 euros).[2] Furthermore, in order to limit the number of ducks being bred (ducks being considered at that time as a probable reservoir for the H5N1 virus), the incubation of duck eggs was officially banned from November 2005 to February 2007 (Agrifood Consulting International 2007).

15.3 Impact of Avian Flu in Vietnam

The economic impact of this sanitary crisis has been evaluated at national level [loss of between 0.3 % and 1.85 % of GNP in 2004 (McLeod et al. 2004)] and at value chain level [effect of concentration and contractualisation (Agrifood Consulting International 2007; Figuié et al. 2013)]. From a political standpoint, Figuié (2013) and Tuong (2010) have demonstrated the local objectives (legitimisation of the Communist Party and the central government) and international objectives (adhesion to the World Trade Organisation) which have influenced the design of H5N1 management policies by the Vietnamese authorities.

At the level of rural households, research works have essentially highlighted:

1. The economic dimension, thereby demonstrating that avian flu has had a particular short-term impact on integrated industrial and industrial farmers (type 1 and 2 according to the FAO classification). However, in the long term, these farmers would have benefitted from their capacity to adapt to new market demands, in particular to new safety standards. Semicommercial farmers (type 3) could have suffered more lasting effects due to their more limited financial capacity to reconstitute their livestock after the crisis and to invest in equipment

---

[1] Moreover, the government intends to modernise poultry farming in the long term and to facilitate the introduction of various biosafety measures, in particular with the support of the agro-industrial sector (e.g. the Thai group Charoen Pokphand) by means of a process of implementing contracts with farmers and relocating farms.

[2] Cost per bird evaluated for flock of approximately 100 animals. It can be broken down as follows: 200 dongs for the vaccination, 550 dongs for the transport certificates and 2,000 dongs for the culling operations carried out in a certified slaughterhouse (with one euro equivalent to approximately 20,000 dongs over the period being studied).

enabling them to improve the safety of the flocks. Sector 4 (backyard poultry farmers) was not particularly affected in terms of income as the poultry is intended for consumption within the household or for sale on a local market less concerned by the transport restrictions imposed (Agrifood Consulting 2007).

2. The cognitive dimension: this was highlighted through studies based on the KAB approach (Knowledge/Attitude/Behaviour). These studies have recorded a poor or incorrect knowledge of avian flu on the part of the farmers, served to justify numerous projects aimed at educating and sensitising farmers with regard to this new risk (UNICEF, Academy for Educational Development, etc.).
3. The nutritional dimension: without really studying them, several expert reports have referred to the potential negative effects of avian flu on the nutritional situation (fall in self-consumption of poultry) with regard to type 4 households (backyard poultry farmers).

These studies failed to analyse the role that farmers play in risk management. Local stakeholders are directly exposed to policies implemented by the States and respond to this pressure. But we make the hypothesis that they have also their own dynamic and logic: no matter the opinion of these stakeholders on messages and recommendations emitted by the national and international authorities to cope with risks, these front-line players keep a relative autonomy in their assessment of the situation. This autonomy mainly relies on laymen knowledge mobilised by these local stakeholders to assess risk, to adapt to it or even to build suitable answers to it.

The aim of the study presented here is therefore to analyse the responses (or absence thereof) adopted by Vietnamese poultry farmers to cope with the outbreaks of the H5N1 virus in Vietnam. Our starting point is to consider poultry farmers as risk assessors and managers rather than as the victims of a new epidemic of which they must be made aware. We therefore want to link the responses implemented with the manner in which the problem has been defined by these social actors. Our hypothesis is that this definition is not only linked to the information they may have received from Vietnamese authorities or from the different media (often identical in the context of Vietnam) but also to local experience of health risks and risks in general as well as to the opportunities that the risk situation might generate.

In July and November 2008, interviews (survey 1) were conducted with 20 poultry farmers from the village of Duyen Yet (commune of Hong Thai, district of Phu Xuyen, province of Ha Tay in the Red River delta in northern Vietnam). These interviews, which form the basis of this work, were in part intended to provide a better interpretation of quantitative data drawn from studies conducted previously in the same zone: study on the farming and commercialisation practices for poultry and poultry products [conducted the same year in the same village, survey 2 (Payne et al. 2009)] and an assessment of the information and education campaign concerning avian flu [conducted in villages in the same district in 2006, survey 3 (Figuié et al. 2006)].

15.3.1 The Village of Duyen Yet

Ha Tay is a province in the Red River delta in northern Vietnam (under the administrative aegis of the city of Hanoi since August 2008). It is an important production area for poultry destined for the Vietnamese domestic market. Duyen Yet is a village in this province, sitting in a bend of the Red River. Before 1993, most of the inhabitants of this village derived their livelihoods from small-scale agriculture (essentially rice) and pig farming. From 1993 onwards, a highly proactive government policy encouraged the zone to specialise in poultry production. A state farm was set up in Dai Xuyen in a neighbouring parish to provide farmers with day-old chickens (DOCs) with a view to rearing broilers. The state farm subsequently encouraged the diversification of poultry farming activities in the area by also supplying parental chicks for the production of chicks and ducklings. In the village of Duyen Yet, the production of chickens which had been developed was for the most part quickly replaced by the production of chicks and ducklings with the installation of several private hatcheries. At the start of the new millennium, a land reorganisation policy enabled the creation of farms devoted to fish farming and intensive poultry farming in the lower parts of the village, thanks to major earthmoving works (allowing the raising of ground for the houses and rearing pens to be built). These farms are called "breeding farms" as opposed to "village farms".

15.3.2 Poultry Farming Systems

At present, all farms practise agricultural activities (essentially rice) while also rearing animals.

A small number of these farms focus primarily on pig farming (maximum of ten animals).[3] Occasionally, these families rear a small number of poultry (traditional breeds) sold at periods when the demand is high (e.g. the New Lunar Year, the Tet festival). These are backyard poultry farmers (type 4 according to the FAO classification).

However, for the majority of the 700–800 agricultural households in the parish, poultry farming represents the main activity (in about 600 households). It is important to distinguish, as mentioned above, between:

- "Village farms". These represent the vast majority of poultry farmers in the parish. They are small farms (100–300 animals per batch) relying on family labour. Half of them have a park adjacent to the poultry house thereby enabling the farmers to rear Muscovy ducks (these last ones are considered as too dirty to be kept in confinement). A small proportion of them (5–10 %) have an adjacent

---

[3] Pig farming is combined with the production of alcohol, with the residues being used as pig feed (in addition to corn produced on land outside the dykes). This generally concerns families with little capital (in particular young couples).

body of water enabling them to rear Peking ducks. These farms correspond to the commercial type (type 3, according to the FAO classification). The main factor limiting the size of the batch in the village is the lack of space.[4]

- "Breeding farms". These farms (there are around 30 of them) are more highly capitalised and specialised than those above. The main activity conducted in these farms is fish and poultry production with generally between 500 and 1,000 chickens per batch (the manure serves to fertilise the ponds). The labour force is based on paid labour. Access to water offers them the advantage of being able to breed Peking ducks in addition to other types of poultry. These farms correspond to the industrial type (type 2, in the FAO classification).

Interviewed farmers consider that breeding farms are less exposed to diseases affecting poultry in general because they are more isolated and better ventilated, unlike village farms.

15.3.3 The Types of Poultry Production

In addition to a limited production of traditional chickens (*Ga ta*) for its own consumption or, as mentioned above, in low-capital farms, the village specialises in the following productions:

- *Broilers*: These chickens can be one of two types: "white chickens" (high-performance industrial breeds with taste qualities judged to be poor by consumers) and more often "red chickens" (Asiatic breed such as *Tam Hoang* or *Lu Phuong* breeds), which are more rustic. Because the broilers' production cycle is short (45 days for white chickens, 3 months for red chickens) compared to laying hens, the farmers produce several batches per year and therefore devote more time during the year to the young chicks, making it a labour-intensive activity. It nevertheless requires very little space (no water pond, no park). As a result of all these considerations, this activity is deemed suitable for farmers with little experience or limited capital.
- *Day-old chickens (DOC)*: These chicks are intended for the production of broilers. They come from Vietnamese breed (*Ga Luon Phuong, Xa So*), Chinese or Thai ones. This accounts for the majority of the production within the village.

The chickens are better adapted to confinement than ducks and are therefore preferred by farmers who have neither a park nor a body of water. Nevertheless, they are sensitive to Newcastle disease which may cause numerous deaths.

- *Day-old ducklings:* Farmers rear parental breeds and sell the day-old ducklings. As already mentioned, these ducklings are of two types: Muscovy ducks and Peking ducks *(ngan* and *vit*, respectively, in Vietnamese). Peking ducks require

---

[4] When rearing laying hens for the production of chicks or ducklings, the farmers consider that a single person can deal with 1,000 animals.

less work (due to the maintenance of their coop) than chickens or Muscovy ducks since they are considered less dirty.

Furthermore, farmers consider Peking ducks to be less sensitive to disease and cold weather than Muscovy ducks (and therefore more suitable for winter rearing). Moreover, Peking ducks have another advantage compared to Muscovy ducks: their embryos can be marketed for consumption. Many farmers nevertheless prefer rearing Muscovy ducks (which account for the second-largest production in the parish after the production of DOCs) because of their higher selling price (a particularly high demand for ducklings in July, August, and September intended for rearing animals to be consumed for the New Year).

15.3.4 Insertion in the Value Chains

Farmers buy chicks and ducklings (parental breed) from the state farms in Dai Xuyen (ducks) and Thuy Phuong (chickens) or from local private hatcheries. The poultry feed is bought in stores located within the parish. Fertilised eggs are incubated either in private hatcheries within the parish or, in the case of almost half of the breeding farms, in hatcheries of the state farms. The hatcheries also act as intermediaries when marketing the chicks (sold to the nearby provinces of Hai Phong and Quang Ninh). Often, the hatchery lends the farmer the money required to purchase the chicks and the feed (in particular, in the case of laying hens when the farmer must wait 6 months before selling the first chicks. In the hatchery we visited, the owner informed us that he offered credit to half of his customers). Broilers and discard layers are sold to the numerous collectors who operate within the village and supply the Ha Vi wholesale market through which passes almost half the chickens supply to the city of Hanoi (Agrifood Consulting International 2007). The farmers are thus integrated into value chains which are geographically limited to northern Vietnam and in which no economic stakeholder would appear to enjoy any marked domination. These value chains are relatively fragmented, thereby making traceability somewhat problematic.

15.4 Avian Flu in the Village of Duyen Yet, Province of Ha Tay

15.4.1 The Presence of the Virus in the Village of Duyen Yet

The H5N1virus was first observed in Vietnam in the province of Ha Tay in June/July 2003. Since then, the province officially declared the presence of the virus in February 2004 and then again in August 2004 (declarations made to the OIE in 2004). According to Delquigny et al. (2004), it can be roughly estimated that between 5 % and 10 % of the birds in the province were affected by the H5N1 virus. Preventive culling affected only 0.5 % of the poultry farms in Ha Tay, primarily the large industrial farms [which explains the much higher percentage of animals culled, reaching 13.6 % of the Ha Tay poultry population (Agrifood Consulting International 2007)]. Despite the fact that outbreaks continue to be declared in the rest of the country, no further outbreak had been declared in Ha Tay province since August 2004 at the moment of the survey (except one very localised outbreak in 2007). Several information sources would nevertheless suggest that the virus continues to circulate there below epidemic thresholds, but with local management of clinically suspicious cases. The fact that these outbreaks are not declared is aimed at protecting the economic interests of the province which is, as already mentioned, the main poultry production site in northern Vietnam.

At the level of the district of Phu Xuyen, only 10 of the 28 communes were officially spared from the virus in 2004 (making it one of the most seriously affected districts in Vietnam in 2004). One of these ten communes was the commune presented in this study (Hong Tay), which declared no outbreaks and was not affected by the massive culling operation.

Nevertheless, several farmers interviewed in Duyen Yet (a village of Hong Tay commune) relate cases of mass mortalities among birds, which were then thrown into rivers, lakes and canals or buried, without the cause of the illness being clearly identified.

One of the farmers interviewed claimed to have lost two thirds of his 800 birds in 2005 to an unidentified illness. Another lost 2,000 of its 7,000 birds in 2007. Before our interview in this farm, another 500 had died (November 2008), and the farmer had quickly sold the surviving birds fearing further deaths and because his farm was flooded. His fish farming activity has enabled him to cope with the situation by providing a stable income.

While the farmers in the commune were not affected by the emergency measures, they were nevertheless affected by the direct loss of their chicken (which they cannot ascribe to a specific infectious agent) and then by the indirect effects of the avian flu outbreak (regulatory constraints and impacts on the markets). Before assessing these indirect effects, we will examine the effect resulting from these losses.

15.4.2 The Avian Flu Reference: SARS or Newcastle Disease?

Within the international community and at domestic level, the avian flu phenomenon was compared to SARS (severe acute respiratory syndrome, which appeared the previous year) and was treated in a similar way, that is, a crisis and emergency linked to the fear of a human pandemic and justified by a high level of uncertainty concerning the very nature of the risk relating to the virus. Was this the case among the farmers in the commune?

According to the farmers, 2004 and 2005 were bad years from the standpoint of animal health, but it is difficult to assess whether or not the deaths recorded really reflect an exceptional situation. Before the emergence of avian flu, the main cause of death of chickens was linked to Newcastle disease (chickens in type 3 or 4 farms are rarely vaccinated; ducks are not affected by this virus), the symptoms of which are very similar to those associated with avian flu.

According to the Agrifood Consulting report (2007), contagious avian diseases such as Newcastle disease have a much higher impact on small-scale Vietnamese farms than the H5N1 virus. In a survey conducted in four provinces of Vietnam,[5] 49 % of poultry farmers claimed to have been affected (between October 2005 and September 2006) by contagious diseases other than the flu compared to only 1 % who claimed to have been affected by the flu itself. Data from the Ministry of Agriculture (Division of Animal Health) confirm a relatively low risk of infection associated with the H5N1 virus, ranging from 0.8 % to 6.5 % at the level of the communes (for the last four of the six waves of the virus). However, the relative incidence of H5N1 and other contagious diseases is difficult to assess in that we do not have data concerning the mortality rates of poultry before the emergence of the H5N1 virus or their causes. The Agrifood Consulting data are based on farmers' declarations and therefore primarily indicate that, in the opinion of the latter, the H5N1 virus (rightly or wrongly) plays only a secondary role in poultry infections (vaccination of poultry against H5N1 has moreover modified the clinical picture and made it more difficult to recognise an outbreak of H5N1) or that the farmers have no interest in declaring cases of flu within their farms.

The emergence of the H5N1 virus became a much more important subject for farmers in relation to its consequences for human health, although only very temporarily. At the beginning of 2005, the province recorded 3 of the 33 deaths caused by the virus in the country since the end of 2003 (WHO 2005). The farmers claimed to have been worried the first year, but then as the number of human cases failed to rise, their concern rapidly disappeared: "People here feared for their safety due to the flu during the first year. We heard a lot about it on the TV. And there was the flu in Dong Thai. But as time went by, the people were no longer worried".

While these deaths alarmed the international community, the small number of victims led the farmers to reject the idea of a risk to human health and retaining only the threat to animal health. At local level, H5N1 therefore shifted away from the SARS model to move closer to that of Newcastle disease and other diseases common to poultry.

With this rapid refocusing on the part of the farmers, avian flu became a relatively classic problem in large part handled as a question of routine. But the manner in which other actors (economic actors, legislators) perceived the problem naturally had indirect effects and may have introduced new elements into this routine.

---

[5] The Agrifood Consulting survey concerns 1,360 outbreaks in the four provinces of Vietnam, including Ha Tay province.

15.4.3 Flu: Another Factor of Instability in an Already Highly Unstable Market

Before considering the indirect effects of the disease, we must first examine another element enabling us to explain the limited importance of the problem for the farmers: while the disease occurs in a context marked by a high level of infectious pressure, it also arises in a context already characterised by a very high level of market instability. Thus, according to one of the parties interviewed in relation to the general instability of agricultural prices, “farming is a bit of a lottery, it’s a question of luck… we can’t plan for every eventuality. Man can’t calculate as well as God”.

This instability is linked to the fact that poultry prices and day-old chicken and duckling prices vary considerably under the effects of a wide range of factors. Many of these factors are seasonal (high consumer demand, in particular at New Year, high demand for ducklings after the rice harvest, low demand for chicks and ducklings in the cold season, etc.). However, beyond these seasonal variations and their complex interactions which are nevertheless more or less predictable, there are other accidental factors. This is the case of the frequent risk of flooding which is particularly important for breeding farms, not only directly affecting the farms (flooded buildings) but also impacting the demand for chicks or ducklings from other farmers. The diseases which regularly affect other species (mainly pigs) also impact the supply of meat and the demand for poultry meat.

The sale price of chicks and ducklings (farm gate prices) recorded in one of the hatcheries in the village is highly variable: for the period January 2006–October 2008, prices varied from 2,700 to 12,400 dongs for a Muscovy duckling (average price of 5,600 dongs for the period for a production cost between 4,000 and 5,500 dongs according to the data provided by the farmers interviewed), from 1,500 to 9,300 dongs for a Peking duckling (average price of 4,700 dongs, no data on production costs) and from 1,400 to 4,800 dongs for a red chicken (average price of 3,100 dongs for a production cost of 2,000 dongs).

According to one farmer interviewed, “there are ups and downs, but on the whole, the economy of the village improves with the development of poultry farming… One year, I earned 20 million dongs while my neighbour earned nothing! Another year, she earned 70 million and I earned 20 million…”.

It is in this context that we must analyse the economic impact of avian flu. In light of the market instabilities, what might be interpreted as a certain fatalism on the part of the farmers (“it’s a bit of a lottery”, “it’s a question of luck”, etc.) is accompanied by practices designed to limit the effects of these hazards rather than the hazards themselves. But first we must examine the new regulations adopted by the government to face H5N1 and how they have been implemented at the local level.

15.4.4 Safety Regulation: Little Restriction at the Field Level

The regulations adopted by the government to limit the propagation of the virus and, more generally, to improve the levels of biosafety in the poultry value chains had highly variable impacts on the farms in the village.

The most significant impact concerned the restriction on transporting animals outside the district imposed at the beginning of 2004 and then again at the end of 2005 (two periods lasting about 2 months when poultry marketing in Hanoi was interrupted).

Nevertheless, these restrictions were to a certain extent circumvented (night transport or circuitous routes, corruption at inspection posts, selling in Hanoi via informal networks, etc.). Compared to the option of discarding the production, the risk of seeing the animals transported being confiscated by the police (in this case the transporter would not pay the farmer who supplied him) was actually a preferable alternative.

The vaccination of animals against avian flu became mandatory at the end of 2005. In theory, chicks and ducklings must be accompanied by a vaccination certificate until they reach the final buyer. In light of the complexity of the traceability, it is difficult to ensure that this regulation is applied meticulously; in practice, certificates would often appear to be issued by the veterinary services without their really having all the necessary documentation to be able to prepare them. These certificates can be subject to inspection, primarily when the animals are being transported. In practice, interviewed farmers declared that transporters prefer running the risk of a fine and the goods being confiscated rather than be subject to this regulation: indeed, there would be a “tax” to be paid in the event of an “inspection” whether there is certificate or not.

The government took the decision also to prohibit the rearing of ducks, but this decision was not followed up by any restrictive measure and did not therefore have any significant effect in our study area (as already mentioned, hatcheries temporarily interrupted their activity as a result of the poultry transport restrictions implemented in 2004 and 2005 and not as a result of any ban in their activity).

15.4.5 Impacts on the Size of the Poultry Flocks

According to the local veterinarian, all the farmers in the parish were affected to different extents by avian flu or the resulting consequences. At the end of 2008, 50 % of them had yet to recover the number of poultry they had before the outbreak of the flu, and 10 % had not resumed their activity. This estimation is completed by survey data (survey 2), according to which 25 of the 71 farmers interviewed (of about 150 farmers in the village of Duyen Yet) had fewer birds than before the flu, 19 had almost as many and 27 had more.

Another study already mentioned (Agrifood Consulting 2007), examining four provinces in Vietnam, confirmed that in 2006, the majority of farmers (more than 90 %) had succeeded in returning to pre-flu levels and that almost 20 % of them had more animals than before the outbreak of the virus.

In many cases, farmers were able to resume their activity by means of credit. Although the different lending organisations were somewhat reticent to lend money to poultry farmers in light of the flu, the Agricultural and Rural Development Bank implemented a credit policy in 2006 at a rate of 8 % intended to enable farmers to resume their activity upon condition that they modernise their farms and improve the "biosafety". This credit policy has primarily targeted breeding farms. Village farmers have resorted to mortgaging their houses or to more informal sources of income involving interest rates of up 20 %. It would be interesting to assess this debt burden more precisely.

The increasing number of contracts signed with private firms, like Charoen Pokphand (supplying credit, inputs and advice and guaranteeing the sale of the production) mentioned by certain experts in the context of Vietnam, was not observed in the village we studied.

15.4.6 The Strategies Developed by Farmers in the Context of Avian Flu

Neighbouring farmers are identified as the main source of contamination, but they are not charged for any "responsibility": it is up to each farmer to protect his farm individually. There are no risk factors, which are perceived to be specific to avian flu, and thus, the strategies developed by farmers to face H5N1 are the ones used usually for poultry diseases. Factors linked to the different species also come into play: Peking ducks are considered as more resistant to diseases than Muscovy ducks.

Safety preventive measures (certain farmers interviewed claimed that they prevented the collector from entering their farm and they disinfected their poultry house when they heard of problems affecting their neighbours) are limited. Major measures aimed at limiting the economic impact of the disease rather than avoiding the disease itself.

15.4.7 Sell

For eggs to be hatched during the closure of the hatcheries in 2004 and 2005, farmers were forced to convert their production of fertilised eggs into eggs for consumption (in particular, as the transport of eggs was subject to limited inspections compared to the transport of animals), representing a major loss of earnings (during the crisis, a hen's egg for consumption was sold at a price of 200–500 dongs, whereas a fertilised egg had a pre-flu value of 3,300 dongs. These "average" figures must be placed in perspective in light of the elements on price instability already presented).

With regard to the disease itself, during the outbreaks of 2004, animals were quickly sold, whenever possible, at very low prices while some were consumed by the farmers themselves or buried (dead birds). One of the farmers interviewed claimed "I put on three kilos during the flu!" With regard to sales, a parallel market usually exists for animals infected with or having died from disease on which the farmers were able to rely. In 2004, according to the farmers interviewed, the price on these markets was generally a quarter of the normal price. The major beneficiaries in these cases were the collectors who would sell the carcasses to restaurants at the price of healthy birds.

Furthermore, consumer demand was greatly affected, with periods of significant falls (in particular, according to the farmers, during periods of strong government communication), as well as periods of high demand (demand remained high during festive periods with consumers keen to maintain tradition), whereas supply was still in decline. The farmers have experienced a period of 6 months when the market was at the lowest point: the farm gate price for broilers price fell to 7,000 dongs per kilo compared to 50,000 dongs before the flu (and to 15,000 from 70,000 dongs for discard layers). Moreover, the competition faced by farmers from imported chicken meat (with the reduction in import duties) was exacerbated by the increased price of food following the global crisis of 2007–2008 (Vietnamese poultry farming is highly dependent on imported corn; e.g. the price of this feed for laying hens available in the village stores increased by a factor of 2.5 at this time).

Farmers therefore had to cope with very low selling prices or even a situation whereby they were unable to sell their eggs or poultry. To minimise this impact, other strategies than the selling and destocking ones were developed.

15.4.8 Wait

In light of the difficulty to sell, one commonly implemented strategy was to "wait until it has passed", the benefits for those able to wait being considerable: "People are used to it. When there is an outbreak of a disease, we try to wait until it passes as prices generally rise afterwards… if not, we lose everything." So in the case of the flu, "people waited hoping to sell their birds at a later date".

This strategy involves increased production costs. For laying hens, farmers try to reduce this increase by reducing their feed and stopping them from laying as they wait for the market to pick up. This strategy entails a certain risk as it is difficult to predict how long one will have to wait.

A much more marginal strategy adopted by some involved storing production by transforming it: one farmer claimed to have prepared dried chicken meat (*ruoc*, usually made with pork). However, we note that the "100-year egg" technique (a traditional means of conserving eggs) was not adopted on this occasion.

15.4.9 Diversify the Species

Considering price instability and different disease's susceptibility between species, the most common strategy is to diversify the poultry species on the farm over the year within the limits of the constraints presented above. Diversification extends beyond poultry species. As we have seen, several farmers also rear pigs or fish, and they were able to offset the lost earnings from their poultry farming activity during outbreaks benefiting from a co-related increase in the price of pork or fish, in particular in 2004 and 2005, as consumption moved away from poultry in favour of these products. Nevertheless, this production is also regularly affected by a range of diseases (foot-and-mouth disease, blue-ear disease, etc.). According to one pig and poultry farmer, "it was more difficult when the pigs were affected by blue-ear disease".

15.4.10 Always Ready to Start Again

All the farmers claimed that they never hesitated in renewing their flock and reinvesting in poultry farming because in any case, "here, you have to combine agriculture and rearing animals," as one farmer succinctly explained. Even in the event of losses linked directly to mortalities, the farmers rebuilt their flocks twice, three times as they do after deaths resulting from Newcastle disease. One claimed to have lost two thirds of his 800 birds to disease in 2005, although he did not know which disease. He mortgaged his land to borrow money to buy new birds. In 2007, he lost a large sum of money, not because of disease but because prices were too low. At present, he only has 80 traditional chickens, *Ga ta*, but as soon as he has saved more money (he cannot borrow any more), he will once again begin with a new flock of broilers.

And as explained by farmers: "We were able to start again quickly because the government said that it was finished. Anyway, here, we have to rear animals because rice doesn't pay well"; or: "We are obliged to continue rearing poultry because the district specialises in it".[6]

The renewed activity did not necessarily involve the same species as before. We have already explained that farmers increase the number of species raised to cope with the hazards of the market. Ducks are considered to be less sensitive than chickens to the H5N1 virus. To what extent did avian flu influence the choice of these species? The answers vary considerably: In several cases, the activity was renewed with broilers as they follow a rapid production cycle and the return on investment is quick. However, according to certain farmers, there are fewer broiler

---

[6] The possibilities for taking up an activity again are limited by financial capacities, borrowing capacity and the availability of chickens from state hatcheries. To overcome this final constraint, many farmers renewed their flock with "false F1s".

chicken farms following the outbreak of avian flu because chickens are more sensitive to the virus and farmers do not want to vaccinate animals with a relatively short cycle. Some farmers believe it is more judicious to rear red chickens rather than white chickens and Peking ducks rather than Muscovy ducks because they are less vulnerable. Others feel that the market is currently highly favourable to Muscovy ducks, thereby explaining why some farmers opt for this species. In light of this wide range of arguments, it is difficult to identify a clear trend in terms of the choice of species; the predominant strategy remains the diversification of species: “Ducks are more resilient than Muscovy ducks and the vaccination of ducks against avian flu is more efficient.[7] During an outbreak of the flu, it is therefore better to keep ducks. But people continue to combine the two”.

15.5 Conclusion

In the opinion of international organisations (FAO, OIE, WHO), H5N1 is an event which justifies unprecedented international mobilisation. This study shows that farmers in the village studied – and who are in the front line of the issue – have considered it as such only during a short period of time, when they feared for their own health. But this fear was transitory, and the problem related to H5N1 only persisted for them, in a much subdued form, as an epizootic disease (transmission from animal to animal) with direct and indirect consequences (economic and regulatory impacts). The pandemic potential (transmission from person to person on a global scale) or even zoonotic dimension (transmission between man and animal) of the virus which justified the international concern does not figure in the local framing of the disease.

Farmers have taken H5N1 into account as a poultry disease, but H5N1 is simply one of a number of problems that farmers have to deal with. There are numerous other poultry diseases. The economic impact of H5N1 has been however quite specific due to the new regulations adopted by the government to face it (under international pressure), but this impact was limited if we consider the context of a generally unstable market. In the past, farmers developed strategies, which they once again called on in the context of the avian flu outbreaks. These strategies aim more to minimise the indirect effects of the disease (i.e. strategies of alleviation) than to avoid the disease itself (i.e. strategies of prevention and precaution) and would appear to have been relatively successful, at the scale of the village.

We can therefore conclude that while avian flu (H5N1) and other infectious diseases affecting poultry are a problem, this problem is not perceived in terms of risk in the sociological sense of the word (i.e. a problem that could be avoided and with identified responsibilities to avoid damages or to pay reparations). Similarly, avian flu has been responsible for a national and international crisis: avian flu outbreaks encouraged to revise scientific knowledge on the ecology of viruses (in particular

---

[7] A Muscovy duck vaccination campaign was launched in 2007 before being abandoned.

with regard to ducks); to review the governance, in particular international health governance; to design new decision-making process in situations of uncertainty; and to rethink the relations of the Vietnamese authorities with the international community, but at the level of the farms in the village concerned by the study, the reaction was limited to a half-hearted criticism of the government (within the limits of what is possible within the country) for what was perceived as excessive communication concerning the flu (and the negative impact that this had on consumption) and on its decision to lower taxes on imported poultry.[8]

The potential contribution of social sciences to the study of infectious diseases is not limited to the analysis of their social factors, in an operational objective, nor to a critical analysis of the inequalities in front of the diseases, in relation with differences in social classes or territories; it is also to contribute to the understanding of the social dynamics that give existence to a phenomenon (Barbier and Prete 2010). Our contribution is to show that this dynamic takes place at different levels, from local to international, mobilising different framings of the disease. These framings evolve with time, with periods of alignment and divergences. These divergences may lead to competing answers to the problem.

References

Agrifood Consulting International (2007) Poultry sector rehabilitation project: the economic impact of highly pathogenic avian influenza – related biosecurity policies on the Vietnamese poultry sector. Prepared for FAO and WHO, Bethesda. p 254

Barbier M, Prete G (2010) Un regard sociologique sur la biopolitique des maladies émergentes et ré-émergentes. In: Barnouin J, Sache I (eds) Les maladies émergentes. Epidémiologie chez le végétal, l'animal et l'homme, Paris, Edition QUAE ed, pp 411–422

Delquigny T, Edan M, Nguyen DH, Pham TK, Gautier P (2004) Evolution and impact of avian influenza epidemic and description of the avian production in Vietnam. Vétérinaires sans frontières, Hanoi, p 119

Desvaux S, Ton DV (2008) A general review and description of the poultry production in Vietnam. Prise, Agricultural Publishing House, Hanoi

FAO, OIE, WHO, UNSIC, UNICEF, WB (2008) The strategic framework for reducing risks of infectious diseases at the animal-human-ecosystems interface. Contributing to one World, one Health [online]. http://un-influenza.org/files/OWOH_14Oct08.pdf

---

[8] Does this mean that avian flu was a case of "much ado about nothing"? Certainly, in light of our study, we might be somewhat surprised by the contrast with certain newspaper headlines seen in the foreign press, such as "Vietnamese farmers ruined by the flu" (Syfia press agency, 03/02/2004). At the same time, we must place this contrast in perspective, noting that the province of Ha Tay adopted a highly defensive attitude most likely by refusing to report any new outbreaks since 2005. In light of the statistics, however, we observe that even in the other provinces, mortalities and culling were not significant in terms of the number of farms concerned. Furthermore, our survey was conducted in 2008, 4 years after the beginning of the events at a time when floods, food prices and import taxes were the main concern of the farmers interviewed. Nevertheless, the flu was still present in Vietnam in 2008 and climatic and economic hazards are part of the daily routine of these farmers.

Figuié M (2013) Global health risks and cosmopolitisation: from emergence to interference. Sociol Health Illn 35(2):227–240

Figuié M, Fournier T (2008) Avian influenza in Vietnam: chicken-hearted consumers? Risk Anal 28(2):441–451

Figuié M, Nguyen MH, Tham TT (2006) Assessment of the pre-tet information, education and communication campaign (IEC) of the joint United Nations-Vietnamese Government Programme to fight highly pathogenic avian influenza (HPAI) in Vietnam. Socialist Republic of Vietnam, FAO, USAID, CIRAD-Malica, Hanoi, Prepared for FAO by CIRAD-MALICA. p 63

Figuié M, Pham AT, Moustier M (2013) Grippe aviaire dans la filière. La réorganisatio du secteur agro-industriel au Vietnam. Revue d'Etudes en Agriculture et Environnement 94(4):397–419

McLeod A, Morgan N, Prakash A, Hinrichs J (2004) Economic and social impacts of avian influenza. FAO, Rome, p 10

OIE (2008) Resolutions adopted by the international committee of the OIE during its 76th general session 25–30 May 2008 [online]. http://www.oie.int/fileadmin/Home/eng/Animal_Health_in_the_World/docs/pdf/A_RESO_2008.pdf/

Payne A, Desvaux S, Chalvet-Monfray K, Renard J-F, Bicout DJ (2009) Flux de volailles et propagations de l'influenza aviaire dans la filière avicole au Vietnam. Epidémiologie et Santé animale 55:137–152

Pfeiffer DU, Minh PQ, Martin V, Epprecht M, Otte MJ (2007) An analysis of the spatial and temporal patterns of highly pathogenic avian influenza occurrence in Vietnam using national surveillance data. Vet J 174(2):302–309

Tuong V (2010) Power, politics and accountability: Vietnam's response to avian influenza. In: Scoones I (ed) Avian influenza: science, policy, politics. Earthscan, London, p 52

WHO (2005) Avian influenza: assessing the pandemic threat. World Health Organization, Geneva, p 64

Chapter 16
The OIE Strategy to Address Threats at the Interface Between Humans, Animals and Ecosystems

Alexandre Bouchot and Marion Bordier

Abstract In our globalised, fast-changing world (deforestation, fast-growing animal protein demand, etc.), animal diseases that have an impact on public health, livelihoods, food security as well as the international trade of products of animal origin are constantly emerging or re-emerging. The complexity of disease emergencies calls for the identification of often collaborative effective strategies, based on both science and proven practical experience, to reduce future threats. The H_5N_1 avian influenza crisis has shown how crucial it is to address persistent global threats at the interface between humans, animals and ecosystems which requires (i) to strengthen animal and human health institutions and (ii) build strong partnerships among players who may have different perspectives on some issues and different levels of resources. To address the gaps in the animal health sector, OIE seeks to build member countries' capacities in policy design and good governance in animal health systems and Veterinary Services. At policy level, the OIE helps its members to enhance their credibility, both at the national and international level, by providing them with efficient tools, such as the strategic planning tools of the Performance of Veterinary Services (PVS) Pathway, with the objective to attract more commitment and more resources from their decision makers and partners. At good governance level, it provides science-based guidance that supports members in detecting, preventing and managing serious animal disease outbreaks through improved surveillance systems, strengthened laboratory networks and improved legislation. OIE promotes strong partnerships, notably with FAO and WHO, especially with regard to two topics that are getting currently a great attention and that require a strong multi-sectoral collaboration at all levels because of their social, economical and ecological determinants: rabies in humans that still kills more than 50,000 persons every year, mainly in Asia and mostly youngsters, and that is believed to be totally

---

A. Bouchot (✉)
OIE – World Organisation for Animal Health, OIE Sub-Regional Representation for South East Asia, c/o DLD, 69/1 Phaya Thai Road, Ratchathewi, 10400 Bangkok, Thailand
e-mail: bouchot.alex@gmail.com

M. Bordier
Animal Health consultant, Les Dambruères, 71 190 La Chapelle sous Uchon, FRANCE
e-mail: marion.bordier@gmail.com

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_16

preventable through effective dog vaccination, and antimicrobial resistance that can hinder the effective treatment and recovery of illnesses in both humans and animals. At regional level and in full collaboration with ASEAN and other partners, the OIE Sub-Regional Representation (OIESRR) for Southeast Asia plays a significant role in regional coordination of animal health and emerging infectious disease management in a region that is often considered as a 'hotspot' for emergence. Along the strategic objectives of the OIE Fifth Strategic Plan, the implementation of its activities to achieve the OIE Strategic Objectives is supported by various programmes and projects funded by donors. Its long-standing flagship regional programme, the Southeast Asia and China Foot-and-Mouth Disease (SEACFMD) Campaign which aims at controlling FMD by 2020 through vaccination promotes socio-economical and participatory approaches as well as assessment of the role of wildlife.

16.1 Introduction

Threats at the interface between humans, animals and ecosystems are numerous. These threats are either socio-economics, related to biodiversity and species conservation or, more immediately visible, related to public health. They are more than often related to animal health.

For instance, the occurrence of SARS (severe acute respiratory syndrome) in 2003 that derived from civets, that of avian influenza known as H_5N_1 in late 2002 or that of Ebola Reston virus in hogs in the Philippines in 2008, have, to varying degrees, threatened or are still threatening the public health. On the animal production side, avian influenza has been, and is actually still, responsible for massive losses in the avian industry by direct mortality or through culling in many countries and especially in Southeast Asia. It has to be noted that these three diseases have originated more than likely from China or Southeast Asia. At the same time, and in addition to these so-called emerging infectious diseases, some other diseases that concern domesticated animals, such as rabies or foot-and-mouth disease, are kind of constantly re-emerging at the interface between humans, animals and the ecosystems and continue, even though less visibly at the first glance, to have serious consequences for human health and for animal health in Southeast Asia and the rest of the world.

As has been declared forcibly by the heads of WHO, FAO and OIE, the challenges facing animal health, beyond diseases transmissible to humans (zoonosis), are critically important and involve food security, agriculture economics and the ensemble of economic activities associated with agriculture. There are in addition some other issues related to public health (xenobiotics, antimicrobial resistances), the environment and animal welfare.

The general observation is that these threats are appearing more and more frequently and that they are more and more complicated to be tackled.

This complexity of disease emergencies or re-emergencies calls for the identification of often collaborative effective strategies, based on both science and proven practical experience, to reduce future threats. The H_5N_1 avian influenza crisis has shown how crucial and challenging it is to address global threats at the interface between humans, animals and ecosystems. The lessons learnt indicate that it requires (i) to strengthen animal and human health institutions and (ii) build strong partnerships among players who may have different perspectives on some issues and different levels of resources.

When speaking about strengthening animal health systems and institution, the OIE is the intergovernmental organisation responsible for improving animal health and welfare worldwide regardless of the cultural practices or the economic situations in its member countries. The need to fight animal diseases at a global level led to its creation through an international agreement signed on 25 January 1924. In May 2003, the office became the World Organisation for Animal Health but kept its historical acronym OIE. It is recognised as a reference organisation by the World Trade Organization (WTO) and in 2011 had a total of 178 member countries. The OIE maintains permanent relations with 45 other international and regional organisations and has regional and sub-regional offices on every continent. To address the gaps in the animal health sector, OIE seeks to build member countries' capacities in policy design and good governance in animal health systems and veterinary services. Simultaneously, OIE promotes strong partnerships, notably with FAO and WHO, especially with regard to emerging issues and two topics that are getting currently a great attention and that require a strong multi-sectoral collaboration at all levels because of their social, economical and ecological determinants: rabies and food-and-mouth disease (FMD) (http://www.oie.int/about-us/).

16.2 Southeast Asia: A Hotbed for the Emergence and Endemisation of Infectious Diseases

In Southeast Asia, the geographical position, the current socio-economic situation and the sociocultural practices all facilitate the occurrence, spread and maintenance of diseases at the human–animal–ecosystems interface. Indeed, the warm and humid climate, as well as richness in wildlife host species, favours the spillover of zoonotic pathogens from wildlife to humans and domestic animals and the transmission of vector-borne pathogens (Jones et al. 2008). Some prevailing sociocultural practices, such as an increasing encroachment of human activities in the forests or the close contact between human and livestock populations, especially in poor and marginalised populations, provide excellent conditions for the frequent exchange of pathogens between animal and human populations. Furthermore, the high human and animal density and the globalisation of trade facilitate the spread of the diseases. Finally, a weakness of medical and veterinarian institutional capacity and a lack of food security and safety are aggravating factors for the endemisation of the diseases (Bhatia and Narain 2010).

Most of the animal diseases, including zoonoses, commonly described in Southeast Asia can be classified as emerging or re-emerging diseases, meaning that they have appeared in a population for the first time or that may have existed previously but are rapidly increasing in incidence or geographic range (http://www.who.int/topics/emerging_diseases/en/). Furthermore, even if Southeast Asia is not among the main hotspots of recent emerging infectious disease events, the region is considered at high risk for the future emergence of zoonotic pathogens from wildlife and vector-borne pathogens (Jones et al. 2008). However, even though they actually did not emerge there, the most recent emerging zoonoses have developed themselves and sometimes geographically been embedded into Southeast Asia – severe respiratory acute syndrome (SARS) virus, Nipah virus (NiV) and highly pathogenic avian influenza (HPAI) virus. The occurrence and spread of zoonoses in Southeast Asia can be explained by the coexistence of different factors that facilitate the interspecies transmission, maintenance and dissemination of pathogens. One of the major reasons is the increased contact between humans, domestic animals and wildlife, due to the exceptionally high growth rate of the human and livestock population, the expansion and intensification of agriculture and human encroachment on game reserves (Cáceres and Otte 2009). The changing lifestyles associated with the globalisation of commerce and trades allow rapid propagation of pathogens. Additionally, in most of the countries in Southeast Asia, neither the health nor veterinary services have sufficient capacity and resources to detect emerging pathogens early and to contain infections in animals (Bhatia and Narain 2010).

It is then interesting to describe the actions that governments take, under the leadership of the international community, to anticipate and limit the impact of animal diseases. How to mobilise outside times of crisis, when it is often too late?

16.3 The One Health Concept

With regard to these existing or emerging threatening diseases at the human–animal–ecosystems interface, there is now an international consensus around the 'One Health' approach that supports and legitimates the need for cooperation between animal, public and environmental health institutions to defeat diseases that threaten both animal and human health (Leboeuf 2011). This collaboration should not be limited to only the international level, but shall be translated as a new and fundamental paradigm at national levels.

While the FAO, OIE and WHO have long-standing experience in direct collaboration, together they have realised that managing and responding to risks related to existing and emerging threats at the human–animal–ecosystems interface is complex and requires a cross-sectoral and multidisciplinary approach. In 2010, they drafted a document, which set out a joint strategy and proposed a long-term basis for coordinating global activities to address health risks at the human–animal–ecosystems interface (FAO et al. 2010). They agreed that the implementation of an efficient multidisciplinary approach requires that (i) both human and animal health systems need to further strengthen their own capacities in the public and private sector and (ii) strong partnerships among players who may have different perspectives on some issues and different levels of resources have to be built. The Tripartite Concept Note provides a background and establishes a strategic alignment and some collaborations and joint actions, as well as the way forward that partners may consider when conducting One Health activities. At the regional level in Southeast Asia, one of the first such efforts was the Regional Workshop on Collaboration Between Human and Animal Health Sectors on Zoonoses Prevention and Control convened in December 2010 in Sapporo, Japan, and co-organised by the FAO, OIE and WHO. The meeting produced several recommendations to strengthen this collaboration. Member countries were called on to establish a functional coordination mechanism between their animal and human health sectors by 2011. The recommendations also called on the FAO, OIE and WHO to continue their collaboration with each other, countries and regional organisations (i.e. ASEAN, SAARC) to strengthen the coordination mechanism (FAO et al. 2010).

Even though a functional coordination mechanism is not always established yet, the way in which public health programmes are designated and funded has changed significantly since the H_5N_1 crisis. Pandemic prevention is now mainly addressed as a development issue, typically funded through emergency response avenues, and consequently, trends in health spending have moved from broad system-based investments to a more specialised, infectious disease model. As a result, basic health infrastructure commitment is estimated to have declined from 11 % to 5 % between 1990 and 2008, although it was found that poor health infrastructure is the main driving factor for outbreaks (Bogich et al. 2012). In this regard, the implementation of global programmes specifically targeting pandemic infectious disease threats through development is sometimes questioned.

The complexity of disease emergencies in a globalised world calls for the identification of effective strategies, based on both science and proven practical experience, to reduce future threats. And, once more, the H_5N_1 avian influenza crisis has shown how a concrete, transparent and consistent approach, based on efficient animal and human health infrastructures, high-quality scientific advice and practical experience, is vital for the management of these threats and for political credibility, both at the national and international level (http://www.oie.int/for-the-media/onehealth/oie-approach/).

In our modern interconnected world, international organisations play an active role in reducing global diseases threats. The concept of public sector governance, in which the state acquires and exercises the authority to provide and manage public goods and services, is an essential element of the One Health approach (Landford and Nunn 2012). Promoting a collaborative 'One Health' approach at national levels will result in a deeper and sustainable political support for the coordinated prevention of high public health and animal impact diseases at the human–animal–ecosystems interface (http://www.oie.int/for-the-media/onehealth/).

However, in this framework, what is the strategy of OIE to further strengthen the governance of the animal health systems and to support effective inter-sectoral collaboration?

16.4 The OIE Strategy

OIE advocates that improving the governance of animal health systems, in both the public and private sector, is the most effective way to safeguard global animal health and human health when diseases occur at the human–animal–ecosystems interface. Therefore, it provides science-based guidance needed by its members to strengthen their veterinary services to detect, prevent and manage serious animal disease outbreaks and efficient tools to enhance their credibility, both at the national and international level. Furthermore, OIE strongly supports activities to expand the scientific basis for effective inter-sectoral collaboration and to identify ways to operationalise One Health in policy and practice. It participates in inter-sectoral networking and technical activities and sponsors and contributes to inter-sectoral conferences, workshops and consultations that are usually co-organised by human and animal health partner agencies (http://www.oie.int/for-the-media/onehealth/oie-involvement/).

16.4.1 The OIE Approach to Strengthen the Veterinary Services

Among the different specific missions included in its mandate, the OIE prepares and adopts relevant standards for animal health and welfare and proposed support programmes to help OIE members to better implement these international standards.

Indeed, in the current trend of globalisation, animal health measures have increasing importance to facilitate safe international trade of animals and animal products while avoiding unnecessary impediments to trade. In light of this, the Agreement on the Application of Sanitary and Phytosanitary Measures (SPS Agreement) encourages the members of the WTO to base their sanitary measures on international standards, guidelines and recommendations, where they exist. The OIE publishes two codes (Terrestrial and Aquatic) and two manuals (Terrestrial and Aquatic) as the principle reference for WTO members (http://www.oie.int/international-standard-setting/overview/): using the Terrestrial Animal Health Code and Aquatic Animal Health Code as a basis is the recognised way to ensure the sanitary safety of international trade in, respectively, terrestrial animals and aquatic animals and their products.

The Terrestrial Code and the Aquatic Code set out standards for the improvement of animal health and welfare and veterinary public health worldwide, including through standards for safe national production and consumption and for safe international trade in animals and their products. All the OIE members have committed that their veterinary authorities shall use the health measures in the Code when importing or exporting animals and their products. The objective is to provide for early detection, reporting and control of agents pathogenic to animals or humans and to prevent their transfer via international trade in animals and animal products, while avoiding unjustified sanitary barriers to trade. To help ensure the effective performance of the Veterinary Services of Member Countries, the OIE has dedicated two chapters (3.1 and 3.2) of the Terrestrial Code to the Quality of Veterinary Services. The development of these standards and recommendations results from the ongoing work of the OIE's Specialist Commissions, which comprise elected members and observers. Upon the expertise of internationally renowned specialists, they prepare draft texts for new chapters of codes or revise existing chapters in light of advances in veterinary knowledge (http://www.oie.int/international-standard-setting/terrestrial-code/; http://www.oie.int/international-standard-setting/aquatic-code/).

The Manual of Diagnostic Tests and Vaccines for Terrestrial Animals and the Manual of Diagnostic Tests for Aquatic Animals provide a harmonised approach to disease diagnosis by describing internationally agreed laboratory diagnostic techniques. The principal target readership is laboratories carrying out veterinary diagnostic tests and surveillance, plus vaccine manufacturers and regulatory authorities in member countries. The objective is to provide internationally agreed diagnostic laboratory methods and requirements for the production and control of vaccines and other biological products. The commissions in charge of these manuals update them regularly as new scientific information is released (http://www.oie.int/international-standard-setting/terrestrial-manual/; http://www.oie.int/international-standard-setting/aquatic-manual/).

The Codes and Manuals are published only once all chapters have been provided for comments to members and fully approved by the World Assembly of Delegates: the views of the National Delegates of OIE members are systematically sought through the circulation of draft and revised texts, and the health measures finally published have been formally adopted by the World Assembly of the Delegates of the OIE members.

To help members to better implement these standards and to improve the governance of veterinary services, the OIE has developed cornerstone support activities, among which the PVS (Performance of Veterinary Services) Pathway specifically focuses on the sustainable improvement of a country's veterinary services, through a global approach and in accordance with their own specific context. A specific methodology has been developed and approved by the members, and the OIE has published the 'OIE Tool for the Evaluation of Performance of Veterinary Services' (the OIE PVS Tool) as the basis for evaluating performance against the international standards published in the Terrestrial Code. A similar tool is available for the evaluation of Aquatic Animal Health Services. The PVS Pathway starts with a PVS evaluation mission which consists of a qualitative assessment of the performance and the compliance of a country's VS (veterinary services) in accordance with the OIE standards on the quality of VS. A PVS Gap Analysis mission follows which facilitates the definition of a country's objectives in terms of compliance with OIE quality standards, suitably adapted to national constraints and priorities. This analysis provides an outline of the corresponding financial action plan, which can be used to legitimate requests for funding from the government or donors. Based on the gaps the country has defined, some activities or projects and programmes are proposed and implemented in the field of the veterinary legislation, public/private partnerships, veterinary education or laboratories. Finally, follow-up missions provide a way of measuring the progress that countries have made in sustainably improving their compliance with the OIE quality standards. Only OIE-certified PVS experts can carry out independent external PVS evaluations of country's Veterinary Services and PVS Gap Analysis. They have undergone training sessions organised by the OIE and funded by donors to the OIE World Fund. All experts use standard tools, indicators and experts' manuals, prepared and published by the OIE Headquarters, which also include template reports (http://www.oie.int/support-to-oie-members/pvs-pathway/).

Although there is still no specific tool officially recognised by WHO and OIE member countries, some PVS 'One Health' missions are currently carried out, using the OIE PVS Tool as a framework in that field.

The first PVS mission was carried out in 2006 in Vietnam, and since then, more than 120 countries in the world have requested OIE to benefit from this programme. Up to now, all the members countries from Southeast Asia, except Malaysia and Singapore, have initiated the PVS Pathway, with different degrees of progress. Many countries, including Vietnam in Southeast Asia, have decided to give a public and free access to their report online. Some main trends arose from the different PVS evaluations worldwide, Southeast Asia not being much different from the average.

All countries have realised the importance of strengthening their veterinary services and are politically committed to improve the situation when needed. First of all, the training and the management of the veterinarians and animal health workers are recognised as the main challenges to ensure a good governance. The initial veterinary education, of varying quality in the area, needs to be strengthened. In some countries, such as Cambodia or Laos, where there were up to now no veterinary schools and where the remaining active vets will retire in the coming years, this need is particularly strong. On the governance side, the efficacy of the chain of command from the central administration to the field is essential to react quickly when an issue arises. Some countries, such as Vietnam and Indonesia, have experienced successive episodes of decentralisation that are often believed to have undermined this process. In addition, the level of remuneration of the staff in charge of the controls, including those at the borders, is sometimes insufficient to prevent them from the temptation of seeking additional revenues for instance through getting a second job or even granting favours. And, along the same line, when financial compensation is lacking or inadequate, farmers hesitate to report diseases for which the total or partial culling of the herd is required.

Following this diagnosis, OIE helps countries in identifying the appropriate prescription, depending on the country's priorities and context. The Philippines and Vietnam, the two pilot countries for the implementation of the PVS Pathway, where the Veterinary Services entered a strong momentum, particularly in terms of public/private partnerships, have developed comprehensive strategic plans for 5 years, which are currently under study for approval at ministerial level. The future will tell, including the forthcoming diagnosis, planned 3–5 years after the first, if the approach is bearing fruit.

16.4.2 The OIE Approach to Enhance the Inter-sectoral Collaboration

OIE strongly supports activities to advance One Health and participates in various inter-sectoral networking and technical activities. Some of the cornerstone activities in this field are presented below.

OFFLU is the OIE-FAO global network of expertise on animal influenza, working to reduce the negative impacts of animal influenza viruses by promoting effective collaboration between animal experts and with the human health sector (http://offlu.net/). Within this network, the animal health community is in charge of providing early recognition and characterisation of emerging influenza viral strains in animal populations and effective management of known infections. This leads to better managing the risk to human health and promoting global food security, animal health and welfare and other community benefits derived from domestic animals and wildlife. The functioning of the network is based on the following activities: (i) exchange of scientific data and biological materials (including virus strains) within the network, to analyse such data and to share such information with the wider scientific community; (ii) offer of technical advice, training and veterinary expertise to member countries to assist in the prevention, diagnosis, surveillance and control of animal influenza; (iii) collaboration with the WHO influenza network on issues relating to the animal–human interface, including early preparation of human vaccine; and (iv) identification of the influenza research needs.

To strengthen laboratory capacity and networking activities in that field, OIE is involved in existing institutional frameworks, mechanisms and networks with partners, particularly with FAO and the WHO. Together, the three international organisations have initiated a number of collaborative projects to help strengthen laboratory capacity and networking. One current FAO/OIE/WHO project, the IDENTIFY project of the USAID-funded Emerging Pandemic Threats Programme, focuses on enhancing the capacity of veterinary laboratories to detect emerging pathogens by improving the ability to accurately and rapidly diagnose animal disease known to occur in a given region or country (http://www.oie.int/for-the-media/onehealth/oie-involvement/identify/). There again, Southeast Asia has been identified as an important area of work.

Within the tripartite partnership with FAO and WHO, OIE is involved in the Global Early Warning System (GLEWS) addressing health threats and emerging risks at the human–animal–ecosystems interface, which is a mechanism to share information on health threats beyond avian influenza. It is recognised that information from the human and animal health sectors, as well as from other relevant sectors such as food, wildlife, land use and agriculture, is most efficiently and appropriately collected by each sector according to its mandate – human and animal health sectors have already established mechanisms to collect data from the field. Once done, it is crucial that the information does not remain within that sector and is shared with other stakeholders (Munford, PMAC p 73). GLEWS allows to combine and coordinate the alert and disease intelligence mechanisms of OIE and FAO and to assist in prediction, prevention and control of animal disease threats, including zoonoses, through sharing of information (http://www.glews.net/).

16.4.3 The OIE Strategy in Southeast Asia Through Two Case Studies

At regional level and in full collaboration with ASEAN and other partners, the OIE Sub-Regional Representation for Southeast Asia plays a significant role in regional coordination of animal health and emerging infectious disease management in a region that is often considered as a ‘hotspot’ for emergence. Along the strategic objectives of the OIE Fifth Strategic Plan, the implementation of its activities to achieve the OIE Strategic Objectives is supported by various programmes and projects funded by donors.

The choice of these two examples has been motivated by the fact that these diseases are key transboundary diseases in Southeast Asia and have major impact in terms of animal and public health in the region. The approach taken is not only considering the disease itself in isolation but also the whole system and its actors. It is thus expected that this approach will improve this two-disease situation as well as the capacities of both human and animal sectors to combat any kind of diseases, including by joining their efforts in collaboration when needed. These following case studies show how cooperative approaches are important between veterinary services, human health services and other relevant government services at the interface between domestic and wild animals, ecosystems and human populations.

16.4.3.1 Foot-and-Mouth Disease (FMD)

Foot-and-mouth disease (FMD) is a severe, highly contagious viral disease of livestock with significant economic impact. The disease is still widespread throughout the world, particularly in Asia, Africa and the Middle East. By the end of May 2012, at the time of the second Global Conference on the topic in Bangkok, more than 100 countries were not FMD-free which means that, beyond the impact of the disease in their territories, they remain a continuous threat to free countries. In developed countries, FMD has catastrophic consequences when declared. It can indeed severely affect and disrupt regional and international trade in animals and animal products causing enormous financial damage. The 2001 outbreak in the UK is estimated to have cost no less than ten billions euros. Australia estimates that an incursion of FMD that would not be immediately controlled would cost 3 % of its annual GDP. In addition, massive culling during outbreaks has created animal welfare and ethical concerns not only in the animal production sector, but in society as a whole. In developing countries, where the adverse effects of FMD are often underestimated, the disease undermines food security and economic development, at the level of both village smallholders and the more organised production chains.

Of the domesticated species, cattle, pigs, sheep, goats and water buffalo are susceptible to FMD. Many species of cloven-hoofed wildlife may become infected, such as deer, antelope, elephant, giraffe and some other species as well. Even though it has not been demonstrated for any other wild species, the African buffalo can serve as a source of FMD infection for domestic animals in Sub-Saharan Africa. Thus, FMD is typically the kind of disease arising at the human–animal–ecosystems interface which is not a zoonotic disease (http://www.oie.int/en/international-standard-setting/terrestrial-manual/access-online/).

FMD epidemiology is complex and this has important implications as it allows to learn many lessons that can be used to strengthen the systems as a whole and that can be reused for many other diseases. The agent which causes FMD is an aphthovirus of the family Picornaviridae. There are seven strains (A, O, C, SAT1, SAT2, SAT3 and Asia1) each one requiring a specific vaccine strain to provide immunity to a vaccinated animal. FMD is characterised by fever and blister-like sores on the tongue and lips, in the mouth, on the teats and between the hooves that can be the symptoms of numerous other diseases. The disease is not a killing disease and mainly causes severe production losses that are easy to be visualised by the owner when it affects dairy production but that are more difficult to assess and to quantify at the first glance when talking about meat cattle production. While the majority of affected animals recover, the disease often leaves them weakened and debilitated. In a susceptible population, morbidity approaches 100 %. Intensively reared animals are more susceptible to the disease than traditional breeds. If the disease is rarely fatal in adult animals, there is however often high mortality in young animals due to myocarditis or by lack of milk when the dam is infected by the disease (http://www.srr-seasia-oie.com/disease-info/foot-and-mouth-disease/).

FMD is, with rinderpest, one of the first severe diseases that has been listed (Chap. 1.2, Article 1.2.3) in the OIE Terrestrial Animal Health Code at the creation of the organisation in 1924. Rinderpest has been declared eradicated from the world in 2011 and the international community is now focusing on FMD. Technically, OIE members are committed by the OIE Terrestrial Animal Health Code, 2009, (Chap. 1.2, Article 1.2.3) to report to the OIE (Chap. 1.1 – Notification of Diseases and Epidemiological Information). FMD is the first disease for which the OIE established an official list of free countries and zones with or without vaccination.

Furthermore, there is a chapter dedicated to FMD in the Terrestrial Code which aims at mitigating the risk of infection and spread of the disease. The chapter provides detailed guidance for the surveillance strategy of the disease (http://www.oie.int/index.php?id=169&L=0&htmfile=chapitre_1.8.5.htm).

The recent epidemiological situation, with the incursion of FMD virus into free (Japan, Korea and Bulgaria) and infected countries (SAT2 in Egypt and Libya), shows that countries remain under threat and must be fully prepared for the emergence or re-emergence of FMD. Trade globalisation has without any doubt increased the risk of spread. It is now assumed that the control of FMD cannot be sustained if good governance of animal health systems, including effective Veterinary Services complying with OIE standards and updated legislation, is not in place and supported by appropriate public/private partnerships (FAO/OIE Global conference on FMD, June 2012, BKK).

In June 2009, OIE and FAO decided to establish an FMD working group under the Global Framework for the progressive control of Transboundary Animal Diseases (GF-TADs) and to prepare a Global FMD Control Strategy, based on the consultation of experts and representatives of national, regional and international institutions. The Global FMD Control Strategy was discussed and published in 2012 and is a combination of three related components, namely, the control of FMD, strengthening the Veterinary Services, and the prevention and control of other major diseases of livestock. The overall aim of the strategy is to reduce the global impact of the disease and to be used as an entry point to achieve sustainable progress in the performance of Veterinary Services and, in turn, improve the animal health status concerning other livestock diseases.

In Southeast Asia, one of the OIE long-standing flagship regional programmes is the Southeast Asia and China Foot-and-Mouth Disease (SEACFMD) Campaign, which aims at controlling FMD by 2020 through vaccination and promotes socio-economical and participatory approaches as well as assessment of the role of wildlife. Australia, through AusAID, and the European Union (via the vaccine bank) are the main funders of such activities. France, the Asian Development Bank, FAO and some other NGOs are also involved. These activities are complying with the recommendations of the Paris Declaration on Aid Effectiveness (www.oecd.org/dataoecd/53/38/34579826.pdf). To summarise, the OIESRR coordinates animal disease control activities between countries and provides technical advice to ensure coherent strategies. Furthermore, it seeks political and financial support to achieve FMD freedom in the region. It was made up of eight members until 2009, namely, Cambodia, Indonesia, Lao PDR, Malaysia, Myanmar, the Philippines, Thailand and Vietnam, and was referred to as the Southeast Asia Foot-and-Mouth Disease (SEAFMD) Campaign. In 2010, in the light of the overall benefits of SEAFMD, Brunei Darussalam, the People's Republic of China (PRC) and Singapore became members of the programme, thereby extending considerably its geographic range. Consequently, SEAFMD has been renamed the Southeast Asia and China FMD (SEACFMD) Campaign (http://www.srr-seasia-oie.com/programs/seacfmd/). Its boundaries are now nearly completely matching the epidemiological entity of cattle trade in the region which is the main driver for the spread of the disease.

The achievements – in terms of political support, awareness, public/private collaboration, knowledge of animal movements and the selling prices, identification of viral types, etc. – are so far satisfying. Now that the current situation is well known, there is a call for the implementation by all the countries of Southeast Asia of activities at larger scale. The strategy is notably to conduct targeted actions, such as specific vaccination campaigns, far less expensive than that of mass vaccination campaigns.

The 18th Meeting of the OIE FMD Sub-Commission for Southeast Asia and China that can be considered a turning point of the campaign was held in Lijiang, Yunnan, China, from 5 to 9 March 2012. One of the key focus points in the sessions was the various, newly introduced FMD control strategies in China, Vietnam, Laos and Malaysia, all of which advanced the implementation of the SEACFMD Campaign in accordance with the SEACFMD 2020 Roadmap.

Currently available opportunities for the region and the mechanisms as to how these can be accessed were also highlighted during the presentations regarding the now operational FMD vaccine bank (and the soon to be operational rabies vaccine bank), as well as the Small Grants Facility (SGF) under the AusAID-funded STANDZ Initiative that allows to implement small ad hoc projects with great flexibility. Country members have now a full set of tools for achieving the vision of an FMD-free region by 2020.

With regard to presence of efficient vaccines and experience of successful programmes for the eradication of the disease in Southeast Asia, socio-economic factors should play a major role in the maintenance of the disease in Southeast Asia. Willingness to tackle the disease is so far not obvious, especially in countries with the most limited resources that are Cambodia, Laos and Myanmar, even though it is assumed that they would substantially benefit from the control of the disease. Dairy farmers, that are few in the area, may be motivated by the direct losses that are clearly visible, it is less obvious for the other farmers aspiring to produce meat or using animals for work. Several factors may motivate this lack of commitment in tackling the disease: the global low impact of the disease on household economy and the lack of perception of the real economic impact by the farmers. More research work to assess the real impact and perception of FMD at these smallholders' level should be undertaken, to gain knowledge about the socio-economic drivers of the disease.

In collaboration with FAO through the GF-TADS, OIE recommends to enhance the analysis of the socio-economic drivers of the disease, such as livelihood, livestock sector strategies and value chain factors, that can guide FMD control programmes to be more successful (Global Conference). In Southeast Asia, the importance of central Burma as a potential source of FMD for the rest of the region has constantly been highlighted as an important number of animals are traded from Myanmar to the rest of Southeast Asia. Controlling FMD in central Burma would require a significant investment to better quantify the incentives as well as the benefits and costs of controlling FMD in this area, beyond the few existing studies identifying FMD risk factors, animal movement patterns and some initial cost–benefit analyses of controlling FMD at the individual farmer level.

Combating diseases of livestock such as FMD in developing countries can contribute significantly to poverty alleviation by generating employment, providing funds for education and training, improving opportunities for trade in livestock and animal products and supplying raw materials to industry.

The outcomes and severity of infectious diseases are the result of complex relationships between the infectious agent, animal husbandry systems, human behaviour and the environment, and disease management can only be effective if these elements are simultaneously taken into consideration in a holistic approach. The 'One Health' strategy offers the necessary conceptual framework, in terms of a multidisciplinary and multi-sectoral approach, and it is appropriate to address zoonoses as well as livestock diseases such as foot-and-mouth disease (FMD) that can have severe impacts on people's livelihood. A special session was held during the 18th SEACFMD Campaign on capacity building and One Health which recognised the importance and the imperious necessity of more and better cooperation between human, animal and environmental health and, in particular, the need to involve more the medical profession, including academia in One Health cross-sectoral collaborations, including joint professional and technical trainings. The opposition to the creation of a specific global or regional institution for the governance of the One Health movement was also reaffirmed (http://www.srr-seasia-oie.com/programmes/seacfmd/activities-report/18th-meeting-of-the-oie-seacfmd-sub-commission/).

16.4.3.2 Rabies

Rabies is a zoonotic disease that is caused by neurotropic viruses of the genus *Lyssavirus* and is transmissible to all mammals. The virus is spread through close contact with infected saliva via bites or scratches. Rabies is present on all continents except the Antarctic and is a neglected zoonosis, while often endemic in countries with poor infrastructure and limited resources for combating disease. Between 50,000 and 100,000 human cases occur each year, mainly in Africa and Asia (OIE Terrestrial Manual, Landford and Nunn). Even though dog bites are responsible for 99 % of cases of rabies virus transmission to humans, bats – including vampire bats – and foxes can act as reservoirs and vectors of the disease, posing a very real threat to animal and public health. The victims, mainly children, die after a period of dreadful suffering. Most of the deaths occur in the absence of postexposure treatment (PET). Rabies is nearly always fatal when left untreated (http://www.who.int/rabies/en/).

Chapter 8.10 of the Terrestrial Animal Code is dedicated to rabies infection and aims at mitigating the risk of rabies to human and animal health and to prevent the international spread of the disease (http://www.oie.int/index.php?id=169&L=0&htmfile=chapitre_1.8.10.htm).

Despite the availability of technology to control rabies in domestic animals, as well as in wildlife, and of technical and institutional know-how gained from successful control programmes, rabies remains a huge public health threat in many areas including Southeast Asia, because of a lack of motivation by governments and the consequent inadequate funding. Many agriculture ministries neglect to seriously implement rabies control in dogs for a number of reasons, including the fact that there is less economic incentive to control rabies in dogs than to fund other disease-control programmes in livestock. Furthermore, despite data and studies underlining the real need to focus on controlling rabies in dog populations to eradicate the disease in humans, many health ministries allocate funds only for human rabies vaccine (Wilde et al. 2013). As a result, the veterinary services are faced with uphill struggle to convince governments in investing resources to control rabies in dogs.

A lack of accurate data on the burden of rabies contributes to the fact that the disease remains a low priority for the global public health community. In Southeast Asia, where data is sparse or cannot be reliably validated, knowledge gaps in key parameters, such as exposure incidence, probability of bite victims receiving PET, and prevalence of rabies in animal population (Hampson 2011). Furthermore, deficient data about the economic impact, both on livestock/working animals and tourism/recreation, is a major constraint to assessing the global burden of the disease.

Beyond the direct impact on local economies when livestock and working animals die due to rabies or infect humans, the need to pay for transport and expensive post-exposure treatment can lead to the unplanned sale of production animals and livelihood assets and further impacts food and economic security (De Balogh 2011). More recently, rabies has also become a concern for the tourism industry with travel advisories issued in countries experiencing a reintroduction of rabies or ongoing endemic disease (Cleaveland et al. Seoul).

The recent case that occurred in Thailand in February 2010 shows two other components that contribute to the unsuccessful control of the disease, both in dogs and humans. The owner of a pet shop, a public health official, was bitten by one of her dogs, a 3-year-old Rottweiler in December 2009. The woman developed rabies symptoms and died in February 2010. The dog later died, followed by another eight pets at the victim's house. She was vaccinating the dogs by herself. This case underlines that there are a circulation of fake vaccines in the region and a lack of awareness of the population about the epidemiology of the disease, even for people working in the field of public health (http://www.promedmail.org/mbds, archive number: 20100225.0623).

The example of rabies highlights both the necessity and the difficulties of implementing an efficient multi-sectoral collaboration to tackle a zoonotic disease at the animal source. Rabies control involves multiple agencies, including those responsible for human and animal (domestic and wild) health, and requires coordinated management across these sectors. An improved exchange of information between sectors is needed for better patient information, planning of personal protective equipment and monitoring the success of dog vaccination campaigns. According to Dr. Bernard Vallat, OIE director general, success in eradicating rabies relies on the close collaboration between public health and veterinary services in designing the control programmes. Good veterinary governance is crucial to applying successfully the technologies and tools available for rabies control but, most importantly, veterinary services have to establish collaboration between different sectors, beyond public health services. The OIE is so committed to supporting the efforts of the international community to achieve worldwide eradication of rabies (Seoul, Sept 2011).

In this context, the OIE SRR for Southeast Asia is recommending to develop a multi-sectoral strategy to control rabies in Southeast Asia that would focus in getting resources from governments, international organisations and other partners to support rabies control in the region. OIE has been campaigning to all governments and international agencies to provide veterinary services worldwide with resources to control rabies in animals. Part of this campaign is to highlight the importance of canine rabies during international meetings and workshops, to tackle not only technical challenges in controlling rabies but also in gaining political support. The SRR has closely worked with ASEAN in getting political commitment from member states to control rabies. Using the recommendations from the OIE Rabies Conference for Eurasia in 2007, the OIE Bangkok worked with the ASEAN through the ASEAN+3 EID project funded by AusAID, in coming up with a policy statement to support rabies control in ASEAN plus three countries. This statement dubbed as 'Call for Action towards the Elimination of Rabies in the ASEAN Member States and Plus Three Countries' was finally endorsed both by the ASEAN Health and

Agriculture Ministers in 2008 and 2009, respectively. It provides recommendations at the national level in terms of policies and legislation, prevention, control, surveillance, partnership, public awareness and communication and at the regional level in terms of prevention, control, information sharing, capacity building, coordination, training and research (www.aseanplus3-eid.info/dl.php?…Rabies_Call_f…). This document will be a useful tool for veterinary services to lobby their governments for support. The OIE, through its SEACFMD Campaign, has a long experience in coordinating regional control of transboundary animal diseases. The SEACFMD 2020 Roadmap could also be used in developing a multi-sectoral rabies control strategy in Southeast Asia. Support from FAO, WHO and other partners is crucial in the development of this strategy.

Furthermore, the OIE is currently managing a rabies vaccine bank in Asia with the financial support of the European Union, under the framework of the regional cooperation programme on Highly Pathogenic and Emerging and Re-emerging Diseases in Asia (HPED). This first regional rabies vaccine bank was launched in early 2012 and could serve as a model for developing other rabies vaccine banks in other regions of the world. The bank delivers vaccines to eligible countries (according to donor requirements) at the request of member countries, allowing effective public/private partnerships between international organisations, national authorities, local authorities, NGOs and private companies to be established. The guidelines for the use of the vaccine bank approved by the eligible countries specify that the applicant country must, in particular, (i) prove that there is an increase in bite rates and human mortality, that the location of the outbreak(s) increases the risk of rabies spreading to people and/or animals and that further spread of the disease may occur, (ii) provide a statement explaining that the National Veterinary Services are engaged and will have the authority to implement or supervise the vaccination of dogs, (iii) submit a specific vaccination control strategy, (iv) specify the nature and quantities of vaccines required, and (v) agree to international transportation conditions. Coinciding with World Rabies Day in 2012, the OIE donated 50,000 injectable rabies vaccines to Lao PDR through the regional rabies vaccine bank (see map). Following this first donation, other countries have requested the OIE for vaccine deliveries. Among them are countries in which GARC (Global Alliance for Rabies Control) has projects, like the Philippines. Other deliveries are under preparation in other Southeast Asian countries (http://www.rabiescontrol.net/news/news-archive/oie-support-to-rabies-endemic-countries-a-vaccine-bank-in-asia.html).

16.5 Conclusion

An integrated collaborative approach to investigating and managing infectious diseases has gained popularity. It is now commonly acknowledged that the integration of the veterinary, medical and environmental sciences necessary to predict, prevent or respond to emerging or re-emerging animal diseases requires effective collaboration and exchange of knowledge across these disciplines. The international organisations regularly reaffirm their opposition to the creation of a specific global or regional institution for the governance of the One Health movement and promote instead that both human and animal health systems strengthen their own capacities and develop strong multi-sectoral partnerships.

If there is now an international consensus around the One Health approach and a call by an international organisation in charge of public and animal health for collaborative initiatives to combat diseases, the multi-sectoral approach is mainly promoted among health disciplines. It is now necessary to improve this integrated collaborative approach with the inclusion of human and social sciences, to take into account the social drivers for emergence, maintenance and spread of diseases. But, there is a dearth of information on the strategies to put interdisciplinarity collaboration into practice and no evidence of its effectiveness. A study carried out by Anholt et al. (2012) shows that the essential components of an ID approach that could support initiatives like the One Health movement were mainly the professional social networks that provide connections across disciplines and the need of trust and respect among disciplines. Education and experiential learning opportunities remain so the best tools to develop interdisciplinarity this time.

References

Anholt RM, Stephen C, Copes R (2012) Strategies for collaboration in the interdisciplinary field of emerging zoonotic diseases. Zoonoses Public Health 59(4):229–240

Bhatia R, Narain JP (2010) Review paper: the challenge of emerging zoonoses in Asia Pacific. Asia Pac J Public Health 22(4):388–394

Bogich TL, Chunara R, Scales D, Chan E, Pinheiro LC, Chmura AA, Carroll D, Daszak P, Brownstein JS (2012) Preventing pandemics via international development: a systems approach. PLoS Med 9(12):e1001354

Cáceres SB, Otte MJ (2009) Blame apportioning and the emergence of zoonoses over the last 25 years. Transbound Emerg Dis 56(9–10):375–379

De Balogh K (2011) Impact of animal rabies on local economy Part I : on livestock and working animals. Paper presented at the OIE global conference on rabies control, Incheon-Seoul

FAO, OIE, WHO (2010) Collaboration sharing responsibilities and coordinating global activities to address health risks at the animal-human-ecosystems interfaces. Retrieved October 3, 2014, from http://www.oie.int/en/for-the-media/press-releases/detail/article/fao-oie-who-collaboration-concept-note-on-health-risks-at-the-human-animal-interface

Hampson K (2011) Reassessment of the socio-economic global burden of rabies: human and animal cost of global rabies. Paper presented at the OIE global conference on rabies control, Incheon-Seoul

Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, Daszak P (2008) Global trends in emerging infectious diseases. Nature 451(7181):990–993

Landford J, Nunn M (2012) Good governance in ‘one health’ approaches. Revue scientifique et technique (Int Off Epizoot) 31(2):561–575

Leboeuf A (2011) Making sense of one health: cooperating at the human-animal-ecosystem health interface. Health and environment reports, n 7. Retrieved October 3, 2014, from www.ifri.org/downloads/ifrihereport7alineleboeuf.pdf

Wilde H, Wacharapluesadee S, Saraya A, Lumlertdacha B, Hemachudha T (2013) Human rabies prevention (comment from a canine-rabies-endemic region). J Travel Med 20(3):139–142

Part VI
Developing Strategies

Chapter 17
Business for Biodiversity and Ecosystem Services

Valérie Boisvert, Hélène Tordjman, and Frédéric Thomas

Abstract Since the end of the 1980s, conservation policies have focused on the search for market solutions to environmental problems. Several attempts have been made over years to turn various parts or facets of nature into economic assets, from genetic resources through ecosystem services. Similarly, several types of institutional arrangements have been in turn presented as markets. The relative failure of these tentative market policies has just led to shifts from one aspect or component of biodiversity to others and to the adoption of new 'business models' as previous arrangements proved ineffective. The latest product of this speculation surrounding nature is attached to ecosystem services that have become an inclusive framework encompassing most environmental issues (climate change, desertification, soil erosion, water, biodiversity, etc.). The concept of ecosystem services has begun spreading after the release of the Millennium Ecosystem Assessment by the mid 2000s. This notion was formed at the interface of science and policy and is grounded neither in ecological nor in economic theories. Setting back ecosystem services in the history of environmental and ecological economics enables to restore the cognitive background from which this notion emerged and to explain both its hegemony and its impacts. Indeed, in line with green economy, it conveys a vision of nature as exempt from any conflict and danger and is quite positive about the feasibility of a harmonious combination of human activities and environmental protection, sustained by market development. It does not provide an adequate framework to deal with vulnerability and risk.

V. Boisvert (✉)
Institute of Geography and Sustainability, Faculty of Geosciences and the Environment,
University of Lausanne, 1015 Lausanne, Switzerland
e-mail: valerie.boisvert@unil.ch

H. Tordjman
CEPN – Université Paris 13, UFR Sciences économiques et gestion,
93430 Villetaneuse, France

F. Thomas
IRD – UMR 208 PALOC, Muséum National d'Histoire Naturelle, Laboratoire
d'Ethnobiologie, 75005 Paris, France

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_17

17.1 Introduction

Ecosystem services have been an important research field from the 2005 *Millennium Ecosystem Assessment* (MEA), and the number of papers devoted to this topic has literally exploded ever since. As illustrated by the recent creation of IPBES (*Intergovernmental Platform on Biodiversity and Ecosystem Services*) – an international expert panel launched in Busan, Korea, in 2010 – the approach in terms of ecosystem services is redefining biodiversity through the services it provides. Ecosystem services are becoming an inclusive framework encompassing most environmental issues (climate change, desertification, soil erosion, water, biodiversity, etc.). They are partly substituted for the latter in policy formulation.

This chapter is an attempt to explain this hegemony. The notion of ecosystem services was formed at the interface of science and policy and is not actually grounded either in ecology, in biology or in economics. Ecosystem services are only very loosely related to the functioning of ecosystems because they are defined only in reference to the benefits they supply to human societies. Otherwise, their economic status is problematic since the term is indistinctly applied to (immaterial) services and to (material) goods or values (MEA 2005).

Setting back the notion of ecosystem services in the history of economics and monetary valuation of the environment enables to restore the cognitive background from which this notion emerged, in order to explain its power. Environmental policies first focused on the valuation of nature to internalise environmental costs into political and economic decision-making processes as a prelude to the development of markets as regulation instruments. Ecosystem valuation has then progressively shifted towards financial tools that aim at turning damages to the environment into market opportunities.

17.2 Ecological Economics and the Value of Nature's Services

The terms 'nature's services', 'ecosystem services' and 'ecological' or 'environmental services' have emerged in environmental literature in the 1970s and have been in widespread use from the end of the 1980s (Gómez-Baggethun et al. 2010; Méral 2012). Their emergence was almost contemporary of the appearance of biodiversity, both as a word and as a policy issue, and of the constitution of ecological economics. Like the latter, the notion of ecosystem services pertains to a global attempt to raise the awareness of both the general public and the decision-makers about the seriousness of the environmental crisis and the urgent need for action and to transform the simplistic representations of ecosystems at the basis of most environmental policy tools. The texts and academic contributions that are usually considered as seminal in this regard are those that established the principles of cost-benefit analysis in the 1960s in the United States and that analysed the components of the total economic value of the environment (e.g. Krutilla 1967), Westman's 1977 article or Paul and Anne Ehrlich's book in 1981.

The major message of Paul and Anne Ehrlich's 1981 book is that the environmental crisis and the question of the limits to growth should be taken seriously. In addition, they argue that these limits are not only energy or material constraints and that they cannot be adequately accounted for by standard economic approaches. Indeed, according to the latter, the progressive depletion of exhaustible resources should automatically lead to an increase in their price, turning other resources and technologies into cost-effective alternatives and favouring therefore the substitution of renewable resources for exhaustible ones and the development of backstop technologies (Nordhaus 1973; Solow 1974). The rent derived from exhaustible resources could be reinvested so as to enable their replacement by reproducible capital and maintain per capita consumption constant (Hartwick 1977). Other authors bring to the fore the notion of critical thresholds, i.e. ecological norms dictated by the assimilative capacity of the environment or the resources renewal rate, which should be imposed on economic activities. This is the 'safe minimum standard' approach advocated by Ciriacy-Wantrup (1952) and developed by Bishop (1978) that has been extended and applied to a wide range of ecosystem functions and values during the 1990s, under the name of 'critical natural capital'.

Indeed in the 1980s, standard environmental economics was based on a representation of ecological dynamics comparable to and compatible with the search for economic equilibrium, lending itself to joint modelling of optimal exploitation paths. Yet ecosystems are complex and their evolution is chaotic. Human societies depend on nature on several counts. If these various and intricate relations are accounted for in a too linear way, the resulting policies are doomed to failure. This observation formed the core and starting point of ecological economics, as expounded in the programmatic texts pleading for a new approach to address the interdependence and coevolution of human economies and natural ecosystems in the first issues of a dedicated journal, *Ecological Economics* (Costanza 1989, 1991). In this context, the question is raised of the limits that should be set on the exploitation of complex ecosystems.

It can be assumed that the notion of ecosystem services is an instrument to communicate on environmental crisis and the urgent need for policy action, without going into the details of ecosystem functioning (Peterson et al. 2009). Ecosystems can be assessed in the light of their ability to provide services, like a capital which is valued and characterised as such only owing to its potential to generate income flows. The concepts of ecosystem services and natural capital are thus closely linked. The tentative genealogies of ecosystem services point that the terminology has been in use in ecological economics from the very outset of this academic field, when the research agenda was set up, in the context of a programme at the Beijer Institute in Sweden, prior to the creation of the International Society of Ecological Economics (EE) and its journal (*Ecological economics*) in 1989 (Gómez-Baggethun et al. 2010).

In the preface to their 1981 book, Paul and Anne Ehrlich introduce the famous metaphor of the rivets of an airplane. Removing only one rivet will not alter the airplane functioning but once a critical threshold is reached, drilling out an additional rivet from the wing flap might result in a crash. Similarly, the production of ecosystem services depends on diversified ecosystems. They can be affected to some degree without perceptible impacts on the provision of services – and the resulting level of human well-being – because of functional redundancy. However, at some point, the loss of an additional species leads to the collapse of the ecosystem and the permanent loss of the functions it performed. This results in an appeal to the precautionary principle: the relations between biodiversity and ecosystem dynamic have not been completely described or analysed, and it is difficult to define precise thresholds up to which sustainable harvesting could be possible. Biodiversity and ecosystems should be protected altogether, and the rate of species extinction should be decreased to ensure the continuous provision of the services on which humankind depends (Ehrlich & Mooney 1983).

Rather than using metaphors, Robert Costanza and his colleagues have chosen to resort to monetary valuation of what they call ‘the services of ecological systems and the natural capital stocks that produce them’. They justify their work as an exercise in pragmatism: *because ecosystem services are not fully ‘captured’ in commercial markets or adequately quantified, they are often given too little weight in policy decisions* (Costanza et al. 1997: 253). They contend that a monetary value should be attached to ecosystem services, to give a notion of the free contribution of nature to the economy, as compared to the world GDP. The authors readily acknowledge and even claim that the total amount they come up with is a very rough estimate. But they contend that its major function is to raise public awareness and discussion (an objective which has been fully met if one thinks of the harsh reactions following the publication of the paper).

The *Millennium Ecosystem Assessment* that began in 1998 and the final reports of which were released in 2005 was a major stage in the dissemination of the reformulated notion of ecosystem services. It gave the first comprehensive assessment of these services at the global level, based on typologies of services and estimations of their contribution to human well-being and economic activities. This global assessment, commissioned by the United Nations, was the result of a consultative process involving the world’s leading scientists on the subject.

Four types of so-called services are identified in the *Millennium Ecosystem Assessment*:

- Provisioning services or the supply of goods of direct benefit to people and often with a clear monetary value, such as timber and medicinal plants.
- Regulating services, the range of vital functions carried out by ecosystems such as the regulation of climate through the storing of carbon and control of local rainfall or the removal of pollutants by filtering air and water. Their valuation proves more challenging since their disruption, which is perceived as a negative externality in standard economics, is not integrated in accounting.
- Cultural services that do not provide direct material benefits but contribute to wider needs and desires of society and therefore to people’s willingness to pay for conservation. They include the spiritual value attached to particular

ecosystems such as sacred groves and the aesthetic value of landscapes. As such, they fall under the category of 'existence values' which is one of the basic tenets of the monetary valuation of the environment.
- Supporting services that do not provide direct benefits but are essential to the functioning of ecosystems and therefore indirectly responsible for all other services (e.g. soil formation, plant growth, photosynthesis).

Quite distinct objects are therefore loosely termed services, including ecological functions, already known or still to be discovered, (material) goods, actual (immaterial) services, values or preferences, that might prove weakly if it all correlated to a given state of the ecosystems. Most of them would not actually fit into the economic definition of a service. Indeed, the term 'service' is applied in this context to material goods and to values that might be the rationale under economic behaviour but that are definitely not the subject of economic transactions. These so-called services are not always defined in relation to specific ecosystems, nor are they observed at the ecosystem level. Some of them relate to the biogeochemical regulation of larger systems, others to given species, to soil types or to forest cover.

There is therefore no unity among the so-called services, neither from an ecological nor from an economic viewpoint. Advances in ecology and life sciences as well as the development of observation devices or the emergence of new social concerns might reveal new 'services' and open therefore prospects of unending developments of the list of ecosystems to be protected and possibly paid for. Ecosystem services therefore appear as the very example of fictitious commodities or constructed entities created for the sake of being traded, without tangible reality beyond their market value (Boisvert and Tordjman 2012).

The all-embracing character and the evolving nature of the notion have probably played a prominent part in its success; it can be appropriated, strategically used and distorted to serve virtually all kinds of purposes and to feed various types of discourses about the environment. It explains its hegemony in the field of conservation; the necessity of preserving ecosystem services is a privileged argument in the legitimation of conservation policies. However, some environmental issues cannot be adequately addressed nor analysed through these lenses: exhaustible resources, noxious substances that cannot be degraded or assimilated by ecosystems at a human time horizon and various damages to the biosphere that cannot be limited to an (reversible or compensable) overexploitation of its cycles and flows.

17.3 Payments for Ecosystem Services and Biodiversity Offsets

The MEA approach is the very illustration of the position of those who are called 'new environmental pragmatists' by Clive Spash (2008, 2009). It goes exactly just far enough to satisfy the alleged desire of decision-makers for monetary valuation, without being actually anchored in any discipline, while referring to many. From the end of the 1990s, the mechanisms characterised as payments for environmental services (PES) have developed (Pagiola et al. 2002). These institutional arrangements are promoted by networks and actors (e.g. FAO and OECD) which are not those involved in the dissemination of the notion of ecosystem services (Pesche et al. 2011). The principle underlying PES is closely linked to the concept of environmental externalities: these mechanisms are designed to have the beneficiaries of a service (carbon sequestration, water regime regulation, recreation value, biodiversity conservation, etc.) pay those who provide or favour this service through their practices. The subject of the transaction is not the service itself (which is to a large extent freely provided by nature). The payment is meant as an incentive to adopt new processes and techniques or as a compensation for stakeholders that might abandon disruptive uses of the environment. The amounts of compensation paid in this context are usually neither related to the assessment of the ecosystem service per se nor to the ecosystem functions. However, the provision of ecosystem services is generally considered as strongly dependent on an operator, who is accordingly kind of granted a concession for the ecosystem.

In addition to PES spreading, the last decade has seen attempts to develop markets or at least market-like mechanisms for ecosystem services (Boisvert and Tordjman 2012). Such project implies the measurement, valuation, standardisation and disaggregation of the environment (Tordjman 2008). New tools and methods were devised for that purpose, relying on the use of a set of emerging techniques pertaining to eco-informatics. They are generally referred to as ‘rapid ecological assessment techniques’. They are used to list, dissect, map and give a price to ecosystem services in order to catalogue them. The Nature Conservancy, WWF, Stanford University’s Woods Institute for the Environment and University of Minnesota’s Environmental Institute are involved in a project entitled *Natural Capital Project* and have recently developed a family of software-based tools for integrated valuation of ecosystem services and trade-offs called InVEST. The same consortium also compiles and archives data on conservation projects and plans to make them freely available in an online free-access database. Similarly, in 2007, several environmental NGOs and research centres launched a project called ARIES (*Artificial Intelligence for Ecosystem Services*) that aimed at providing free access to a rapid biodiversity assessment service and to information about biodiversity values at several levels from the regional to the global. The models are based on extensive inventories and database that are in constant evolution and make it possible for users to work out maps of the main ecosystems and the services they provide as well as estimations of the potential economic value of the latter. A further step in market development would be to establish international payment systems in order to attract funds and to finance far-reaching conservation activities. These payment schemes require monetary valuation. A price is given to ecosystem services in using conventional – and debated – environmental valuation methods:

1. Ecosystem use values can be captured by the restoration or replacement costs in cases of degradation, defensive or protective expenditures and hedonic approaches

(travel costs to value recreation sites and housing prices to value environmental attributes that are parts of the amenities paid for when buying a house).

2. Non-use values, especially existence value, are estimated thanks to contingent valuation methods, i.e. direct questioning aiming at having respondents disclose their willingness to pay for a preserved ecosystem or their willingness to receive for its degradation.

The emergence of ecosystem services as the mainstay of environmental policies has led to reconsider existing mitigation policies, especially in the United States. It has favoured the development of biodiversity offsets. In offsetting schemes, the developers can purchase the number and type of 'biodiversity credits' required to offset the damages they caused to have the latter mitigated, as required by the law. The number of credits they need is defined by the administration in charge of conservation – the US Fish and Wildlife Service or the National Marine Fisheries Service depending on the cases. If they destroy a given acreage of the habitat of a particular species, the developers must contribute through their payment to the maintenance or restoration of a comparable area of the same species habitat. The whole difficulty is of course to define this area, in quantitative as well as in qualitative terms. This is the 'no-net loss' principle brought to the fore in the context of wetland mitigation (Robertson 2000). The places where money is invested in order to offset damages caused to biodiversity are called 'conservation banks'. Private or public, they are considered as critical habitats, because they host endangered or endemic species or because they have scenic or heritage value. According to speciesbanking.com, a website specialised in data collection on that subject, there are 102 conservation banks in the United States, and each of them is operating under its own rules, indicators and definition of ecological equivalence. The credits emitted within those different offsetting systems are not fungible. In a recent report commissioned by the US Department of Agriculture Office of Environmental Markets, the Willamette Partnership surveyed a sample of 35 measurement systems used to measure biodiversity (Willamette Partnership 2011). Yet their homogenisation and standardisation are major concerns and targets of policies, and the US Office of Ecosystem Services and Markets has been created in 2008 under the Department of Agriculture (USDA), expressly to address this issue. The purchase of credits tends now to be presented as a genuine monetary compensation – in other words as the price – for biodiversity destruction. The development of habitat valuation techniques and of an associated body of experts, consultants and brokers has been instrumental in this respect.

At an international level, several interrelated think tanks and networks of individuals and organisations – e.g. *Forest Trends*, *the Katoomba Group*, *the Ecosystem Marketplace* and *the Business and Biodiversity Offsets Program* – were launched in the 2000s with the professed objective of contributing to the advancement of markets and payments for ecosystem services. The programmes and projects on these topics have substantially increased and always imply the same actors and networks (big environmental NGOs, United Nations agencies and programmes, transnational corporations, various representatives of corporate interests, the private banking and financial sector, auditing and consulting firms, etc.). They all agree that there is an urgent need for standardisation of the emerging market instruments, based on the adoption of common definitions, guidelines and management tools.[1]

The initial objective of market-like mechanisms in the field of conservation policies was to internalise environmental externalities and to have them accounted for in decision-making. Since the inception of the ecosystem services concept, environmental assets tend to be defined specially for the sake of being traded on globalised markets. The TEEB (*The Economics of Ecosystems and Biodiversity*) initiative was a decisive step in this regard: it marked a turning point from the commodification to the financialisation of the environment (TEEB 2010; The Economics of Ecoystems and Biodiversity 2010). Like the MEA, the objective of the TEEB initiative was to raise awareness about the economic benefits of conserving biodiversity, the losses associated with its erosion and the need for action and for innovative financial mechanisms. It was hosted by UNEP and was initiated following a proposal made by the German government at the meeting of the environment ministers of the G8+5 countries that took place in Potsdam in March 2007. The TEEB reports that were released at the tenth Conference of the Parties in Nagoya in October 2010 are intended for different 'end users' as they are referred to ecologists and economists, international and national policymakers, local and regional policy, citizens and above all business.

The TEEB reports bring to the fore the lost opportunities associated with environmental degradation and make the case for the development of financial tools that would enable to invest in ecosystem services. The ecosystem services are reinterpreted so as to turn them into assets that would be traded on financial markets to be developed.

The various business risks – hence potential costs – biodiversity loss or improper management might induce are gathered under the all-embracing heading of 'biodiversity business risks' (BBR) and they are converted into valuable assets. The website associated with the TEEB report and developed to raise public awareness about biodiversity erosion and the economic potential of ecosystem services is called *Bank of Natural Capital*.

17.4 Conclusion

The emergence of the notion of ecosystem services is inseparable from a particular kind of environmental policy. The thrust of ecosystem services management is to introduce and spread market-based instruments, which are supposed to allow the surfacing of the full ecosystem values. Indeed, according to the standard economic theory, the main threat to services is due to their nonmarket nature. Because of the latter, the value of ecosystem services would be systematically underrated because

---

[1] See Ecosystem Marketplace website, created in 2004 which is presented as an information portal on markets for ecosystem services.

it would not be – at least not fully – accounted for in the price system. Ecosystem services would in addition be affected by a lack of recognition, because they are not appropriated. Nobody would therefore feel responsible for their conservation. Most policy instruments regarded as possible solutions to these issues are therefore incentives, meant to correct and complement missing market information so that economic actors take the right decisions: subsidies, taxes, and royalties, fees and payments for ecosystem services, etc. The favoured solution is to have beneficiaries pay for the services, on a more or less voluntary basis, rather than to impose a polluter (or destroyer)-pays principle.

The debate on the valuation of ecosystem services is inspired by standard economics and associated representations of the policies to be promoted rather than by an actual analysis of ecosystem functioning. It conveys a vision of nature as exempt from any conflict and danger and is quite positive about the feasibility of a harmonious combination of human activities and environmental protection, sustained by the development of markets and contracts.[2] Using the terms 'ecosystem services' implies to consider that moderate exploitation is compatible with conservation. Pursuant to this representation, human activities, if properly channelled, are not threats but opportunities for ecosystem services. The justification register referred to is that of incentives rather than restriction, ban, coercion and repression. The underlying message is a liberal and positive one. The emphasis is placed on promise and reward rather than on responsibility and sanction. The less pleasing aspects of ecosystems – for instance, as sites for the breeding of mosquitoes or various other vectors of diseases or as sources of vulnerability for human activities – are overlooked. The notion of disservice has made a modest appearance in the literature, but it is far from meeting with the success enjoyed by the notion of ecosystem services. The values of ecosystem services estimated in monetary terms are capitalised and appear as assets in a natural capital balance sheet without debts or liabilities.

A new branch of finance devoted to biodiversity and ecosystem services is under development (Boisvert and Tordjman 2012; Tordjman and Boisvert 2012), though its practical relevance and feasibility are far from demonstrated (Wendland et al. 2010; Karousakis 2009). Ecosystems are compared to services portfolios, made up of various environmental assets (biological diversity, carbon sinks, etc.) which could be turned into financial assets and traded on dedicated markets. Such a prospect seems most promising to funding agencies and environmental think tanks that consider it might have a leverage effect, especially sought after in a context of growing scarcity of funding. As a result of a reversal that is commonplace in finance, debts can be securitised and turned into valuable assets; similarly, biodiversity erosion and the loss of ecosystem services can be turned into assets if the associated risks and costs have been identified and provisioned for into business management

---

[2] The communication agency that was in charge of the International Year of Biodiversity in 2010 recommends the adoption of a 'new nature message', the so-called love message, based on emotions of awe and wonder associated with biodiversity, rather than the 'loss message' that induces guilt and headshaking at the state of the world but no action (Futerra 2010).

plans. In this situation, the legitimacy and soundness of the ecosystem services concept to promote conservation policies can be questioned. Indeed, the ensuing markets or market-like instruments are based on expectations about ecosystem deterioration or biodiversity depletion. How could these very tools be used to check environmental degradation?

Since the inception of the ecosystem services notion, there has been a shift in environmental policies from a tentative integration of environmental costs in investment choices implying serious environmental impacts to the promotion of green investment. Environmental issues are no longer presented as constraints or impediments for economic growth but as possible profit opportunities. This rhetoric is quite powerful: the environment cannot be saved without an alliance with the business sector. In this perspective, nature is the major producer of goods and services, and as a consequence, it makes sense to invest heavily in its development. Not surprisingly, the business and finance sectors are spearheading the diffusion of the ecosystem services concept that ultimately discredit coercive regulation for environmental protection depending on public control and funding, considered as inordinate in times of recurring economic and financial crises, while promoting the development of market-based instruments.

References

Bishop RC (1978) Endangered species and uncertainty: the economics of a safe minimum standard. Am J Agric Econ 60(1):10–18

Boisvert V, Tordjman H (2012) Vingt ans de politiques de conservation de la biodiversité: de la marchandisation des ressources génétiques à la finance « verte ». Economie appliquée LXV(2):107–136

Ciriacy-Wantrup S v (1952) Resource conservation. University of California Press, Berkeley

Costanza R (1989) What is ecological economics? Ecol Econ 1:1–7

Costanza R (ed) (1991) Ecological economics: the science and management of sustainability. Columbia University Press, New York

Costanza R, d'Arge R, de Groot R, Farber S, Grasso M, Hannon B (1997) The value of the world's ecosystem services and natural capital. Nature 387:253–260

Ehrlich P, Ehrlich A (1981) Extinction: the causes and consequences of the disappearance of species. Random House, New York

Ehrlich P, Mooney H (1983) Extinction, substitution and ecosystem services. BioScience 33(4):248–254

Futerra (2010) Branding biodiversity: the new nature message. http://www.futerra.co.uk

Gómez-Baggethun E, de Groot R, Lomas P, Montes C (2010) The history of ecosystem services in economic theory and practice: from early notions to markets and payment schemes. Ecol Econ 6:1209–1218

Hartwick JM (1977) Intergenerational equity and the investing of rents from exhaustible resources. Am Econ Rev 67(5):972–974

Karousakis K (2009) Promoting biodiversity co-benefits in REDD. OECD environment working papers, no. 11, OECD Publishing

Krutilla JV (1967) Conservation reconsidered. Amer Econ Rev 57:777–786

Méral P (2012) Le concept de service écosystémique en économie: origine et tendances récentes. Nat Sci Sociétés 20:3–15

Millennium Ecosystem Assessment (MA) (2005) Ecosystems and human well-being: a framework for assessment. Island Press, Washington, DC

Nordhaus W (1973) The allocation of energy resources. Brookings Pap Eco Act 3:529–576

Pagiola S, Bishop J, Landell-Mills N (eds) (2002) Selling forest environmental services: market-based mechanisms for conservation and development. Earthscan, London

Pesche D, Méral P, Hrabanski M, Bonnin M (2011) Services écosystémiques et paiements pour services environnementaux: les deux faces d'une même logique? Document de travail SERENA, 2011–01

Peterson MJ, Hall DM, Feldpausch-Parker AM, Peterson TR (2009) Obscuring ecosystem function with application of the ecosystem services concept. Conserv Biol 24:113–119

Robertson M (2000) No net loss: wetland restoration and the incomplete capitalization of nature. Antipode 32(4):463–493

Solow R (1974) The economics of resources and the resources of economics. Am Econ Rev 64(2):1–14

Spash C (2008) How much is that ecosystem in the window? The one with the bio-diverse trail. Environ Values 17:259–284

Spash C (2009) The new environmental pragmatists, pluralism and sustainability. Environ Values 18:253–256

The Economics of Ecosystems and Biodiversity (2010) The economics of ecosystems and biodiversity: ecological and economic foundations. Earthscan, London

Tordjman H (2008) La construction d'une marchandise: le cas des semences. Annales Histoire Sciences Sociales 63:1341–1368

Tordjman H, Boisvert V (2012) L'idéologie marchande au service de la biodiversité? Mouvements 70:31–42

Wendland KJ, Honzák M, Portela R, Vitale B, Rubinoff S, Randrianarisoa J (2010) Targeting and implementing payments for ecosystem services: opportunities for bundling biodiversity conservation with carbon and water services in Madagascar. Ecol Econ 69:2093–2107

Willamette Partnership (2011) Measuring up: synchronizing biodiversity measurement systems for markets and other incentive programs. A report funded by the U.S. Department of Agriculture, Office of Environmental Markets

Chapter 18
Bridging the Gap Between Conservation and Health

Angela Yang, Peter M. DiGeronimo, and Alexandre Azevedo

Abstract Health is frequently in the news, whether it is the “bird flu” headlines or woven into the core of climate change reports. And in these articles, health is the common thread that connects humans, animals, and the environment; however, this underlying link is often undervalued, leaving a “gap” that challenges our ability to prevent and mitigate major global catastrophes. The Ebola virus disease has ravaged West Africa, leaving a swath of devastation and unanswered questions in its wake, but it highlights the alarming potential of a zoonotic disease, one of hundreds that pass between animals and humans. Climate change continues to fuel controversy, but it is undeniable that our exploitation of the Earth is impacting the fundamental resources that form the foundation of our existence. The state of our ecosystems is integral to the conservation and sustainable management of our wildlife and natural resources. The health of the environment cannot be segregated from our own health; thus, we need to examine health from a global stance. Our traditional perspectives of “health” and “disease” are outdated, and it is prime time for us to reevaluate our approaches to engage a comprehensive audience as well as holistic strategies to address these issues as “One Health.”

18.1 Introduction

The genesis of this chapter originated from a meeting in Bangkok of the same title as this book, a forum where regional experts discussed and deliberated the vital minutia of individual human health and disease projects. The malaria researchers concluded that incidence and prevalence of the disease in humans could be reduced

---

A. Yang (✉)
Biodiversity, Wildlife and Ecosystem Health, MSc.,
The University of Edinburgh, Edinburgh, UK

Wildlife Conservation Society, Bronx, New York, USA
e-mail: angela.yang987@gmail.com

P.M. DiGeronimo • A. Azevedo
Biodiversity, Wildlife and Ecosystem Health, MSc.,
The University of Edinburgh, Edinburgh, UK
e-mail: pmdigeronimo@gmail.com; ax.c.azevedo@gmail.com

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_18

if there were no trees. While this may seem logical to human health experts examining the world through one end of a microscope, they need peer beyond the Petri dish: what would this world be like without trees? Herein lies the crux of our conundrum: the divide between health and conservation.

In a human-centered world, the term "health" unfailingly conjures images of disease and the human condition. However, this is merely one element in the broader definition of health that bridges humans, animals, and ecosystems. It is this "One Health" that binds our well-being to that of our surroundings in a complex, interdependent web upon which our existence is delicately, yet critically balanced. We must remember that health applies not only to individual organisms but to living systems as well: the intricate relationships between living organisms and the environment are often obscured, further challenging efforts to define and evaluate the state of ecosystems, their goods and services, as well as the dynamics of "One Health." Yet, the speed and scope of anthropogenic change and the lack of recognition of the long-term ecological impacts of our decisions only magnify this intense situation, creating an ever-evolving discord that tests the boundaries and resilience of the natural world.

Like the air that we breathe, humanity is part of the global environment that forms the basis for life on Earth. However, we, and our unabated population growth, have had an increasing hand in manipulating the state of the world and that of our future. Our influence over Earth's dynamics through the millennia has contributed to the degradation of ecosystems and the exploitation of natural resources, also referred to as "ecosystem goods and services." Ecosystems and their goods and services—food, air, water, nutrient cycling, for example—are the foundation for our health and well-being. These essential functions sustain human health and, in effect, life as we know it (MEA 2005). Even subtle shifts in ecosystem services can topple this fragile equilibrium and trigger social, economic, political, and demographic changes that potentially endanger our future. Thus, the ubiquitous, ever-expanding human footprint has fuelled unprecedented resource demands that have led to the urgent need to manage and conserve our natural capital in hope of a sustainable future. For example, we "consume" in one way or another as much as 40 % of all solar energy trapped by land plants (Erlich and Wilson 1991), a selfish action that not only threatens other species but that of our own (eds Grifo and Rosenthal 1997). Forests provide numerous ecosystem services that are fundamental to "health," including energy production, climate regulation, and nutrient cycling, but with the current rate of deforestation measured in acres per minute, our myopic actions defy logic, hence jeopardizing the future of this planet (Fig. 18.1).

Conservation and the sustainable management of our natural world have direct bearing on "health" in the broader context. In a concept that is simultaneously rudimentary and revolutionary, the "One Health" paradigm examines these challenges through a new multidisciplinary lens, addressing the issues through a consilience of human, animal, and ecosystem health, but this concept faces an uphill battle against tradition to gain traction. In June 2012, Rio + 20, the United Nations Conference on Sustainable Development, fell short on many fronts, but in its singular focus on economic development, failed to consider the social and environmental pillars that

Fig. 18.1 The "hard edge" between Bwindi Impenetrable National Park in Uganda and converted agricultural land (Photo: A. Yang)

are integral to sustainable development. Science-based evidence on global health issues were overshadowed by ideology and the final outcome "*The future we want*" omitted health as a cross-sectoral priority in sustainable development. Nevertheless, the general approach of this document allows for an unprecedented opportunity to engage health sectors, in all their incarnations, in the dialogue towards sustainable development goals (Langlois 2012).

18.2 Redefining Conservation

A general definition of conservation in this context is the act of preserving, protecting, managing, or restoring wildlife, habitats, and natural resources. Thousands of international and local conservation organizations and scores of professional scientists excel at quantifying conservation needs in order to objectively develop science-based strategies that counter present and future threats, with the goal of balancing man and nature. Conservation organizations, constrained by their areas of expertise and financial resources, focus on protecting species and habitats in a progressively anthropogenic arena. However, delineating national park boundaries and building fences to physically separate humans and wildlife animals is a less viable tool nowadays, particularly in developing countries where there is extensive interdependence between livelihoods and ecosystem services and where resource competition is fierce. Conservationists increasingly acknowledge that the root of many conservation issues stems from conflicts over space and resources and clashes with social or cultural beliefs, the underpinnings of which may fall outside of their sphere of knowledge and influence. As a result, conservationists need to look beyond their traditional strongholds and collaborate with other sectors, including social, political, and health: conservation alone can no longer protect biodiversity.

Even among and within conservation organizations, biologists working exclusively within their expertise or particular projects fail to recognize opportunities, capitalize on synergies, or bridge the gaps that could maximize efficacy. This proclivity is not limited to the world of science as we have all been accused of not “thinking outside the box” at some point. When implementing potential solutions, conservation strategies may require broader, multidisciplinary approaches to meet any realistic expectation of success, but conservationists often lack the time, capacity, or resources to engage the appropriate sectors that can better address social-, political-, and/or economic-based challenges.

The narrow focus of projects, sometimes imposed by donors, further reinforces segregation and isolation. Projects that target wildlife ecology may overlook the opportunity to collect biological samples that could assist with management strategies, as the knowledge of baseline population health can help detect trends and identify potential new threats. Ecological studies that require animal capture, such as radio-collaring, offer a unique opportunity to collect biological samples. When pronghorn antelope were radio-collared in the Upper Green River Basin, Wyoming, to identify migration corridors (Fig. 18.2), measurements and biological samples were simultaneously collected to test for pregnancy rates and stress levels as part of a comprehensive effort to establish comprehensive baseline information about pronghorn antelope ecology (Beckmann et al. 2008). Gillespie et al. (2008) discuss multiple invasive and noninvasive sampling techniques to monitor for infectious disease and parameters of health in wild primates for both the conservation of wild animals and the safeguarding of human health. While humans and wild primates are at particular risk of epizootic and zoonotic disease due to our close evolutionary relationship, the same sampling techniques and data can be used across taxa for similar means.

Fig. 18.2 Net-capturing pronghorn in Wyoming (Photo: J. Berger)

The illegal trade in wild flora and fauna or parts is another global issue that threatens biodiversity and health but is confounded by regional, social, political, and cultural divides. Despite international and national regulations, the lack of capacity and global coordination hampers law enforcement in the illicit movement of wild species worldwide. Fuelled by greed and ignorance and sheltered by cultural and social beliefs, this billion-dollar trade offers an unparalleled "free ride" for species and their pathogens to travel the globe, enter new environments, and invade or infect naïve populations. Gomez and Aguirre (2008) identified 29 pathogens diagnosed and documented in illegally traded wildlife included numerous epizootic, zoonotic, emerging and re-emerging infectious diseases. Conservation organizations need to collaborate within and among themselves as well as engage influential sectors beyond conservation to tackle the source of the problem, as well as develop strategies to mitigate the effects. In November 2012, US Secretary of State Hillary Clinton called for a "concerted global response" (WWF 2012b) to address wildlife trafficking, a multinational criminal activity that rivals drugs and human trafficking—and only with the joint efforts between countries and between disciplines can this trade be halted.

With human populations surpassing the seven billion mark in 2011, the rate of anthropogenic change is accelerating and conservationists need to capitalize on all available resources, including fellow scientists, local communities, as well as experts from the development, health, and policy arenas. Preconceived ideals and standard definitions need to evolve in order to keep pace with society, science, and development, and a holistic approach that recognizes the new conservation paradigm—one that includes people and livelihoods—is an important strategy for shared goals and, ultimately, our shared future.

18.3 Redefining Health

The traditional, antiquated, and most common definition of health as the "absence of disease" applies primarily to human health and is limited in scope, depth, and applicability in the twenty-first century. Even the meaning of human health, as it stands, can be contested and needs further rejuvenation to connect with a globalized world. Health is an elusive term that can be defined as a continuum between illness and wellness, partly determined by each individual's ability to cope with and adapt to stress (Lyon 2000). Health is not "black and white," but encompasses a range of indices including physiological, psychological, spiritual, cultural, and developmental. Perhaps, health needs to always be used in conjunction with "well-being," the latter encompassing all non-disease factors, particularly those that pertain to our environment? Nevertheless, we need to realize that health, a constant undercurrent in our daily lives, affects living organisms, the environment, and even global economies. Just as the term "conservation" needs reevaluation, health requires an updated characterization beyond merely remedying a malady.

The epidemiology and transmission of infectious disease are altered by rapidly changing environments, particularly in light of burgeoning human populations that decrease proximity between and among humans and animals, degrade natural habitats, and deplete resources. In developing countries already plagued with overpopulation, flagging economies, corruption, and the lack of capacity, resources, and education, diseases can have resonating impacts on the immediate populations of humans and animals as well as the ecosystem, further underscoring the importance of understanding the linkages between all three. Through complex, integrated mechanisms that we still struggle to comprehend, the health of one can have cascading and/or compounding effects on the others, and the condition of the environment can directly or indirectly affect the health and well-being of humans, with the most obvious consequences at the nexus of livelihoods and the environment. These relationships need to be recognized and health needs to be addressed as a whole. Simultaneously, the human health community needs to appreciate that while human health is the priority, it is closely linked to animal and ecosystem health, and any imbalance in this trifecta can topple the delicate equilibrium, affecting the status of all three.

18.4 Disease: An Ecological Concept

The last century witnessed vast changes in our understanding of disease. Germ theory revolutionized human healthcare, providing scientific grounds to identifiable pathogens as agents of disease. Two medical milestones quickly followed: the development of vaccines and antibiotics as the cornerstones of preventive care and treatment, respectively. Prior to this, medicine could treat clinical signs and provide palliative therapy, such as cough suppressants and fever reducers, but afterwards, we could identify and treat the proximate cause of disease by preventing and eliminating infection of causative agents. Subsequently, we have increasingly recognized more ultimate causes of disease such as diet, exercise, lifestyle, and heredity. Discoveries in the field of genetics and the development of molecular medicine have transformed how we understand and approach predisposition to and development of disease. We increasingly understand that infectious disease is not as the simple result of infection by a specific pathogen, but as the end product of ecological processes.

Understanding health as an ecological concept requires that we understand disease as a natural process. It is inaccurate and presumptuous to assume that the sole absence or presence of disease equates a healthy or unhealthy individual, community, or environment. Individuals and populations are likely always to naturally harbor pathogens or other organisms. Understanding the health continuum is far more pragmatic than attempting to purge each individual or population of disease. So we must approach health at the ecosystem level rather than at the organismal level and adopt a comprehensive, well-rounded definition of "health."

Examples of the advantages of understanding disease at an ecosystem level and applying this knowledge have already begun to appear. In one case, the use of locally occurring copepods (crustaceans) to control mosquito (*Aedes aegypti*) populations resulted in drastic reductions of the incidence of dengue disease in several communes in northern and central Vietnam (Nam et al. 2005). The implementation of community-based programs to educate and build capacity in local communities allowed the eradication of the vector by populating the mosquitoes' breeding sites with local predacious copepods. In this example, a strong community approach addressing a predominant human health problem through a collaboration of health education and understanding of vector ecology resulted in strong and sustainable outcomes, whereas the application of pesticides would probably result in greater costs and dependence of the communities, unpredictable side effects on the environment, and, most importantly, a less effective control of the disease.

Using such an ecological approach to address disease redirects our focus from treatment to prevention. Rather than intervene after the emergence of a disease, might it not be more pragmatic, beneficial, and cost-effective to detect and prevent the occurrence where possible? Instead of treating patients stricken with malaria, it would be more effective to prevent the initial infection by minimizing vector-host interfaces, a measure that may involve understanding the fields of vector ecology, sociology, health, and education.

The severe acute respiratory syndrome (SARS) epidemic, which caused close to 800 human deaths worldwide between 2002 and 2003 (CDC 2005), is caused by a coronavirus infection that manifests as a respiratory disease in humans. Through globalized air travel, an outbreak rapidly escalated and teetered on pandemic status, infecting over 8,000 people in 37 countries. However, SARS could have been detected and potentially prevented through disease surveillance in wild animals and the enforcement of policies on the illegal movement and consumption of wildlife in Southeast Asia. Three species of cave-dwelling bats were ultimately found to be the reservoir for SARS-like coronaviruses (Li et al. 2005). These animals are often sold

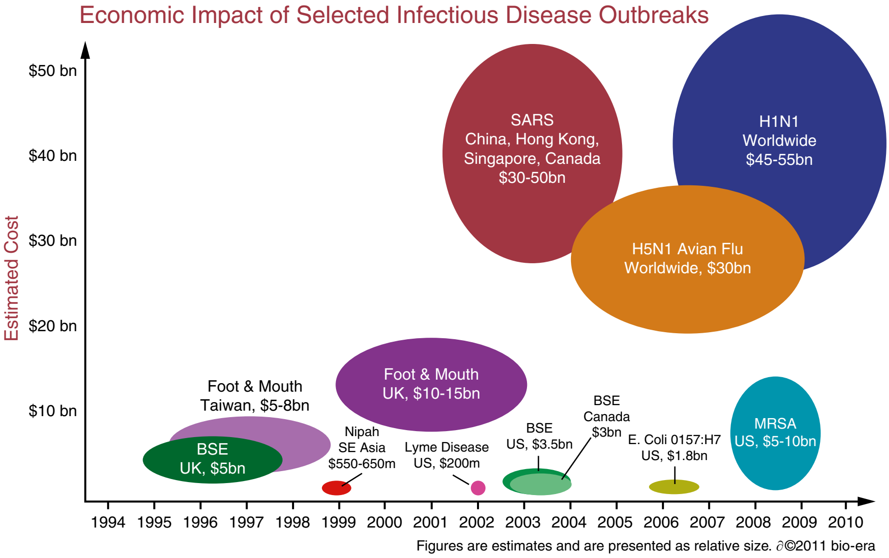


Fig. 18.3 Disease economics (Credit: bio-era)

in wet markets, and although the transmission dynamics are not clearly delineated, this virus likely infected humans through intermediary hosts like civets, which are heavily traded for food (Black 2005). While scientific laboratories and pharmaceutical companies are vying to develop vaccines, perhaps human health and conservation partners should simultaneously collaborate with governments and communities to stop the trade in wild species which would benefit all sectors? This trade not only impacts biodiversity and health but also global economies (Fig. 18.3). Increasing pressure, particularly from governments, national Ministries of Health, and multilateral agencies such as the United Nations, would add weight to flagging policies and possibly bolster national enforcement, as evidenced by US Secretary of State Hillary Clinton's speech to strengthen the enforcement of wildlife laws globally (Staziuso 2012).

18.5 Healthy Animals, Healthy People, Healthy Ecosystems

We like to tackle health and conservation as separate entities: conservationists work with wildlife and human health experts work with people. Meanwhile, threats to the two sectors can be one and the same, or both can face similar challenges where synergy could facilitate or expedite resolutions. However, despite years of attempting to engage multiple disciplines and "cross-pollinate" to address the broader issues, there have been few successes to date, and we continue our compartmentalized approaches to conservation and health. Not only is this unproductive, but as we progress along our path of rapid development, conservation and health may both suffer if we do not capitalize on linkages and alliances.

Human and animal health are affected by changes in ecosystem health, which include biodiversity loss and climate change. It is difficult to quantify the net impact of biodiversity loss on human health and well-being, but because biodiversity is necessary for functioning ecosystems, its loss results in decreased nutritional security, medicinal resources, and critical ecosystem-derived goods and services. The World Wide Fund for Nature's (WWF's) Living Planet Report (WWF 2012a) indicates that between 1970 and 2008, biodiversity declined by 30 % (60 % in the Tropics), and this trend seems to be continuing. While the direct consequences of water and food shortages are easily recognized, many impacts of ecosystem degradation on humanity can be difficult to assess due to displacement in time and space. The underappreciation of these fundamental relationships, particularly by policymakers and the public, results in conservation and natural resource management being a low priority (Grifo and Rosenthal 1997). However, we must recognize that our health derives from ecosystem health and we need to value healthy ecosystems for our own sake.

Malaria, a vector-borne disease caused by *Plasmodium* parasites, relies closely on its environment. Within the parasite's complex life cycle, transmission requires appropriate habitat for the mosquito vector, such as standing water, and human activities, such as changing land-use patterns, that bring the host in contact with the vector. In many parts of tropical Asia, vast tracts of primary forests are being razed for rubber and oil palm plantations at an astonishing rate. In addition to the loss of the forests, biodiversity, and associated ecosystem services (Ziegler et al. 2009), land-use changes are likely altering disease incidence as well: rubber plantation workers may be at greater risk for contracting malaria due to increased exposure and vector proliferation (the standing water caught in sap collection cups provide habitat for mosquito larvae). The malaria researcher at the end of the microscope attributes increased disease prevalence to the trees, but in fact the true problem originates with deforestation, the conversion of forests to agricultural monocultures, and the system of rubber production. Ecosystem imbalances are largely unpredictable but seem to favor the dominance of generalist species that often become overabundant hosts or vectors (Molyneux et al. 2008). Given that expanding monoculture rubber plantations are a major threat to native forest ecosystems in parts of the world, we must consider that in this case there can be a solution that satisfies human health as well as conservation objectives. This interface is where malaria researchers, industry, health experts, policymakers, and conservationists need to focus.

A plethora of other indirect and deferred health impacts of environmental change also exist, including those resulting from climate change: increasing sea level, ocean temperatures, and acidity as well as severe weather events. Global climate change and its major driver, the burning of fossil fuels, are altering the ecology of disease by their effects on vectors and hosts and the exacerbation of the intensity and frequency of weather extremes. Global warming drives changes in vector and host distribution, and hence, vector-borne diseases are expected to expand to higher latitudes and altitudes. The increase in weather events such as hurricanes and droughts creates opportunities for the rapid expansion of vector and host numbers and range. When coupled with infrastructural damage and human displacement, these events can have catastrophic and enduring impacts on all sectors.

Predicted shifts in global temperatures and precipitation are anticipated to increase incidence of diseases such as yellow fever, plague, Lyme disease, malaria, and avian influenza (Dell'Amore 2008). Leptospirosis, a waterborne bacterial disease disseminated by rodent urine, is often associated with flooding, and outbreaks followed the severe floods in the wake of Hurricane Mitch in Central America. The abundance of the dengue vector mosquitoes (*Aedes aegypti*) has been shown to increase with warmer temperatures in Thailand, Honduras, and Nicaragua (Molyneux et al. 2008). Cholera, a waterborne bacteria (*Vibrio cholerae*), is generally considered a disease of poor sanitation, but studies have shown that cholera is also influenced by the environment (rainfall, sea surface temperatures), hydrology, and weather patterns (Shah 2011), and these can play a pivotal role in the disease dynamics (Koelle 2009). The effective management of future cholera outbreaks requires collaborations between bacteriologists, human health experts, climate scientists, meteorologists, ecologists, and hydrologists.

The study of climate change is a relatively "new" science, and baseline research to evaluate its impacts on human health and well-being has only just begun. Despite unpredictability and the possibility that distribution changes may not necessarily imply changes in the net range of these diseases (Laferty 2009), the shift in pathogen, vector, or host distributions itself implies exposure of naïve human and animal populations to novel pathogens and the creation of new equilibriums. In addition to changes in disease dynamics, the fluctuations in temperatures, and the associated environmental alterations and interactions, could test the resilience of life on Earth. Climate change challenges the adaptability of human settlements by altering water and food security, affecting shelter availability, generating extreme climatic events, and promoting population migration (Costello et al. 2009). With this in mind, ecosystem services that regulate climate change and protect healthy ecosystems from extreme weather events are integral to "One Health" as well as conservation. Being able to predict climate change effects and subsequent ecological changes will be essential to allow early detection of trends and development of measures to mitigate the effects of these changes on global health.

Often linkages between climate change and health are indiscernible because, besides displacement in time and space, the resulting consequences are biased by global inequities in resource consumption: the people suffering the most severe impacts may not be the primary drivers of environmental degradation or resource exploitation. WWF's Living Planet Report (WWF 2012a) indicates that high-income countries have ecological footprints fivefold greater than that of low-income countries, yet our consumption of natural resources continues to increase: we have now exceeded the Earth's capacity to support our activities. The United States comprises 5 % of the world's population but consumes 25 % of the world's fossil fuel resources (World Watch Institute 2012). It is this disparity that further confounds assessments of linkages between climate change, environmental degradation, biodiversity loss, and human health.

Threats to human health and environmental degradation are often fueled by the same socioeconomic factors and may in turn exacerbate them. Therefore, to focus on only one of these domains will ultimately result in modest and short-lived results. We must recognize these trends and identify their socioeconomic drivers in order to address them in a proactive, pragmatic, and comprehensive manner by intervening at the most effective entry points. Deforestation, rapid agricultural development, water mismanagement, urbanization, and climate change increase the burdens of infectious and noninfectious disease. Measures that threaten biodiversity in order to benefit human health or vice versa are short-sighted, are contradictory, and have the potential to jeopardize both.

In order to maintain healthy people, healthy animals, and healthy ecosystems, there is an imperative need for a collaborative approach that exploits multidisciplinary expertise and resources, while circumventing conflicting measures and policies. This is the key resolution for working towards a sustainable future, where solutions to one problem will not generate yet another, present or future: we cannot discount the interdependence between the health of animals, people, and the environment in global development.

Infectious disease spans the complex animal, human, and environmental interface. While we increasingly recognize the risk of contracting disease from our environment, this epidemiological perspective is limiting and merely identifies unidirectional linkages of disease from human patients to outside sources instead of in a more representative compound model that incorporates fluctuating social, cultural, political, economic, and ecological dynamics. Pathogens do not discriminate, selecting their hosts on the basis of suitability, and human health, while significant to us, is merely one small component of disease dynamics.

Infectious disease is a natural part of all ecosystems; however, anthropogenic pressures on wildlife populations can include and amplify their consequences (Brito et al. 2012). By influencing and possibly altering disease ecology, we not only exacerbate the threat of extinction for some species but also expose the health of humans and animals to the emergence and reemergence of pathogens (Daszak et al. 2000). This interdependence is illustrated by the emergence of the Nipah virus, a lethal zoonotic paramyxovirus that killed over 100 people in an outbreak in Malaysia in the late 1990s (Daszak et al. 2013). The outbreak investigation revealed that the zoonotic pathway of the disease originated from fruit bat droppings that spilled over to humans through the infection of domestic pigs. However, both the reservoir (fruit bats) and the virus were shown to occur historically in the area, and it is likely that they have long coexisted with pig farms. Daszak and colleagues (2013) postulated that two major changes allowed the intensification of this interface upset the balance, allowing the Nipah virus to “spill over” into humans. According to the authors, agricultural intensification—increased pig farming—created a pathway for repeated transmission of the virus from fruits bats to pigs, which could also have been exacerbated by alterations in bat distribution due to forest fires and climatic oscillations. The second condition was the priming effect that the first infections had on the pig populations, allowing the animals to acquire enough immunity to sustain the virus within the population long enough to transmit it to humans, instead of just resulting in massive pig mortalities. This outbreak clearly demonstrates the consequences of toppling the fragile equilibrium between the health of ecosystems, animals, and humans.

The reality is that the health profession, human or animal, alone is not equipped to consider all ramifications of decisions made on this scale. Continuing with the malaria example, a physician's training is not intended to estimate the devastating effects deforestation can have on the health and well-being of a community, even if models suggest it can reduce malaria-bearing mosquitoes. The analogy to classical medicine would be that the negative side effects of the treatment (in this case, deforestation) could greatly outweigh the elimination of the targeted sickness (in this case, malaria). Destroying forests to eradicate malaria, the most direct action in this microcosm, is irrational once we look beyond the microscope. This course of action would be as irresponsible as the wanton use of antibiotics. In the light of the emergence of drug-resistant pathogens, for example, multi-drug-resistant *Staphylococcus aureus* or extensively drug-resistant tuberculosis, the medical profession now calls for judicious use of medicines in order to be ever mindful of the global consequences of our choices.

Similarly, the unintentional release of the nonsteroidal anti-inflammatory drug diclofenac into the environment in the 1990s decimated vulture populations in Pakistan and India. In this region, vultures fulfill a vital ecological role scavenging animal and human remains and rapidly divesting of decomposing matter before the onset and proliferation of pathogens. In essence, vultures recycle nutrients back into the ecosystem and reduce disease incidence in the environment, but their role extends into cultural, environmental, and socioeconomic benefits (Markandya et al. 2008), all directly or indirectly contributing to human health and well-being. With

Fig. 18.4 White-rumped vulture (*Gyps bengalensis*), a species that is now critically endangered due to the unintended release of pharmaceuticals (diclofenac) in the environment (Photo: A. Michaud)

up to a 99 % decline in white-rumped vulture (*Gyps bengalensis*) populations across the Indian subcontinent (Prakash et al. 2003), the loss of vultures has potentially caused a rise in other scavengers such as rats and dogs, increased pollution from decomposing carcasses, economic losses resulting from dog bites, and the spread of diseases such as rabies (Fig. 18.4). Thus, the unintentional introduction of a pharmaceutical drug into the environment has triggered events that have profound implications on both biodiversity and health.

The construction of the Three Gorges Dam in China's Yangtze River system provides yet another striking example of the ecological underpinnings of health (Kittinger et al. 2009). While the ultimate purpose of the dam was to improve human well-being through energy production, flood control, and economic stimulus, its construction altered an expanse of the Yangtze riparian system, a biodiversity hotspot. This ecological disturbance likely contributed to extinction of the Yangtze River dolphin (*Lipotes vexillifer*) and jeopardizes the habitat of several threatened terrestrial species, including flagship species such as the golden monkey (*Cercopithecus mitis*). The redistribution of water and the creation of the reservoir may also increase the incidence of waterborne diseases such as schistosomiasis and allow for the accumulation of environmental pollutants such as heavy metals, toxins, and human and animal waste. Expanded habitat for the gastropod vector of schistosomiasis and the increased exposure interface resulting from the displacement of up to four million people could cause this debilitating and infectious zoonotic parasite to proliferate. The Three Gorges Dam massively altered an important waterway and disrupted vital ecosystem under the guise of improving human livelihoods and temporary economic gain, but at what cost? Do the negative and irreversible costs to the environmental and health outweigh its short-lived benefits? Misgivings about the net benefits of the project raised by the conservation sector are not merely about the protection of charismatic species, nor do they intend to deny people the benefits of affordable electricity or flood control. Critics of the dam cite a range of issues from human rights to human health. A systematic and holistic evaluation of the project underscores what we have reiterated in this chapter from the outset: that human health and well-being derives from the health of an entire ecosystem and extreme disruptions of ecosystems jeopardize all of our well-being.

The Three Gorges Dam is considered by many to be a catastrophe, not only from the conservation and environmental perspective. Projects that alter ecosystems raise concerns that span conservation and health, as well as many other related or outwardly disparate disciplines, including the political and cultural sectors. If we continue to work within our professional "bubbles," solutions will remain elusive, fragmented, and difficult to implement in a manner that addresses cross-sectoral issues such as conservation and health. From lessons learned, we should be equally conscientious when recommending treatments, interventions, and solutions for ecological disease processes such as vector-borne and waterborne disease. To approach health and disease management at the ecosystem level, we must see beyond just the end goal and consider the value of the ecosystem as a functional unit from which countless services are derived. This ecological approach to community, population, and global health requires cross-trained professionals, multidisciplinary teams, and broad-spectrum, multilateral cooperation.

18.6 Health in a Globalized World

People, animals, and food move at an unprecedented pace in our globalized world. This happens at a scale that confounds traditional knowledge of disease epidemiology and transmission and thwarts detection, prevention, and mitigation. Pathogens can "hitch" rides on hosts and via airplanes, trains, buses, and boats and can be on the other side of the globe among a naïve population of humans and animals within days, maybe even hours—"biological warp speed," as coined by virus hunter Nathan Wolfe (Wolfe 2009). The increasing density and connectivity of human settlements create the perfect environment for rapid escalation of an outbreak into epidemics and pandemics.

The scale and rate of the global food trade encumbers detection and control of food-borne illnesses, and the once local impacts of salmonella outbreaks, for example, can nowadays assume a totally different scale due to rapid mass distribution. This is evidenced in the periodic Eshcerichia coli (E coli) outbreaks in recent years that were able to spread far and wide prior to their detection and identification (WHO 2011). Globalization also has the power to accelerate and amplify the natural processes of genetic recombination and viral mutations as seen in new, more virulent strains of E. coli (Muniesa et al. 2012) as well as highly pathogenic avian influenza (HPAI) virus.

Moreover, it is important to understand the far-reaching social and economic consequences of diseases in a globalized world. Even diseases that are not fatal to humans or animals can have profound social and economic effects, hampering development and ultimately affecting human health and livelihoods. Foot-and-mouth disease (FMD), an infectious viral disease in wild and domestic cloven-hoofed animals, is endemic in seven out of ten Southeast Asian countries. While mortality is relatively low with this disease, morbidity impacts livestock production and national economics by limiting the growth of the livestock trade through international export. FMD-free countries will not import meat from endemic countries, and the economic losses cascade through the production chain, affecting human livelihoods. The inability of developing countries to advance their livestock production sector limits national economic growth and potential livelihood income, underscoring the direct and indirect linkages between animal and human health and well-being.

Sobering cases of globalization and the spread of disease emerged, and reemerged, with periodic Ebola outbreaks, severe acute respiratory syndrome (SARS), and highly pathogenic avian influenza (HPAI). The very real and rapid spread of these viruses captured the global spotlight and their sensationalization brought the reality of our growing dilemma to the public domain: while information (accurate or otherwise) is transmitted around the globe instantaneously, our preparedness to contend with epidemics and pandemics lags behind. In 2002 and 2003, a coronavirus, SARS, confirmed this reality by spreading from Hong Kong to 37 countries in a matter of weeks and nearly achieving pandemic status. It took the threat of pandemic avian influenza in the mid-2000s to prompt large-scale, multilateral, multidisciplinary projects to predict and prevent emerging pandemic threats—efforts that continue today.

This new globalized reality has led to the need for an updated approach to "One Health" that can complete the medical view with perspectives on social, environmental, and demographic dynamics on a global scale. Addressing health and disease holistically, and looking beyond geographic, political, social and scientific boundaries, will be the only course to keep pace with globalization.

18.7 Bridging the Gap

As with all complex, global issues that transcend geographical, social, cultural, and political boundaries, there is no panacea. However, the innovative "One Health" approach and its arsenal of tools can help bridge the divide between conservation and health and facilitate effective, collaborative strategies. The recurring theme in this chapter emphasizes the need to recognize critical linkages and capitalize on multidisciplinary expertise to strategically address cross-sectoral challenges make pragmatic decisions that consider the long-term ramifications of cross-sectoral tactics.

We can no longer work, isolated, in our respective realms of expertise: we need to address conservation and health as a unified entity, engage appropriate groups, identify synergistic opportunities, develop multidisciplinary strategies, and implement projects that bridge areas of expertise that may appear to be dissimilar. Acknowledging the limitations of our own capabilities is the first hurdle. Few conservationists excel at developing social projects, and likewise, not many wildlife veterinarians have the skills to effectively engage policy makers. While each individual and each field is constrained, there are potentially endless expert partners and innovative synergies.

So it does not end with the malaria expert, the microscope, and the Petri dish. Back at the meeting, the sole conservationist in the room raised her hand and asked: "The trees seem to be responsible for development's short-sightedness: what if we could work with human disease experts and the rubber plantation owners to develop strategies as simple as covering the sap collection cups to reduce mosquito breeding and educate plantation workers on disease prevention?"

References

Beckmann JP, Berger KM, Young JK, Berger J (2008) Wildlife and energy development: pronghorn of the Upper Green River Basin – year 3 summary. Wildlife Conservation society, Bronx. Available at: http://www.wcs.org/Yellowstone

Black R (2005) Bats a 'likely source' of Sars. BBC. Available at: http://news.bbc.co.uk/2/hi/science/nature/4291386.stm

Brito D, Moreira DO, Boutinho BR, Oprea M (2012) Ill nature: disease hotspots as threats to biodiversity. J Nat Conserv 20:72–75

CDC (2005) SARS basic fact sheet. Centers for Disease Control and Prevention. Available at: http://www.cdc.gov/sars/about/fs-SARS.html

Costello A, Abbas M, Allen A, Ball S, Bell S, Bellamy R et al (2009) Managing the health effects of climate change: Lancet and University College London Institute for Global Health Commission. Lancet 373:1693–1733

Daszak P, Cunningham AA, Hyatt AD (2000) Emerging infectious diseases of wildlife – threats to biodiversity and human health. Science 287:443–449

Daszak P, Zambrana-Torrelio C, Bogich TL, Fernandez M, Epstein JH, Murray KA, Hamilton H (2013) Interdisciplinary approaches to understanding disease emergence: the past, present, and future drivers of Nipah virus emergence. Proc Natl Acad Sci 110(Supplement 1):3681–3688

Dell'Amore (2008) http://news.nationalgeographic.com/news/2008/10/081007-climate-diseases.html

Erlich PR, Wilson EO (1991) Biodiversity studies: science and policy. Science 253:758–762

Gómez A, Aguirre AA (2008) Infectious diseases and the illegal wildlife trade. Ann N Y Acad Sci 1149(1):16–19

Gillespie TR, Nunn CL, Leendertz FH (2008) Integrative approaches to the study of primate infectious disease: implications for biodiversity conservation and global health. Yearbook Phys Anthropol 51:53–69

Grifo F, Rosenthal J (eds) (1997) Biodiversity and human health. Island Press, Washington, DC

Kittinger JN, Coontz KM, Yuan Z, Han D, Zhao X, Wilcox BA (2009) Toward holistic evaluation and assessment: linking ecosystems and human well-being for the Three Gorges Dam. EcoHealth 6:601–613

Koelle K (2009) The impact of climate on the disease dynamics of cholera. Clin Microbiol Infect Suppl 1:29–31

Laferty KD (2009) The ecology of climate change and infectious diseases. Ecology 90:888–900

Langlois EV, Campbell K, Prieur-Richard A-H, Karesh WB, Daszak P (2012) Towards a better integration of global health and biodiversity in the new sustainable development goals beyond Rio_+ 20. Ecohealth 9(4):381–385

Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, Field H, Daszak P, Eaton BT, Zhang S, Wang LF (2005) Bats are natural reservoirs of SARS-like coronaviruses. Science 310(5748):676–679

Lyon B (2000) Stress, coping and health: a conceptual overview. In: Rice V (ed) Handbook of stress, coping and health: implications for nursing research, theory, and practice. Sage, Thousand Oaks, pp 3–23

Markandya A, Taylor T, Longo A, Murty MN, Murty S, Dhavala K (2008) Counting the cost of vulture decline—an appraisal of the human health and other benefits of vultures in India. Ecol Econ 67:194–204

Millennium Ecosystem Assessment (2005) Ecosystems and human well-being: health synthesis. United Nations Environment Programme/World Health Organization. Available at: http://www.unep.org/maweb/documents/document.357.aspx.pdf

Molyneux DH, Ostfeld RS, Bernstein A, Chivian E (2008) Ecosystem disturbance, biodiversity loss and human infectious disease. In: Chivian E, Bernstein A (eds) Sustaining life. How human health depends on biodiversity. Oxford University Press, New York, pp 287–324

Muniesa M, Hammerl JA, Hertwig S, Appel B, Brüssow H (2012) Shiga toxin-producing *Escherichia coli* O104:H4: a new challenge for microbiology. Appl Environ Microbiol 78(12):4065–4073. doi:10.1128/AEM.00217-12

Nam VS, Yen NT, Phong TV, Ninh TU, Mai LQ, Lo LV, Nghia LT, Bektas A, Briscombe A, Aaskov JG, Ryan PA, Kay BH (2005) Elimination of dengue by community programs using *Mesocyclops* (Copepoda) against *Aedes aegypti* in Central Vietnam. Am J Trop Med Hyg 72:67–73

Prakash V, Pain DJ, Cunningham AA, Donald PF, Prakash N, Verma A, Gargi R, Sivakumar S, Rahmani AR (2003) Catastrophic collapse of Indian white-backed *Gyps bengalensis* and long-billed *Gyps indicus* vulture populations. Biol Conserv 109:381–390

Shah S (2011) Climate's strong fingerprint in global cholera outbreaks. Yale Environment 360. Available at: http://e360.yale.edu/feature/climates_strong_fingerprint__in_global_cholera_outbreaks/2371/

Staziuso J (2012) Efforts to combat illegal wildlife trade will be stepped up. Says Hillary Clinton. 9 Nov 2012, Huffington Post. Available at: http://www.huffingtonpost.com/2012/11/09/illegal-wildlife-trade-trafficking-us-clinton_n_2100844.html

WHO (2011) Bulletin of the World Health Organization 2011;89:554–555. doi:10.2471/BLT.11.040811

World Watch Institute (2012) The state of consumption today. World Watch Institute. Available at: http://www.worldwatch.org/node/810#3

Wolfe N (2009) Nathan Wolfe: the jungle search for viruses. TED Talks. [video file] Available at: https://www.ted.com/talks/nathan_wolfe_hunts_for_the_next_aids

WWF (2012a) Living planet report 2012. World Wide Fund for Nature. Available at: http://wwf.panda.org/about_our_earth/all_publications/living_planet_report/

WWF (2012b) WWF applauds Hillary Clinton's call to stop wildlife crime. 8 Nov 2012. Available at: http://wwf.panda.org/?206664/WWF-applauds-Hillary-Clintons-call-to-stop-wildlife-crime

Ziegler AD, Fox JM, Xu J (2009) The rubber juggernaut. Science 224:1024–1025. Available at: https://c3.nasa.gov/nex/static/media/publication/Science5-22-09.pdf

Chapter 19
Implementation of the One Health Strategy: Lessons Learnt from Community-Based Natural Resource Programs for Communities' Empowerment and Equity Within an EcoHealth Approach

Aurélie Binot and Serge Morand

Abstract In the sectors of public health, animal health and environment, several international organizations develop policies and initiatives, which are awkward to be implemented at the national and local levels. Local communities are the targets of numerous initiatives and policies particularly in developing countries, mainly through nongovernmental organizations, in the domains of health, rural development and conservation biology. Assessing the interactions between health and biodiversity raises many research questions linked to its implementation regarding the ecological and epidemiological patterns, the associated indicators and stakeholders involved in monitoring at local level. Getting communities involved, beyond passive participation, remains a tricky challenge in the framework of One Health/EcoHealth approaches. It deals with the issue of power sharing and communication gaps between communities and "risk specialists" as well as within communities. This chapter reviews how lessons are learnt from several community-based, participatory and adaptive management initiatives since the nineties could be promoted in the frame of a One Health approach's implementation, in order to improve risk communication and to help turning rhetoric into reality.

A. Binot (✉)
CIRAD-AGIRs, Kastetsart University, Bangkok, Thailand
e-mail: aurelie.binot@cirad.fr

S. Morand
CNRS-CIRAD AGIRs, Centre d'Infectiologie Christophe Mérieux du Laos,
Vientiane, Lao PDR

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3_19

19.1 Introduction: Accepting Complexity

The impact of global changes on the relationships between biodiversity and health is claimed by international organizations and supported by several international programs (Chivian 2003). Particularly, changes affecting biodiversity may increase the risk of zoonotic disease emergence (Morand and Guégan 2010; Morand et al. 2014). In this framework, several initiatives such as the MEA (Millennium Ecosystem Approach 2005) or the One Health Initiative have emphasized the importance of an ecosystem approach, claiming for integrated approaches implementation (www.onehealthinitiative.com, FAO 2008). However, in the sectors of public health, animal health and environment, several international organizations develop policies and initiatives, which are awkward to be implemented at the national and local levels. In this framework, local communities are the targets of numerous initiatives and policies particularly in developing countries, mainly through nongovernmental organizations, in the domains of health, rural development and conservation biology. Since Rio 1992, numerous community-based initiatives have been implemented in the framework of sustainable development. One has to admit that community-based strategies to cope environmental issues were rarely investigated and/or taken into account, local communities being often viewed as passive and not actors of these management processes (Hutton et al. 2005; Igoe and Brockington 2007; Nelson and Agrawal 2008).

Different integrative initiatives were initiated after Rio UN conference merging environment and human well-being within a holistic paradigm emphasizing ecosystem regulation functions and associated services. As an example, the paradigm of Ecosystem Service for disease regulation (ESDR) provides an interesting conceptual framework to understand how biodiversity provides regulation of pathogens and reservoirs or vectors (MEA 2005). But this pathway for assessing the interactions between health and biodiversity raises many research questions linked to its implementation regarding the ecological and epidemiological patterns and the associated indicators and stakeholders involved in monitoring at local level.

First, a controversy remains within scientific communities about the ambiguity of this conceptual framework merging biodiversity and health interactions. As biodiversity erosion and environmental changes clearly increase the risk of zoonotic disease emergences (Blasdell et al. 2011), the diversity of the living, including pathogens, may also be perceived as a source of potential “danger”. Nevertheless, since 2005 the paradigm of ecosystem services frames for scientists, institutions and civil society the role that biodiversity plays in terms of disease regulation. However, we still know few about these regulation mechanisms and functions in the field of zoonotic diseases (Jones et al. 2008). If these functions have already been studied and partly understood in the framework of agriculture pests, few are currently known about the regulation mechanisms that biodiversity provides for animal and human health protection.

Then, one has to fully accept how intrinsically complex this type of research is. It calls for multi- and interdisciplinary methods and topics. On one hand, understanding biodiversity and ecological dynamics refers to complex system modelling.

On the other hand, health is also in itself a complex issue merging biomedical, social, cultural and psychological factors. A fortiori, interlacing biodiversity and health issues by understanding their interactions will lead to the modelling and designing of joined complex systems. If ecosystem approach to human health such as ecosystem services or the EcoHealth initiative can provide an interesting conceptual framework, one has to be aware how difficult it is to put them in practice.

Last, ecosystem approaches to health also call for multilevel analysis, as addressing global stakes can only be achieved by crosscutting several local and regional issues. This last point adds complexity in the modelling and analysis approaches involving change of scale and taking into account geographical specificities. Beyond spatial and geographical scales overlapping, one has to add social networks overlapping and crosscutting at different levels, again from local to international stages. Perception, definition and understanding of "ecosystem services" to human and animal health would vary a lot regarding different stakeholders. This perception will be influenced by the dependence of stakeholders to commodity chains involving natural resources (including livestock and agricultural products), by dependence on market balance and by understanding what human well-being is. However, this complex understanding is necessary to design appropriate indicators for the monitoring of ecosystem services to human and animal health.

Denying this complexity and looking for "recipes" and standard guidelines would lead to the same pitfalls community-based approach to natural resource management and integrated conservation have undergone since the nineties. Despite their huge potential in terms of integrative complex socio-ecosystems management, intersectorial and participatory approaches to natural resource management clearly failed their implementation in developing countries. They revealed huge gaps between rhetoric and practices. Integrative participative conceptual frameworks did not succeed in avoiding sectorial top-down projects implementation.

19.2 Toward an Integrated Framework for Risk Assessment and Management?

This brings us to other questions: How are the global changes and their impacts perceived by different types of stakeholders, from international decision makers to natural resources users, and scientists? How do these various actors understand the patterns of zoonotic disease emergence and the interactions between environment and health? How does it interfere with cultural background, scientific disciplines, or traditional knowledge? In short, what are the representations that could provide a basis for Ecosystem Services and Disease Regulation's (ESDR) implementation and monitoring in different cultural and socio-cognitive contexts? How different social groups perceive the notion of "zoonotic disease", merging animal and human health? How do they understand the risks at play within environmental changes, their causes and their impacts?

Assessing and monitoring health risks, from the “experts’” and scientists’ point of view, consists in the challenge of integrating disciplines from health, social sciences and biodiversity fields. Several experiments and applied research projects, for example, in the field of surveillance programs, have implemented such integrative approaches, merging together ecological and epidemiological data in multidisciplinary information systems (Witt et al. 2011). Geographic information systems involving remote sensing and earth observation merge epidemiology, ecology, modelling of ecological and climate events into surveillance programs, highlighting diseases’ vector-habitat expansion, animal and human population dynamics, land use changes, public health infrastructures, etc. This is clearly a first step toward a One Health practical application, by integrating heterogeneous data into multidisciplinary programs.

But beyond “experts-based knowledge”, the integration of communities’ risk perceptions and knowledge could also lead to innovative models for zoonotic risk-coping strategies, innovative risk governance and innovative communication schemes. This very challenging process could help to build more bridges between risk managers and the users of natural resources, who are also the populations at risk. It could also provide new pathways in the framework of risk analysis, in order to improve risk communication between different interest groups. Indeed, communication remains an issue roughly neglected by risk assessors and risk managers (Roger 2012).

19.3 Innovative Participatory Approaches for Risk Mapping

Participatory approaches, like participatory epidemiology or community-based natural resource management (CBNRM), have an important potential in terms of data extraction with different interest groups. They could be used in order to collect users’ knowledge about environmental and health risks, at the scale of a specific territory. They can also lead to collecting data to highlight the behaviour’s rules when people are facing risks, taking into account socioeconomic or sociopolitical stakes at play.

Then, through participatory risk mapping or experimental economics experiments, innovative geographic information systems could be developed, including information layers defined by local communities. This would be really innovative in so much as it could also bring into the geographic information systems data regarding the natural landscape representation and management. The spatial definition of what ecologists used to call a “landscape” should be investigated regarding the functional definition of a landscape making sense for communities involved. This could be very helpful for the definition of a functional scale for ecosystem services regulation diseases’ implementation at the level of a social territory.

This participatory approach to risk mapping raises different research questions, leading to a “new” socio-environmental model for risk assessment: What are the patterns of zoonotic disease emergence and the interaction between environment and health at local level? How does it interfere with local practices and cultural background in terms of natural resource management, health perception and cultural landscapes? Does the spatial definition of what ecologists use to call "landscape" fits with the functional definition of a landscape at community level in southern countries context? How indicators for monitoring the disease regulation functions according to experts' knowledge could fit communities' knowledge? How are risks perceived at the landscape level? To which local knowledge does it refer (e.g. within Buddhism or animism cultural background to understand the causes of diseases)? Such approach to risk mapping could help in developing innovative geographic information systems including layers that make sense for communities: risk factors, risk manageability, socio-spatial stakes at play, environmental patterns, socioeconomic resources, perceived seasonality and periodicity of risk emergence.

Beyond the potential in terms of managing risks, designing such information systems constitutes a collaborative process of representation sharing involving heterogeneous stakeholders.

19.4 Lessons Learnt from the 1990s: "Community-Based Natural Resource Management" (CBNRM) Programs for Innovative Decision-Making Process Within an EcoHealth Approach

Regarding risk governance and management involving various stakeholders, we really need, through social sciences inputs, to better understand what are the social and political spaces and networks where effective decision is taken by social actors, in order, for example, to open the negotiating table to the communities' functional political leaders and to improve communication pathways between them and the institutional and technical risk managers. To that purpose, the huge experience and lessons learnt from CBNRM projects could be valorized regarding empowerment and sociopolitical tensions management, for example, knowing how risk assessment and management can be a sensitive issue. We now have more than 20 years of experiencing community-based approach to natural resource management, as a strategy for rural development, local empowerment and conservation. Led by new ideas about the merits of decentralized, collective resource governance regimes and creative field experiments (such as Zimbabwe's CAMPFIRE), these community-based approaches evolved in a wide range of ecological, political and social contexts, mainly across Africa. These community-based programs aimed poverty alleviation, economic development and nature conservation objectives.

Community-based natural resource management (CBNRM) models work to strengthen locally accountable institutions for natural resource use and management, enabling local groups of people to make better decisions about the use of land and resources. It involves the transfer of authority over natural resources to local communities, including potentially valuable resources such as wildlife and timber.

Thus, CBNRM programs are mainly dealing with major institutional reforms and fundamental changes in power for land tenure devolution, elite's role, communities' empowerment, economic development and environmental governance. In all instances CBNRM involves some degree of co-management of resources between central authorities, local government and local communities, which share rights and responsibilities through diverse institutional arrangements. The various forms of CBNRM and their many locally specific adaptations have greatly diversified approaches to natural resource governance with heterogeneous stakeholders (Binot et al. 2009). As underlined by IIED authors, "Through its potential to develop more sustainable natural resource governance regimes, CBNRM is an important strategy for pursuing the goals of various multilateral environmental treaties, such as the Convention on Biological Diversity (CBD), the Convention to Combat Desertification (UNCCD) and the UN Framework Convention on Climate Change (UNFCCC)" (Roe et al. 2009). Reviewing innumerable CBNRM case studies, this IIED review has emphasized how focus needs "to be placed on supporting CBNRM in a 'demand-driven' fashion, rather than conventional centralized project models that attempt to implement CBNRM through central government agencies. Emphasis should be placed on supporting local communities and civic organizations by building their capacity to engage in collective action that builds stronger political constituencies for resource governance reforms" (Roe et al. 2009).

Looking forward on more than 20 years of CBNRM projects, one should also note how participatory monitoring approaches involving appropriate indicators are needed. Despite the vast amount of CBNRM projects, quantitative and qualitative data on their social, economic and environmental impacts of community-based projects are lacking. Part of the problem lies with poor or incomplete design and a lack of understanding by project implementers of what it is that really should be measured. As underlined by Roe et al. (2009), "(…) part of the solution lies with community engagement in monitoring project successes (and failures). (…) subsequent monitoring is empowering for communities and instructive for project implementers. Properly designed and structured projects will provide for quantitative and qualitative self-assessments of project impacts by communities themselves long after the project has departed".

It is well known that One Health initiative has to face the huge challenge of going beyond sector-based policies and top-down approach (Roger 2012). Lessons learnt from community-based environmental governance schemes could be valorized toward "new" governance models for risk management. Indeed, within the ecosystem approaches to human health considering humans as integral parts of ecosystems (cf. EcoHealth), "local-level-involvement" appears as one of the key objectives to be achieved.

Since its first steps in 1996, EcoHealth approaches have strongly supported transdisciplinarity, systemic approach, multi-stakeholder participation, equity, environmental sustainability and evidence for community-based interventions (Charron 2012). CBNRM projects have experienced institutional design that creates effective local incentives for collective action under communal tenure arrangements. This governance framework could be explored to risk management strategies at the scale of a natural landscape within an EcoHealth approach, for example. As underlined by Charron (2012), "The ultimate objective of Ecohealth research and practice is to develop environmentally sustainable, community-based interventions to improve the health of affected communities. Much success has resulted from the incorporation of community transformation and empowerment as key project objectives".

On the same line, a new approach, called community-based adaptation (CBA), aims at helping poor people at greatest risk from climate change to adapt to its impacts. Indeed, climate change's impacts are disproportionately affecting poor communities, and it is vital that these communities are helped to adapt to climate change and cope with any future risks related to climate change. Providing international aid to poor countries does not guarantee reaching the poor and most vulnerable communities. In order to achieve this challenging goal, community-based adaptation (CBA) constitutes new community-based development activities, practices, research and policies (as developed by Dr Saleemul Huq, senior IIED fellow, IISD 2007). CBA really seems to be in line with both CBNRM and EcoHealth, as it proposes to merge natural and social sciences and participatory approaches in order to identify and support the most vulnerable communities to climate change. "These are generally very poor, depend on natural resources and occupy areas already prone to shocks such as floods or droughts. Once a community's vulnerability has been established, using the best available science on climate change impacts, the process of engagement with the communities can begin".

As for CBNRM projects, challenges remain to the implementation of an EcoHealth approach and no recipes can be offered. Functional and equitable partnerships have to be built taking into account the complexity of the processes. As for CBNRM projects, EcoHealth emphasizes the involvement of communities as a key parameter for success, before government's role. As for CBNRM projects, EcoHealth stresses social equity and promotes strategies for community participation and empowerment, respectively, for the solution of environmental and health problems.

19.5 Sharing Knowledge and Power Within Risk Governance

Getting communities involved, beyond passive participation, remains a tricky challenge in the framework of One Health/EcoHealth approaches. It deals with the issue of power sharing and communication gaps between communities and "risk specialists" as well as within communities.

Considering risk management, the heterogeneity of perceptions and social representations of risks at play has to be taken into account. Recently, the Food and

Agriculture Organization (FAO) of the United Nations underlined the fact that classical risk-based approach to animal disease risk management has to better take into consideration the knowledge, perceptions, behaviour and reactions of people (FAO 2011). As such, FAO experts recommend the implementation of strategies that are both "risk based" and "people centred". These new approaches emphasize the importance of understanding human behaviour in value chains, focusing on behaviours that can either moderate or exacerbate risk. They take into account people's perception of risks, drivers of behaviour (economics, knowledge and understanding, peer pressure, morality), in an effort to determine how to influence behaviour. "Different groups may have very different perceptions of a particular risk and very different ideas of the assessed risk. Both of these issues require good risk communication to achieve an effective risk management policy. (…) In this respect, it becomes important to fully comprehend the roles and motivations of the different people involved in the value chain" (FAO 2011).

Some participatory modelling experiments have proposed very interesting pathways in order to share co-designed representation of dynamic socio-ecosystems, integrating various actors' perceptions. This approach, even if time consuming, provides a detailed analytical framework for the interactions and stakes at play between various stakeholders, even when it raises conflicts. It aims at revealing the diversity of points of view. It provides a conceptual model of socio-ecological interactions at work in a given system, involving various stakeholders.

These participatory methodologies, such as ComMod (Etienne et al. 2011), involve different types of actors of a given sociobiological system. It enables to consider, with the same level of importance, the different types of social and environmental knowledge, brought by the different stakeholders (Bousquet et al. 2011). They build together one or several conceptual models, which can, if relevant, be implemented on a computer and are used to design a role-playing game involving the stakeholders. Thus, the resulting co-designed model is used as the instance of the shared representation in game sessions where the different actors play their own role or interchange their role with each other. Here, the models are not intended to forecast. They are the result of a participative process for a shared representation between the stakeholders of the system of interest (Bousquet and Trébuil 2005). The main idea is that companion modelling, by rendering explicit known and hidden processes, as well as actor strategies, can be used by stakeholders themselves to deal with their own problems for identifying commonly accepted solutions and consultation pathways. The role of scientists here is mainly to frame and backstop the modelling process and to implement the model into game sessions.

As ComMod approach has been successfully applied for natural resource management in different multi-stakeholder contexts (Dumrongrojwatthana and Trébuil 2011), its application to ecosystem health approach seems to be very relevant and should be explored in order to promote participatory and consensual risk governance pathways.

19.6 Lessons Learnt from Applied Ecosystem Management Projects

Ecosystem approach to health deals with the issue of both environmental risks, on one hand, and health risks, on the other hand. Beyond research experiences, lessons should also clearly been learnt from applied goal-driven frameworks such as ecosystem management approaches, applied by Man and the Biosphere (MAB) projects in the 90s (Harwell et al. 1999). Ecosystem management integrates scientific understanding of ecological relationships within societal contexts. It emphasizes the need for a shared vision for ecosystem use and development, including access to decision making and various perceptions of "geographical" development. It promotes the positive coupling of environmental and economic security within an adaptive management process, sustainable at landscape level. Thus, ecosystem management is fully enrolled into an environmental risk characterization process exploring outcomes of various scenarios, beyond natural resource management issues. Then, identifying the "at-risk systems" and its social actors and populations is the key issue in terms of problem formulation within an ecosystem management process (Stern and Fineberg 1996). To this issue, a huge range of different data is needed, from ecological to political, through social and economics.

Even if ecosystem management aims at environment protection, it clearly calls, in its application, for interdisciplinary risk characterization aiming at reducing uncertainties within an adaptive decision-making process. In its philosophy, adaptive ecosystem management potentially fits an EcoHealth approach.

19.7 Conclusion

Lessons learnt from several community-based, participatory and adaptive management initiatives since the 90s could be promoted in the frame of a One Health approach's implementation, in order to improve risk communication and to help turning rhetoric into reality.

Regarding how difficult it is to deal with these multilevel, multi-stakeholder and multidisciplinary issues, we, as researchers, should accept that the improvement of risk communication pathways within a One Health/EcoHealth approach constitutes a key research question and calls for the co-designing of shared socio-ecosystem representation. This could lead to the characterization of functional socio-ecosystems, to the definition of relevant scale for managing environmental health risks, allowing monitoring approaches that involve local communities.

This type of approach raises research perspectives at the edge of ecology, epidemiology and social sciences for a better management of zoonotic risks involving diverse stakeholders.

Multilevel (planet/village) and multi-stakeholder diagnostics are then necessary to identify relevant social networks, opening new political spaces. Improving communication between stakeholders at each level, through participatory approaches, implies to share knowledge and perceptions between researchers, decision makers, targeted communities, natural landscape users, etc. Knowing that, we should definitely accept (and force decision makers and donors to accept) that integrative risk management is a long-term "learning process," iterative and time consuming.

References

Binot A, Blomley T, Coad L, Nelson F, Roe D, Sandbrook C (2009) Community involvement in natural resources management in Africa – regional overviews. In: Roe D, Nelson F, Sandbrook C (eds) Community management of natural resources in Africa: impacts, experiences and future directions, vol 18, 13th edn, Natural resource issues. IIED, London, p 54

Blasdell KR, Morand S, Chaval Y, Herbreteau V, Douangboupha B, Jittapalapong S, Cosson J-F, Buchy P (2011) Hantaviruses and the dilution effect in Southeast Asia. BMC Proc 5(Suppl 1):P53

Bousquet F, Trébuil G (2005) Training on multi-agent systems, social sciences, and integrated natural resource management: lessons from an Inter-University Project in Thailand. In: Bousquet F, Trébuil G, Hardy B (eds) Companion modelling and multi-agent system for integrated natural resource management in Asia, 309th edn. IRRI Publications, Los Banos, p 326

Bousquet F, Etienne M, D'Aquino P (2011) Introduction. In: Etienne M (ed) Companion modelling. A participatory approach to support sustainable development, 11th edn. Quæ, Versailles, p 20

Charron DF (2012) Ecohealth research in practice: innovative applications of and ecosystems approach to health, insight and innovation in development. Springer/International Development Research Centre, New York/Ottawa

Chivian E (2003) Biodiversity: its importance to human health. Harvard Med School, Boston

Dumrongrojwatthana P, Trébuil G (2011) Northern Thailand case: gaming and simulation for co-learning and collective action; companion modelling for collaborative landscape management between herders and foresters. In: van Paassen A, van den Berg J, Steinggrover E, Werkman R, Pedroli B (eds) Knowledge in action: the search for collaborative research for sustainable landscape development, vol 11, 191st edn, Mansholt publication series. Wageningen Academic Publishers, Wageningen, p 219

Etienne M, Bousquet F, Le Page C, Trébuil G (2011) Transferring the ComMod approach. In: Etienne M (ed) Companion modelling. A participatory approach to support sustainable development, 255th edn. Quæ, Versailles, p 270

FAO (2011) A value chain approach to animal diseases risk management – technical foundations and practical framework for field application, vol 4, Animal production and health guidelines. FAO, Rome

FAO, OIE, WHO, UN, UNICEF, WB (2008) Contributing to one world, one health, a strategic framework for reducing risks of infectious diseases at the animal–human–ecosystems interface, 14 October. ftp://ftp.fao.org/docrep/fao/011/aj137e/aj137e00.pdf

Harwell MA, Myers V, Young T, Bartuska A, Gassman N, Gentile JH, Harwell CC, Appelbaum S, Barko J, Causey B, Johnson C, McLean A, Smola R, Templet P, Tosini S (1999) A framework for an ecosystem integrity report card. BioScience 49(543):556

Hutton J, Adams W, Murombedzi J (2005) Back to the barriers? Changing narratives in biodiversity conservation. Forum Dev Stud 32(341):370

Igoe J, Brockington D (2007) Neoliberal conservation: a brief introduction. Conserv Soci 5(4):432–449

IISD reporting service (2007) Community based adaptation to climate change bulletin. A summary of the second international workshop on community-based adaptation to climate change, 135(1). International Institute for Sustainable Development (IISD), in collaboration with IIED. Sunday, 4 Mar 2007. http://www.iisd.ca/ymb/sdban/

Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, Daszak P (2008) Global trends in emerging infectious diseases. Nature 451:990–993

Millennium Ecosystem Assessment (MA) (2005) Ecosystems and human well-being: current state and trends. Island Press, Washington, DC

Morand S, Guégan JF (2010) How the biodiversity sciences may aid biological tools and ecological engineering to assess the impact of climatic changes. Rev Sci Tech 27(2):355–366, Review

Morand S, Moutou F, Richomme C (eds) (2014) Faune Sauvage, Biodiversité et Santé, Quels Défis ? Editions Quae, Paris, 192p

Nelson F, Agrawal A (2008) Patronage or participation? Community-based natural resource management reform in sub-Saharan Africa. Development and Change 39:557–585

Roe D, Nelson F, Sandbrook C (eds) (2009) Community management of land and resources in Africa: impacts and experiences, vol 18, Natural Resource Issues. IIED, London, p 160

Roger F (2012) Control of zoonotic diseases in Africa and Asia. The contribution of research to One Health. Perspective Policy Brief No. 18, CIRAD, p 4

Stern PC, Fineberg HV (eds) (1996) Understanding risks. Informing decisions in a democratic society. National research Council of the National Academies, The nationala Academies Press, Washington, DC

Witt CJ, Allen LR, Masuoka PM, Foley DH, Buczak AL, Musila LA, Richardson JH, Colacicco-Mayhugh MG, Rueda LM, Klein TA, Anyamba A, Small J, Pavlin JA, Fukuda MM, Gaydos J, Russell KL (2011) The AFHSC-division of GEIS operations predictive surveillance program: a multidisciplinary approach for the early detection and response to disease outbreaks. BMC Pub Health 11:S10

Index

© Springer Science+Business Media Singapore 2015

S. Morand et al. (eds.), *Socio-Ecological Dimensions of Infectious Diseases in Southeast Asia*, DOI 10.1007/978-981-287-527-3