Wageningen UR Frontis Series

Environmental Change and Malaria Risk

Global and Local Implications

Edited by
Willem Takken, Pim Martens,
and Robert J. Bogers

Springer

ENVIRONMENTAL CHANGE AND MALARIA RISK

Wageningen UR Frontis Series

VOLUME 9

Series editor:

R.J. Bogers
Frontis – Wageningen International Nucleus for Strategic Expertise,
Wageningen University and Research Centre, Wageningen, The Netherlands

Online version at http://www.wur.nl/frontis

ENVIRONMENTAL CHANGE AND MALARIA RISK

Global and Local Implications

Edited by

WILLEM TAKKEN

Laboratory of Entomology,
Wageningen University and Research Centre,
Wageningen, The Netherlands

PIM MARTENS

International Centre for Integrative Studies,
Maastricht University, Maastricht,
The Netherlands

and

ROBERT J. BOGERS

Frontis-Wageningen International Nucleus for Strategic Expertise,
Wageningen University and Research Centre,
Wageningen, The Netherlands

Springer

A C.I.P. Catalogue record for this book is available from the Library of Congress.

ISBN-10 1-4020-3928-X (PB)
ISBN-13 978-1-4020-3928-7 (PB)
ISBN-10 1-4020-3927-1 (HB)
ISBN-13 978-1-4020-3927-0 (HB)

Published by Springer,
P.O. Box 17, 3300 AA Dordrecht, The Netherlands.

www.springer.com

Printed on acid-free paper

Printed in the Netherlands.

Contents

Preface

The workshop "Environmental Change and Malaria Risk: Global and Local Implications" was held to conclude a 5-year collaborative research project on environmental change and malaria risk, with field research in Kenya and Brazil. It was fitting that such a large group of specialists was able to attend the workshop and contribute with a chapter in which the predicted environmental changes were viewed from different angles. We would like to thank the Netherlands Foundation for the Advancement of Tropical Research (WOTRO) and the National Programme for Research on Climate Change and Air Quality (NOP) for having funded our work so generously. Wageningen UR – Frontis is thanked for having arranged the workshop and for its financial contribution. We would especially like to thank Petra van Boetzelaer for having assisted with the logistics of the workshop, and Paulien van Vredendaal for having spent many hours in the type editing of the chapters, making publication of this book possible.

The editors,

Willem Takken
Pim Martens
Rob Bogers

Wageningen, March 2005

Colour pages

Chapter 2.
Pim Martens and Chris Thomas; Figures 2 and 3

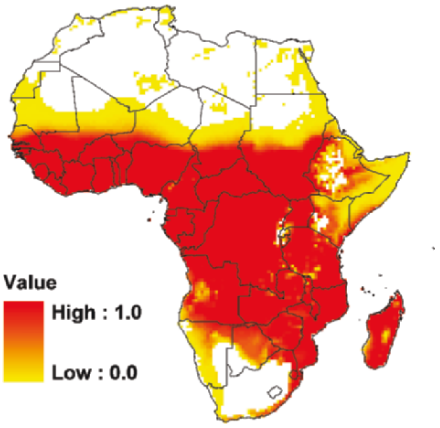


Figure 2. MARA/ARMA index of climatic suitability for *P. falciparum* transmission in four consecutive months

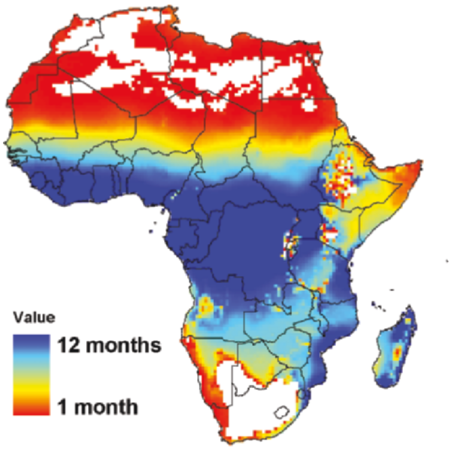


Figure 3. Number of consecutive months with a MARA/ARMA index of climatic suitability for *P. falciparum* transmission of p Σ0.9 in each month

Chapter 5.
M.B. Hoshen and A.P. Morse; Figures 5 and 7

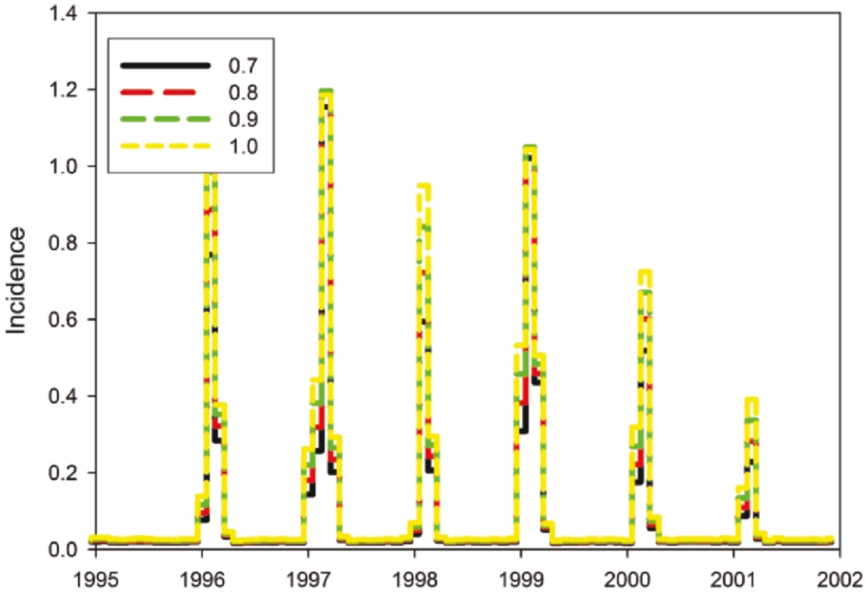


Figure 5. Inoculation efficiency as a determinant of incidence, for 17.5°S 25.0°E using ERA-40 weather. Simulated incidence patterns for 1995-2001 for varied values of α

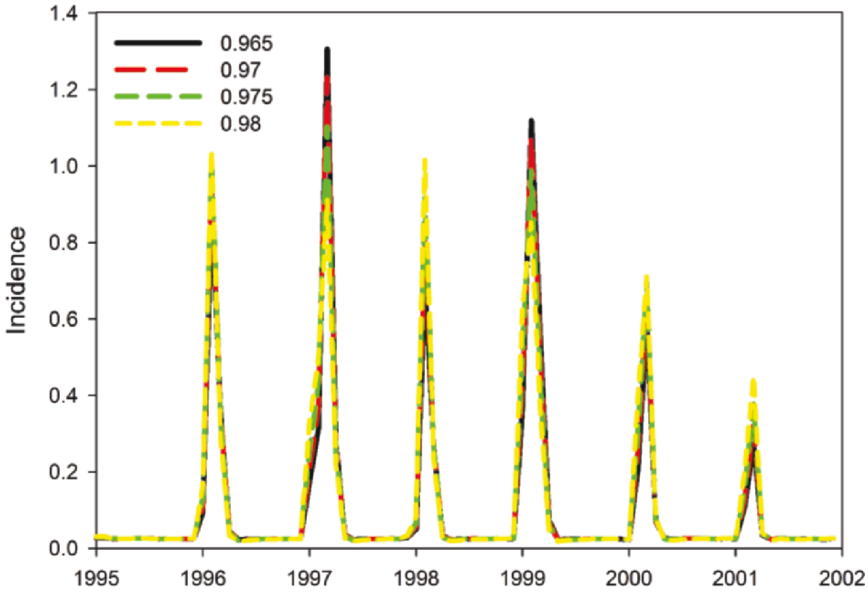


Figure 7. Sensitivity of model to human parasite clearance. Simulated incidence, for 17.5°S 25.0°E using ERA-40 weather. Simulated incidence patterns for 1987-2001 for varied values of human clearance

Chapter 8.

Michael van Lieshout; Figures 1, 3, 4, 5, 7, 11 and 14

Figure 1. Map of the study area, Kisumu region, Kenya (indicated by the square)

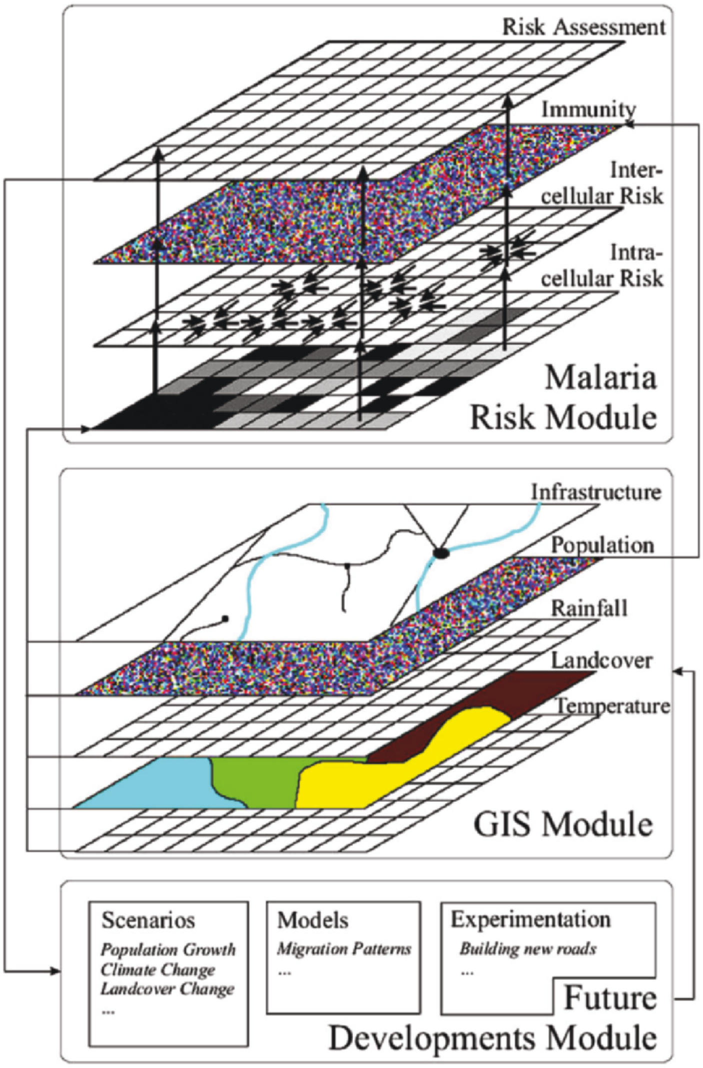


Figure 3. Lay-out of LEMRA model (De Vries 2000)

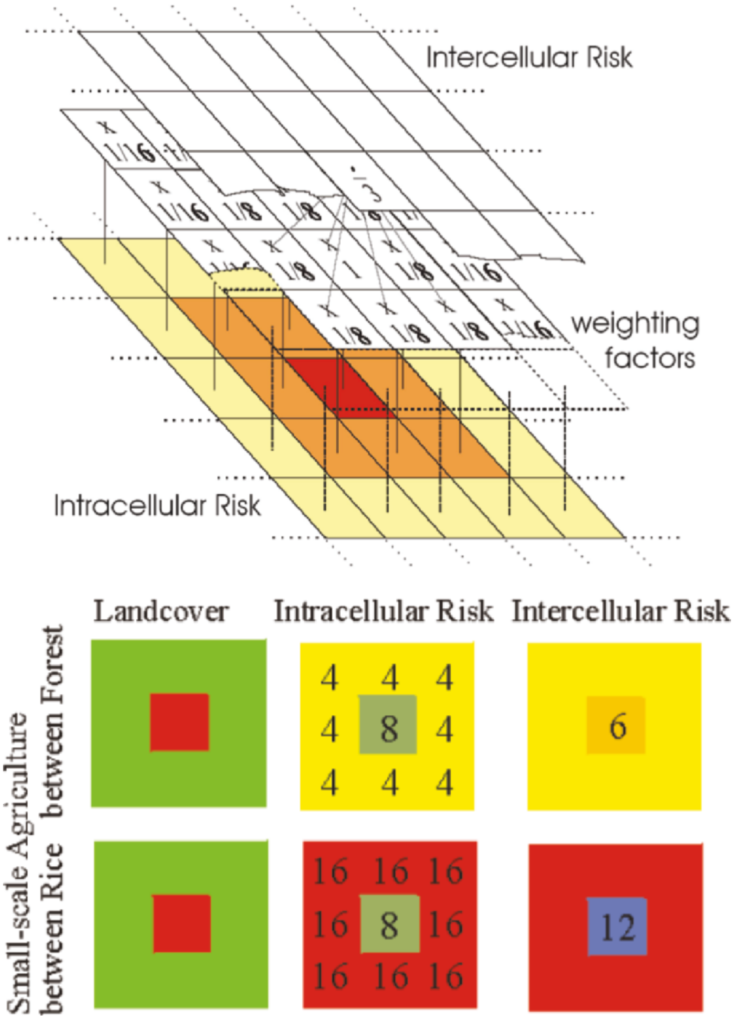
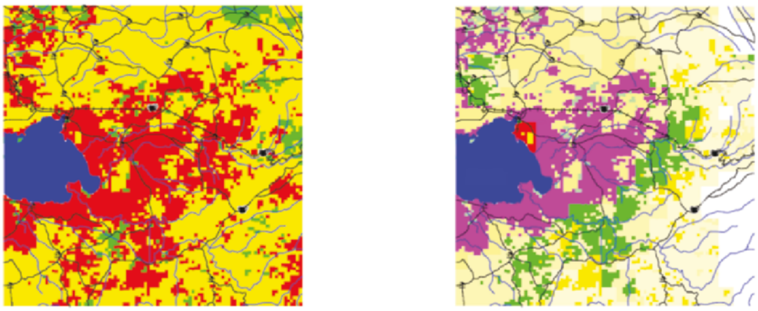


Figure 4. Intra- and intercellular malaria risk



(a) land cover only

(b) land cover + temperature

(c) land cover + temperature + precipitation

(d) land cover + temperature+ precipitation + infrastructure

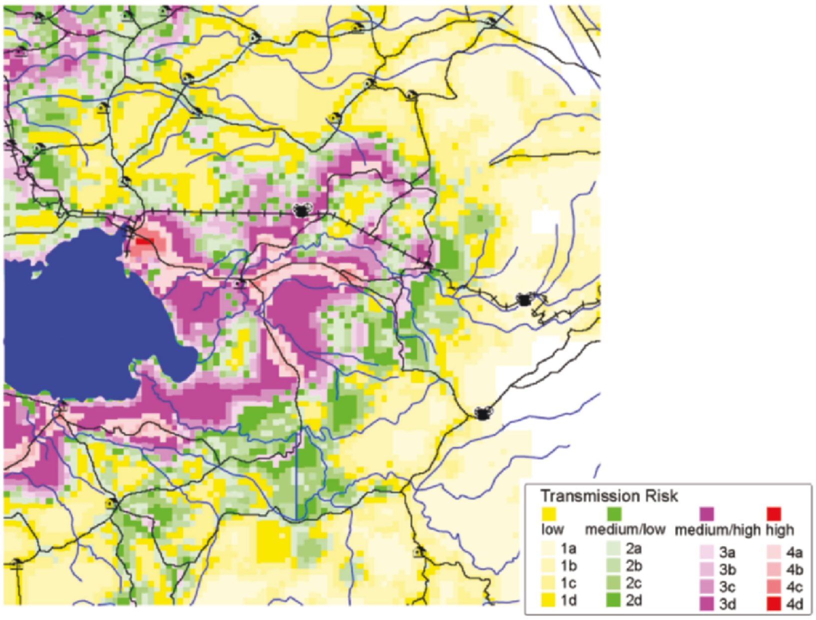


Figure 5. Modelling malaria risk in relation to environmental and land-use parameters

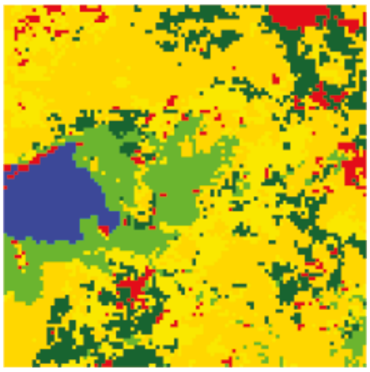


Figure 7. Land cover in Kisumu region

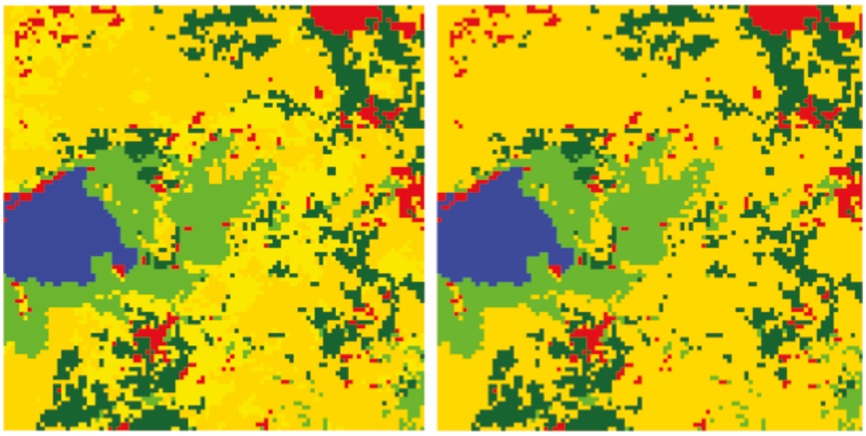


Figure 11. Illustration of land-use change (left: current; right: Flying Geese 2020)

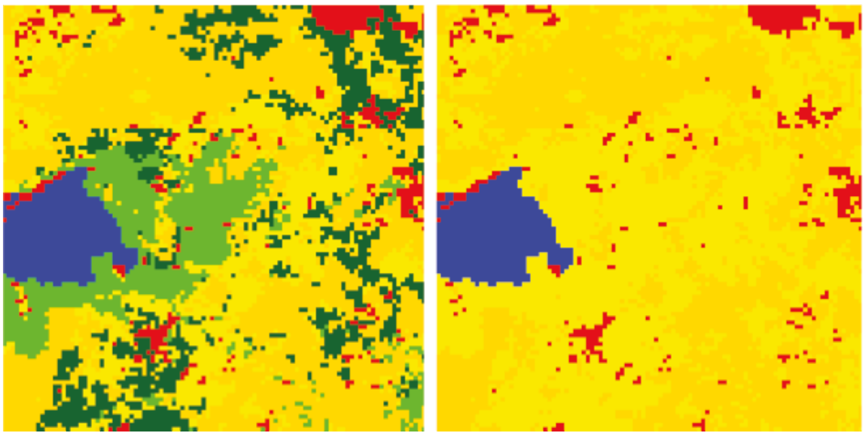


Figure 14. Illustration of land use change (left: current; right: El Niño 2020)

Chapter 10.
Paulo de Tarso R. Vilarinhos; Figures 1, 2 and 4

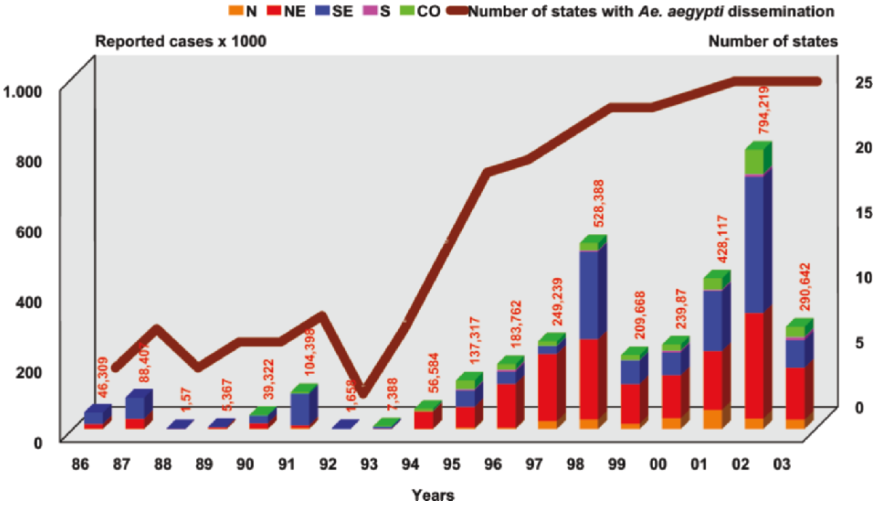
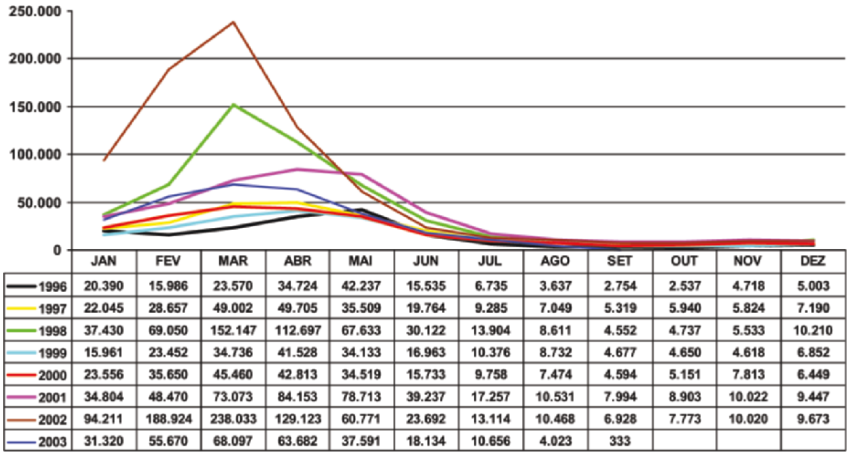


Figure 1. Number of dengue cases reported per geographic region of Brazil, 1986-2003 (Source: SVS)



	JAN	FEV	MAR	ABR	MAI	JUN	JUL	AGO	SET	OUT	NOV	DEZ
1996	20.390	15.986	23.570	34.724	42.237	15.535	6.735	3.637	2.754	2.537	4.718	5.003
1997	22.045	28.657	49.002	49.705	35.509	19.764	9.285	7.049	5.319	5.940	5.824	7.190
1998	37.430	69.050	152.147	112.697	67.633	30.122	13.904	8.611	4.552	4.737	5.533	10.210
1999	15.961	23.452	34.736	41.528	34.133	16.963	10.376	8.732	4.677	4.650	4.618	6.852
2000	23.556	35.650	45.460	42.813	34.519	15.733	9.758	7.474	4.594	5.151	7.813	6.449
2001	34.804	48.470	73.073	84.153	78.713	39.237	17.257	10.531	7.994	8.903	10.022	9.447
2002	94.211	188.924	238.033	129.123	60.771	23.692	13.114	10.468	6.928	7.773	10.020	9.673
2003	31.320	55.670	68.097	63.682	37.591	18.134	10.656	4.023	333			

Figure 2. Dengue cases reported per month in Brazil, 1996-2003 (Source: SVS)

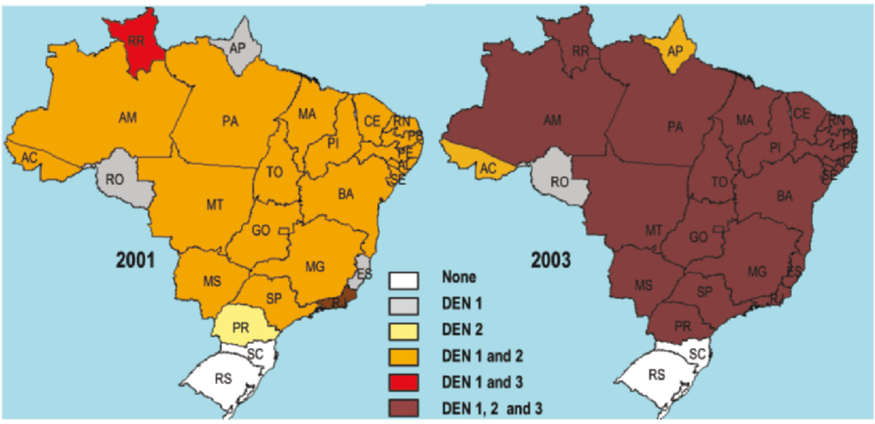


Figure 4. Dengue serotypes circulating in Brazil, 2001-2003 (Source: SVS)

Chapter 11.

Willem Takken, Paulo de Tarso R. Vilarinhos, Petra Schneider and Fatima dos Santos; Figures 1 and 5

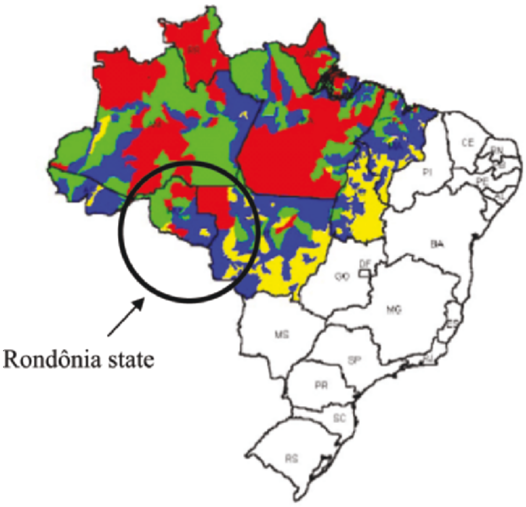


Figure 1. Map of Brazil and malaria-risk areas. Blue: low risk; green: medium risk; red: high risk (source: PNCM 2003)

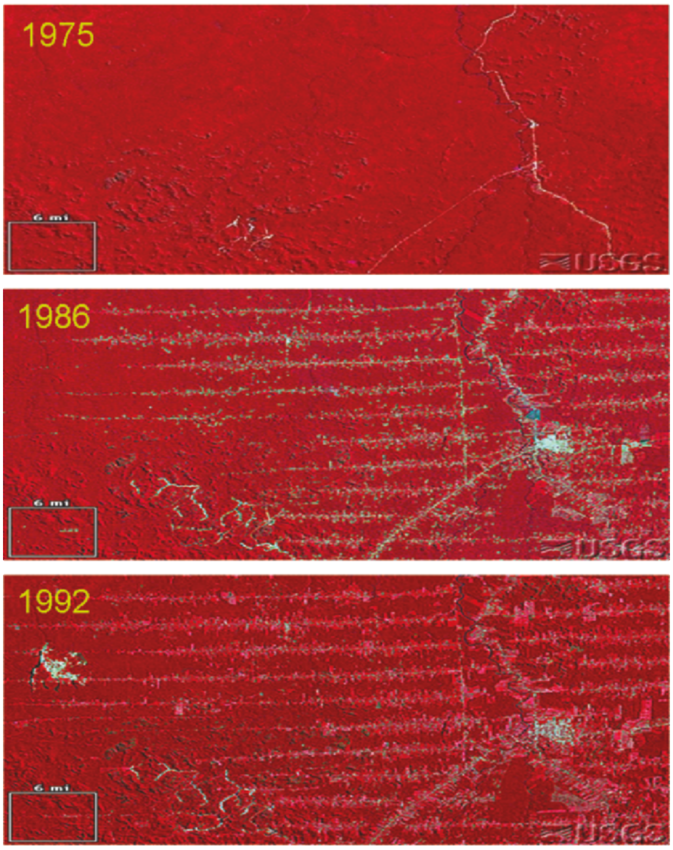


Figure 5. Satellite images of Rondônia, Brazil, showing the changes in land use following deforestation. The town on the right-hand side is Arequimes, the centre of the timber industry (source: Skole and Tucker 1993)

Chapter 12.

B.V. Purse, P.S. Mellor and M. Baylis; Figures 1, 2, 3 and 4

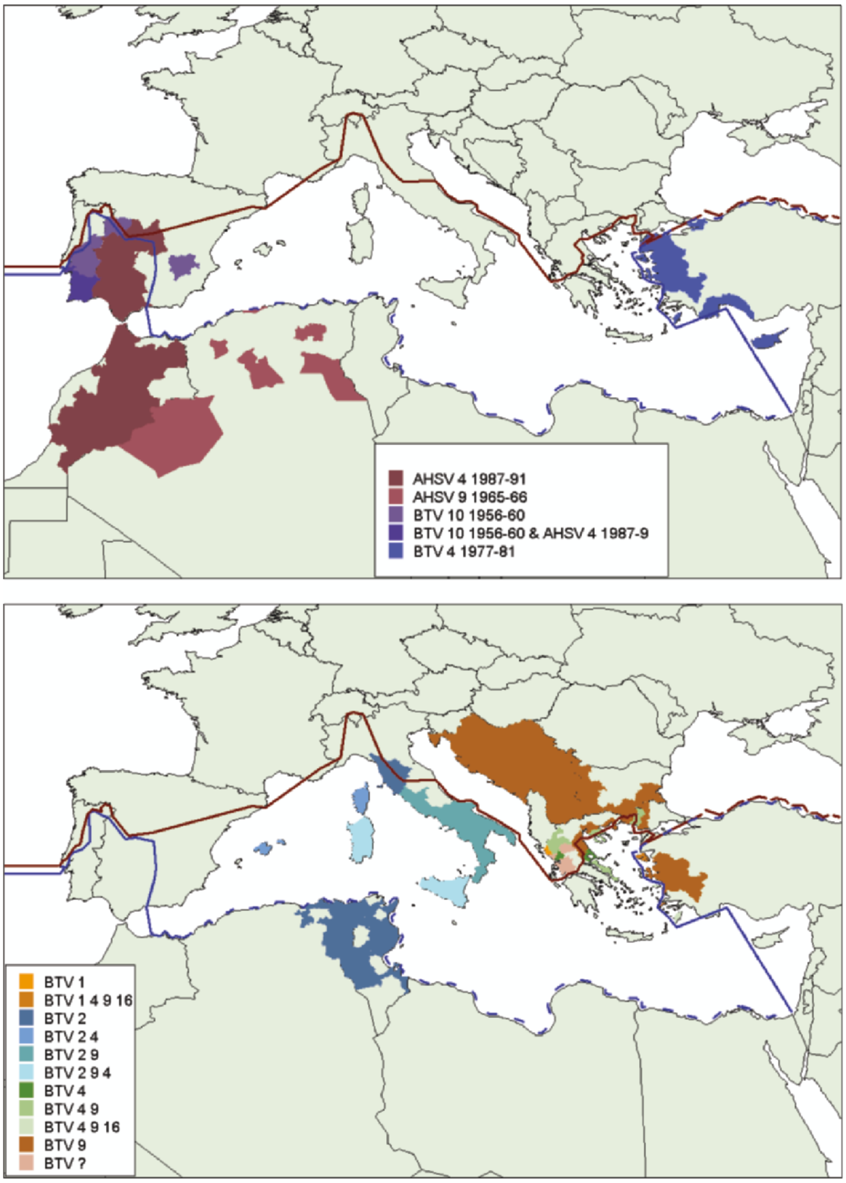


Figure 1. (a) Provinces or regions affected by bluetongue (BT) and African Horse Sickness (AHS) up to 1998. The key gives the virus, serotype and the years of the outbreak.
(b) Provinces or regions affected by bluetongue (BT) between 1998 and 2003. The key gives the serotypes of the outbreak.
In both (a) and (b) the blue line indicates the known distribution of *C. imicola* from light-trap catches made before 1998 and the red line indicates the current known distribution of *C. imicola* from light-trap catches made between 1998 and 2003. These lines are broken where they cross regions that have not been sampled for *Culicoides* in either period

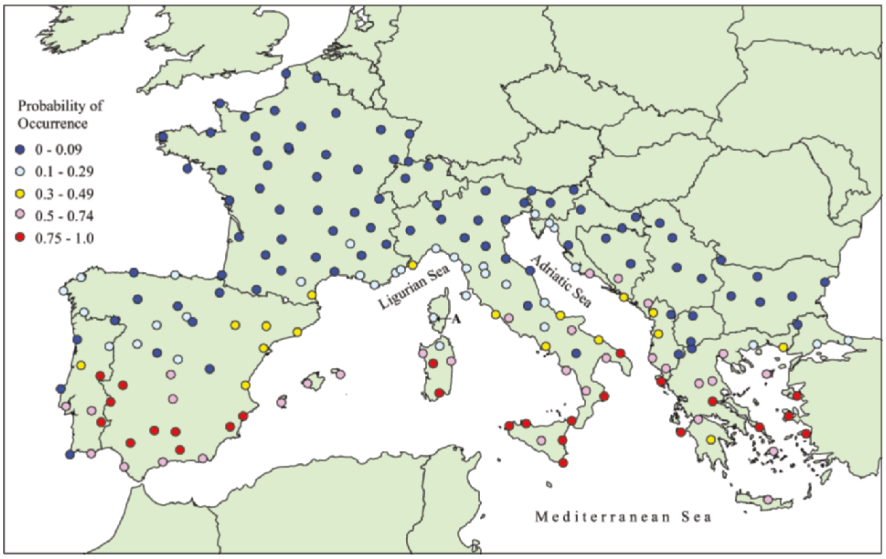


Figure 2. Suitability of sites in Europe for the occurrence of *C. imicola*, based on a logistic regression model established for Iberia (Reprinted from Wittmann, Mellor and Baylis 2001, with permission of the OIE)

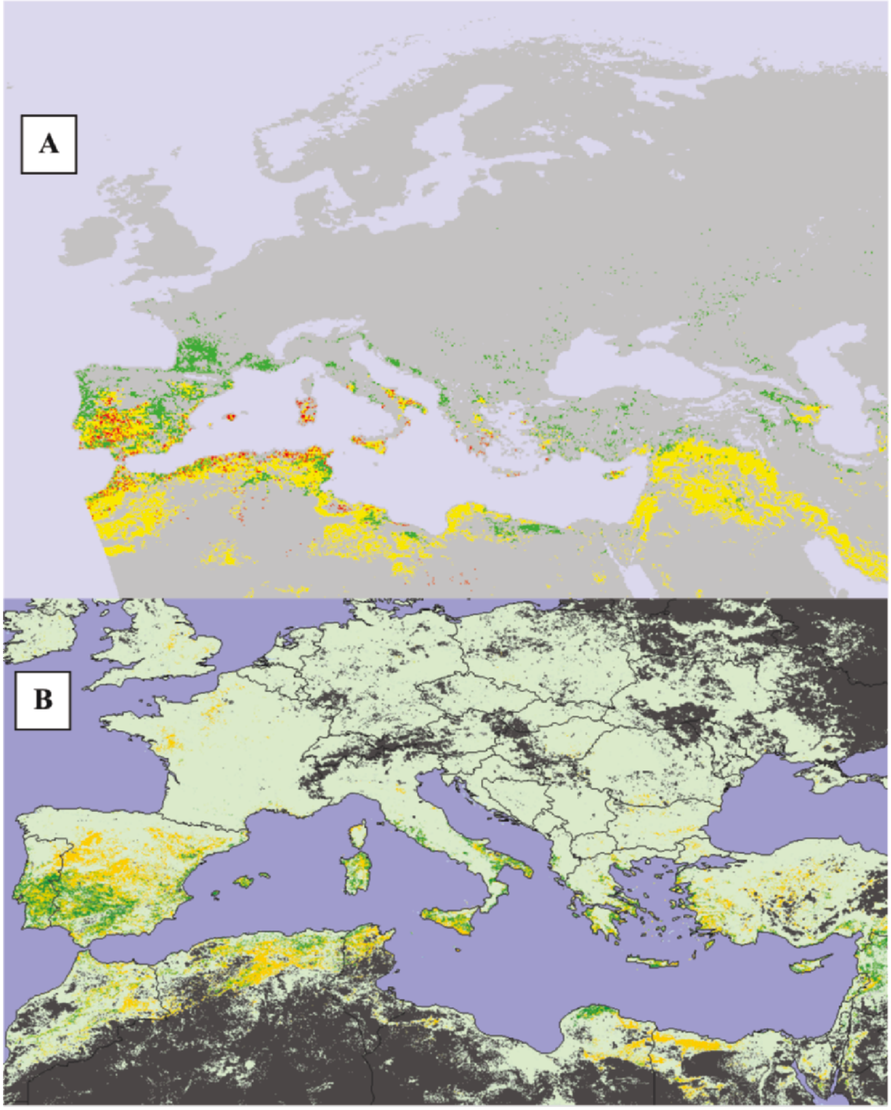


Figure 3. (a) Abundances of *C. imicola* around the Mediterranean predicted by a model derived from the observed abundances at 44 sites in Iberia and Morocco. Key: red = high *C. imicola* abundance; yellow = medium *C. imicola* abundance; green = low *C. imicola* abundance; grey = no prediction (since the environment is too dissimilar from the training set pixels). (Reprinted from Baylis et al. (2001) with permission from Veterinary Record). (b) Abundances of *Culicoides imicola* around the Mediterranean predicted by a model derived from the observed abundances at 87 sites in Portugal. Key: dark green = high *C. imicola* abundance; yellow = medium *C. imicola* abundance; light green/blue = low *C. imicola* abundance; grey = no prediction (since the environment is too dissimilar from the training set pixels). (Reprinted from Tatem et al. (2003) with permission from Elsevier)

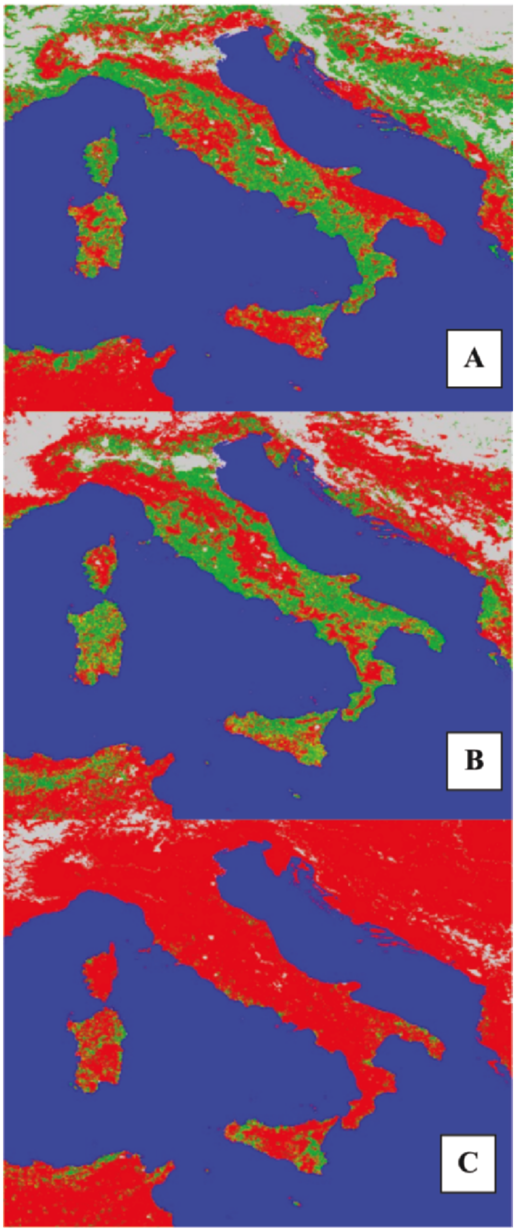


Figure 4. Predicted distribution of *Culicoides* species in Sicily and Italy; a. *C. pulicaris* b. *C. obsoletus* c. *C. imicola*. For a and b, from a model derived from the observed presence–absence data for each species at 268 sites in Sicily, sampled between May and October. For c, from a model derived from the observed presence–absence data for *C. imicola* at 142 sites in Sicily, sampled between July and October. Key: green = model prediction of species presence; red = model prediction of species absence; grey = no prediction since Mahalanobis distance between a pixel and its assigned probability or class was two or more times greater than the maximum distance observed between any one of the sites in Sicily and the classes to which they belonged

1

Introduction

Willem Takken[#] *and Pim Martens*[##]

Global warming as a result of excess production of greenhouse gases has been on the forefront of scientific debate in the last decade. The United-Nations-sponsored Conference on Environment and Development (UNCED) in Rio de Janeiro in 1992 was the first international platform at which these issues were discussed. The predicted increase in global temperatures was expected to seriously affect natural environments, affecting the balance of ecosystems and threatening the livelihoods of thousands of people. Because of much uncertainty, fuelled by incomplete climate models and the potential costs of mitigating measures, few governments at that time were prepared to take measures to counteract or reduce the predicted effects or consider reduction of gas emission rates. This has now changed with the activation of the Kyoto Protocol of the United Nations Framework Convention on Climate Change. This protocol became active in February 2005 and recognizes the harmful effects of greenhouse gases on the environment.

One of the undesired side effects of climate change is the change in geographic distribution and intensity of transmission of vector-borne diseases such as malaria, leishmaniasis, dengue fever and Lyme disease. Several studies have predicted that under the most conservative estimate of change, these diseases will shift their boundaries to higher latitudes or altitudes, benefit from changes in precipitation and possibly increase or decrease in incidence. The vectors (insects and ticks) of these infectious diseases are cold-blooded, and their distribution is confined by a temperature range outside which environmental conditions become hostile. The parasites that they transmit usually benefit from increased temperatures, as the development rate of them is then also increased. Much of this work has remained speculation in view of the uncertainties associated with the predictions of climate change. It seems, however, prudent to examine the potential effects on health under the predicted changes, because millions of people and animals might be affected by changes in disease risk. For example, a slight rise in ambient temperature and rainfall can extend the duration of the season in which mosquito vectors are transmitting disease with several weeks. In turn, this may affect a larger fraction of the population compared to the current situation. Governments, then, need to be prepared to invest more in preventive health care and curative measures than would be the case if business were as usual.

In November 2003 we organized a workshop on Environmental Change and Malaria Risk. Participants of the workshop were drawn not only from the world of malaria but also from scientists active on the more general effects of climate change on ecology and from those working on other vector-borne diseases. Papers presented at the workshop are included in these proceedings, which give a broad overview of the problems, as well as in-depth insights in specific aspects of global change and disease

---

[#] Laboratory of Entomology, Wageningen University, The Netherlands

[##] International Centre for Integrative Studies, Maastricht University, The Netherlands

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 1-2.

risk. From the combined work presented here it becomes clear that many of the models used for the prediction of the effects of climate change on health need to be verified by field work. However, the models all serve as a framework from which questions pertinent to the specific issue can be developed. We hope that the enclosed work will serve as a stimulus for others to refine the models and to undertake field work needed to strengthen and substantiate the theories that predict the effects of climate change on health.

2

Climate change and malaria risk: complexity and scaling

Pim Martens[#] *and Chris Thomas*[##]

Abstract

The impact of climate change and other environmental changes on population health poses radical challenges to scientists. A fundamental characteristic of this topic is the pervasive combination of complexity and uncertainty. This chapter seeks to identify the nature and scope of the problem, and to explore the conceptual and methodological approaches to studying these relationships, modelling their future realization, providing estimates of health impacts, and communicating the attendant uncertainties.

Keywords: complexity; scale; modelling

Introduction

The impact of climate change and other environmental changes on population health poses radical challenges to scientists. The exploration of these systems-based risks to human health seems far removed from the tidy examples that abound in textbooks of epidemiology and public-health research (with only a few exceptions (Martens and McMichael 2002; Aron and Patz 2001)). Yet there are real and urgent questions being posed to scientists here. The wider public and its decision-makers are seeking from scientists useful estimates of the likely population health consequences of these great and unfamiliar changes in the modern world.

Clearly, there is a major task for health scientists in this topic area. This chapter seeks to identify the nature and scope of the problem, and to explore the conceptual and methodological approaches to studying these relationships, modelling their future realization, providing estimates of health impacts and communicating the attendant uncertainties.

Challenges

A fundamental characteristic of this topic area is the pervasive combination of complexity and uncertainty that confronts scientists. Policy-makers, too, must therefore adjust to working with incomplete information and with making 'uncertainty-based' policy decisions. Here we outline several aspects of this research domain: (i) complexity and surprises; (ii) uncertainties; and (iii) determinants of population vulnerability and adaptive capacity to these environmental changes.

[#] International Centre for Integrative Studies, Maastricht University, The Netherlands

[##] Institute of Ecosystem Science, School of Biological and Biomedical Sciences, University of Durham, Science Laboratories, Durham, UK. E-mail: c.j.thomas@durham.ac.uk

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 3-14.

Complexity and surprises

Predicting the impact of a changing world on human health is a challenging task that requires an interdisciplinary approach drawn from the fields of evolution, biogeography, ecology and social sciences. It relies on a variety of methodologies such as integrated-assessment (IA) modelling (see below) as well as historical analysis, among other things. When even a simple change occurs in the physical environment, its effects percolate through a complex network of physical, biological and social interactions, which feed back and feed forwards. Sometimes the immediate effect of a change is different from the long-term effect; sometimes the local changes may be different from the region-wide alterations. The same environmental change may have quite different effects in different places or times. Therefore the study of the consequences of environmental change is a study of the short- and long-term dynamics of complex systems.

Uncertainties

The prediction of environmental change and its health impacts encounters uncertainties at various levels. Some of the uncertainties are of a scientific kind, referring to deficient understanding of actual processes – for example, knowing whether or not increased cloud cover arising because of global warming will have a positive or a negative feedback effect. Some of the uncertainties refer to the conceptualization and construction of mathematical models where the specification of linked processes may be uncertain or where key parameter values are uncertain. For example, what is the linkage between changes in temperature, humidity and surface water in the determination of mosquito breeding, survival and biting behaviour? Some uncertainties are essentially epistemological, referring to what we can and cannot reasonably foresee about the structure and behaviour of future societies, including for example their future patterns of emissions of greenhouse gases. And, finally, there is of course the familiar source of uncertainty that arises from sampling variation, and which leads to the need for confidence intervals around point estimates.

Vulnerability and adaptation

Human populations vary in their vulnerability to health hazards. A population's vulnerability is a function of the extent to which a health outcome is sensitive to climate change and of the capacity of the population to adapt to new climate conditions. The vulnerability of a population depends on factors such as population density, level of economic development, food availability, local environmental conditions, pre-existing health status, and the quality and availability of public health care.

Adaptation refers to actions taken to lessen the impact of the (anticipated) climate change. There is a hierarchy of control strategies that can help to protect population health. These strategies are categorized as: (i) administrative or legislative; (ii) engineering, or (iii) personal (behavioural). Legislative or regulatory action can be taken by government, requiring compliance by all, or by designated classes of, persons. Alternatively, an adaptive action may be encouraged on a voluntary basis, via advocacy, education or economic incentives. The former type of action would normally be taken at a supranational, national or community level; the latter would range from supranational to individual levels. Adaptation strategies will be either reactive, in response to observed climate impacts, or anticipatory, in order to reduce vulnerability to such impacts.

Modelling the impact of climate change on malaria

Models incorporating a range of meteorological variables have been developed to describe a specific ‘bioclimate envelope’ for malaria. Multivariate statistical techniques can be used to select predictive variables (whether meteorological or environmental, ground-based or remotely-sensed). Models that match the presence of a particular species with a discrete range of temperature and precipitation parameters can be used to project the effect of climate change on vector redistribution.

Some mosquito species have been successfully mapped in Africa using meteorological data (Lindsay, Parson and Thomas 1998). Meteorology is usually recorded at ground level, but coverage can be relatively sparse or inappropriate, especially in developing countries (Hay et al. 1996). Grid surfaces interpolated from these data often form the basis for modelling the relationship between vectors/disease and climate, though averaging and interpolation to large grid boxes leads to (as yet unresolved) methodological problems of scaling when making inferences to point estimates (Patz et al. 2002; Hay et al. 2002). Remotely-sensed imagery from space satellites is often used as surrogate for instrumental meteorological data and has the advantages of wide coverage, fine resolution, consistency and providing a synoptic view. In addition, compound indices may be useful: the Normalized Difference Vegetation Index (NDVI), based upon the difference ratio of reflected red and near-infrared energy, correlates well with photosynthetic activity of plants, rainfall and saturation deficit and has also been correlated with the distribution of vectors and disease (Hay et al. 1996).

Rogers has mapped the changes of three important disease vectors (ticks, tsetse flies and mosquitoes) in Southern Africa under three climate-change scenarios (Hulme 1996). The results indicate significant changes in areas suitable for each vector species, with a net increase for malaria mosquitoes (*Anopheles gambiae*). The final objective of such work is to map human disease risk but the relationship between vector-borne disease incidence and climate variables is complicated by many socio-economic and environmental factors.

Another example of an empirical statistical model is the CLIMEX model. This model, developed by Sutherst, Maywald and Skarratt (1995), maps the translocation of species between different areas as they respond to climate change. The assessment was based on an ‘ecoclimatic index’, governed largely by the temperature and moisture requirements of the malaria mosquito. CLIMEX analyses conducted in Australia indicate that the indigenous vector of malaria would be able expand its range 330 km south under one typical scenario of climate change. However, these studies clearly cannot include all factors that affect species distributions. For example, local geographical barriers and interaction/competition between species are important factors that determine whether species colonize the full extent of suitable habitat (Davis et al. 1998). Assessments may also include additional dynamic population (process-based) models (Sutherst 1998).

Martin and Lefebvre (1995), using a similar approach, developed a Malaria-Potential-Occurrence-Zone (MOZ) model. This model was combined with 5 GCMs (General Circulation Models) to estimate the changes in malaria risk based on moisture and minimum and maximum temperatures required for parasite development. This model corresponded fairly well with the distribution of malaria in the 19th century and the 1990s, after allowing for areas where malaria had been eradicated. An important conclusion of this modelling exercise was that all simulation runs showed an increase in seasonal (unstable) malaria transmission, under climate change, at the expense of perennial (stable) transmission.

Rogers and Randolph (2000), using a multivariate empirical-statistical model, found that, for the IS92a (business as usual) climate-change scenario, there is no significant net change by 2050 in the estimated portion of the world population living in malaria-transmission zones: malaria increased in some areas and decreased in others. The outcome variable in this model is based on present-day distribution limits of malaria. However, using current distribution limits in the estimate may have yielded a biased estimation of the multivariate relationship between climatic variables and malaria occurrence, since the lower temperature range in temperate zones (especially Europe and southern USA), would have been treated as climatically unsuitable for malaria. However, it may be that these portions of multivariate climate space were captured in the model because malaria persists in climatically similar regions (e.g. parts of Asia). These hypotheses are currently being tested by sensitivity modelling (Thomas in prep.).

An integrated, process-based model to estimate climate-change impacts on malaria (that is part of the MIASMA modelling framework), has been developed by Martens and colleagues (Martens 1995b; 1995a; 1999). This model differs from the others in that it takes a broad approach in linking GCM-based climate-change scenarios with a module that uses the formula for the basic reproduction rate (R_o) to calculate the 'transmission or epidemic potential' of a malaria-mosquito population. The use of the basic reproduction rate is defined as the number of new cases of a disease that will arise from one current case when introduced into a non-immune host population during a single transmission cycle (Anderson and May 1991). This goes back to classical epidemiological models of infectious disease. Model variables within R_o that are sensitive to temperature include: mosquito density, feeding frequency, survival, and extrinsic incubation period. The extrinsic incubation period (i.e., the development of the parasite in the mosquito) is particularly important. The minimum temperature for parasite development is the limiting factor for malaria transmission in many areas.

Tol and Dowlatabadi (2001) integrated the results of MIASMA within the FUND framework, developed by Tol, to estimate the trade-off between climate change and economic growth on malaria risk. The first results of this exercise show the importance of economic variables in estimating changes in future malaria risk. Although this exercise indicates the importance of including the economic dimension in analysing climate-change impacts upon future malaria risk, their approach may be too simplistic (Martens and McMichael 2001).

Gallup and Sachs (2001) explored the correlation between the malaria index and income levels. They took into account some of the factors that also affect malaria risk (e.g. low agricultural productivity, presence of other tropical diseases, colonial history and geographical isolation). The malaria index is defined as the fraction of the population living in areas of high malaria risk in 1994, times the fraction of malaria cases in 1990 that are of the malignant *Plasmodium falciparum* species. The malaria index showed a strong negative association with income levels, indicating that income grows more slowly in countries where the disease is present. This trend appears to apply equally to countries in Africa and in other continents. In countries that include large malaria-free regions (e.g. Brazil, Venezuela, Malaysia, Indonesia, Turkey, Kenya and Ethiopia), the prevalence of infection correlates with poverty. Malaria, of course, is not the sole determinant of poverty, just as poverty alone does not explain the distribution of malaria.

All of the examples discussed above have their specific disadvantages and advantages. For example, the model developed by Rogers and Randolph (2000) incorporates information about the current social, economic and technological modulation of malaria transmission. It assumes that those contextual factors will apply in future in unchanged fashion. This adds an important, though speculative, element of multivariate realism to the modelling – but the model thereby addresses a qualitatively different question from the biological model. The biological model of e.g. Martens and colleagues (1998; 1999) assumes that there are known and generalizable biologically mediated relationships. Also, this modelling is only making a start to include the horizontal integration of social, economic and technical change. The statistical model is based on socio-economically censored data. It derives its basic equation from the existing (constrained) distribution of malaria in today's world and climatic conditions, and foregoes much information on the malaria–climate relationship within the temperate-zone climatic range. Yet this range is likely to be considerably important in relation to the marginal spread of malaria under future climate change.

Characterizing the relationship between socio-economic development and malaria incidence is difficult for various reasons: First and foremost, malaria incidence is hugely influenced by geography and prevailing climate. Hence, since the world's poorest countries tend to be in high-risk tropical and subtropical regions, it is inevitable that national rates of malaria incidence correlate with per capita income. Apportioning malaria causality between environment, income and social practices is, therefore, problematic. Other related reasons include: i) The income per capita at a country or regional level is an inadequate description of how that wealth is distributed within a society and to what public uses it is applied (e.g. Costa Rica and Cuba, with lower per capita income, outperform Brazil in social and health indices); ii) Political instability can undermine the influence of development (i.e. Russia, Azerbaijan); iii) Economic development can increase transmission temporarily (e.g. deforestation, population movement, water development projects); iv) Many control programmes depend on external/donor funding (e.g. Viet Nam) from richer, developed countries.

Furthermore, the quality of malaria data is very poor in most developing countries. National indicators of malaria include national mortality or morbidity data. Mortality data generally reflect *P. falciparum* transmission as *P. vivax* is rarely fatal. Further, in areas with very high levels of transmission where nearly everyone is infected, with or without immunity, the morbidity figures are meaningless. Estimates can vary considerably from year to year because of changes in reporting rather than a true change in disease transmission. For these reasons therefore, a straightforward relationship between national income per capita and malaria status is not very likely.

Little research has been carried out on the determinants of vulnerability of populations to malaria, so it is difficult to develop assumptions about future adaptation to changes in disease risk associated with climate change and economic development. Populations can respond to changes in local malaria transmission associated with climate change. With planning and development of adaptation capacity, potential increases in disease incidence associated with climate change may be largely prevented. However, the effectiveness of adaptation responses will vary depending on the circumstances of the population at risk.

In tropical countries, successful prevention and control in the future would probably involve *technical, political* and *socio-economic adaptation*. Technical adaptation includes for example the use of insecticides. Political adaptation involves adequate administration of control programmes, funding of research and training, investments in health infrastructure etc. It should be noted here that, after the initial success of global eradication programmes of the 1950s and 1960s, resources available from international agencies have declined along with those of national governments. The disease is now resurgent in many countries where it previously had been controlled. However, the relation between the level of malaria incidence and political willingness to adapt policy is unknown. In the meantime, it is not clear to what extent economic growth on its own will reduce the incidence of malaria.

A matter of scale

The problem of modelling the impacts of global (environmental) change processes on human health is that it has to cope with a variety of processes that operate on different temporal and spatial levels and differ in complexity.

First, modelling has to connect disciplinary processes that differ by nature: physical processes, monetary processes, social processes and policy processes. Because of the multitude of disciplinary processes to be combined, a representation as simple as possible of disciplinary knowledge is preferable. There is, however, no unifying theory how to do this. In addition, the processes to be linked are usually studied in isolation from each other. This isolation is needed as part and parcel of the classic model of scientific progress and discovery. However, when the constraints of isolation are removed, there is a variety of ways in which to connect the reduced pieces of disciplinary knowledge. This manifold of possible integration routes, for which there is no unifying theory, is one of the reasons why quality control is so difficult to achieve in IA modelling. For instance, in order to link the reduced pieces of disciplinary knowledge in a systemic way, one can use elements from classical systems analysis, or the method of system dynamics, or a sequential input–output analysis, or a correlation-based approach, or a pressure–state–impact–response approach.

Second, modelling has to deal with different spatial scale levels. One of the ultimate challenges in modelling is to connect higher scale assessments with lower scale ones. So far, there has been hardly any experience with playing around with scale levels in modelling. Down-scaling or up-scaling the spatial level of a model has profound consequences. This is related to the question to what extent the processes considered are generic or spatially bound in character. In other words: does a relationship at one scale hold at larger or lower scale levels?

Third, modelling is faced with a multitude of temporal scales. Short-term needs and interests of stakeholders have to be considered. However, biogeochemical processes usually operate on a long time scale, whereas economic processes operate on short to medium time scales. Another challenging aspect of modelling is to interconnect long-term targets as specified as a result of analysing processes operating on longer-term time scales, with short-term goals for concrete policy actions. Unfortunately, there is not yet a sound scientific method how to do this, thus far only heuristic methods have been used.

In Figure 1, for example, some important factors determining malaria risk are depicted along ‘temporal’ and ‘spatial’ scale axes. Looking at the climate, human and mosquito system, it is apparent that they vary in their spatial and temporal scale: mosquito larval development takes place at the level of puddles and at time scales varying from days to weeks, climate change is a process influencing the global climate system at time frames of years to centuries or more, whereas economic processes operate on short to medium time scales. Furthermore, short-term needs and interests of stakeholders have to be considered.

Although the assessment of malaria risk may be done on a variety of geographical scales – varying from a village to an entire country, region or the world as a whole – so far there has been no formal analysis of the effect of scaling on models or our understanding. Varying geographical (extent) and measurement (resolution) scales has profound implications for spatial analysis. This is formalized as the Modifiable Areal Unit Problem (MAUP) (Openshaw 1984), and is fundamental to the analysis of geographical data (Flowerdew, Geddes and Green 2001). MAUP has become an important but overlooked issue for our understanding of malaria as many studies are now geographically based. An equally important issue, already alluded to, is scaling mismatches when interpreting events at one scale against data measured at another. In the pilot analysis presented below we explore these differences in spatial scale (the same effects will be evident in mismatched temporal series).

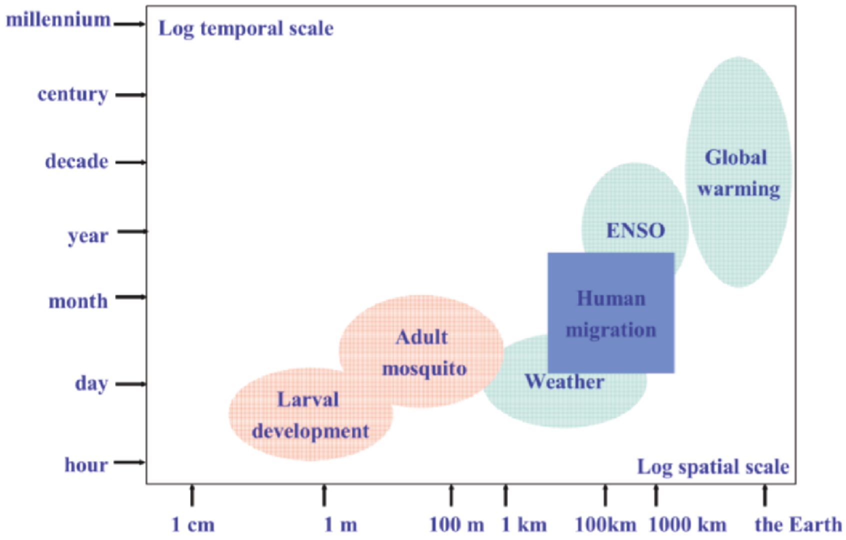


Figure 1. Some processes on different temporal and spatial scales that affect malaria epidemiology

In seeking spatial structure it is instructive to compare the variation in measurements among locations at increasing distances, in the likelihood that locations closer together will be more similar than locations further apart. Here we employed an exploratory geostatistical approach by calculating the semivariance (Oliver 2001) (as variance among locations increases, the semivariance also increases) in four measurements relevant to malaria in Africa. The first two are estimates of the climatic suitability for *falciparum* malaria transmission based upon 0.5-degree grid cell length surfaces of 1961-90 observed mean climate (http://ipcc-ddc.cru.uea.ac.uk) using the MARA/ARMA spatial fuzzy-logic model (Craig, Snow and Le Sueur 1999): i) spatial extent (Figure 2, see Colour pages elsewhere in this book) – the suitability for malaria transmission in four consecutive months (fuzzy values from 0 to 1); ii) seasonal extent (Figure 3, see Colour pages elsewhere in this book) – number of consecutive months suitable for transmission (fuzzy values from 0 to 12). We used this index as a proxy fro climate, rather than a single measure such as temperature because it incorporates both temperature and precipitation thresholds for disease transmission.

The second two measurements are entomological values (biting rate and entomological inoculation rate, EIR) recorded in the field at specific locations across Africa (Figure 4) and compiled by Hay et al. (2000).

Our analyses were designed to indicate general differences in spatial structure and are not exhaustive (a variety of lags and bounding regions could have been tried) or complete (for instance there are methodological inconsistencies in the entomological measurements, see Hay et al. (2000)).

Figure 4. Locations where EIR and (for a sub-set) biting rate have been recorded (derived from Hay et al. (2000))

Climate-based estimates of malaria distribution and seasonality showed long-range variation, with a sill variance (asymptote) at around 30 degrees separation. As might be expected from interpolated values, variance increased smoothly with increasing separation (Figure 5 a,b). In contrast, semivariograms of location-specific biting rates and EIR showed no obvious spatial structure, with measurements varying randomly over space (Figure 5 c,d) at least for lags of 0.5 degrees.

The lack of spatial structure in biting rate and EIR will likely be due to sampling errors and inconsistencies and, more importantly, local variation in environment not captured at 0.5-degree lags. In other words, to compare biting rate and EIR usefully with climate it would be necessary either to aggregate entomology measures to climate grid boxes or to use meteorological data local to the entomological studies. For the former, we urgently need to know the spatial structure (if any) of malaria entomological and clinical measurements, and how this varies among regions, so that we can determine optimal aggregation scales and hence relate them to other aggregated variables such as climate. For the latter, we need more consistent long-term measurements tied to local meteorological stations. Initiatives such as the INDEPTH network (see chapter by Sankoh and Binka in this volume) are an essential step forward for both solutions.

Geographical scaling is not the only important issue. For instance, an early version of the malaria model developed by Martens et al. (1995) uses a composite measure of different species of *Anopheles*. This globally aggregated model assumed that there are universal relationships that are sufficiently dominant to ensure a valid approximate overall forecast. Later versions of the model (Martens et al. 1999) include species-specific relationships (as far as available in literature) between climate and transmission dynamics. Even so, the equations within a global model may well be inappropriate for particular local conditions. This example of hierarchical (in this case, taxonomic) scaling demonstrates another area where informed decisions need to be made in modelling.

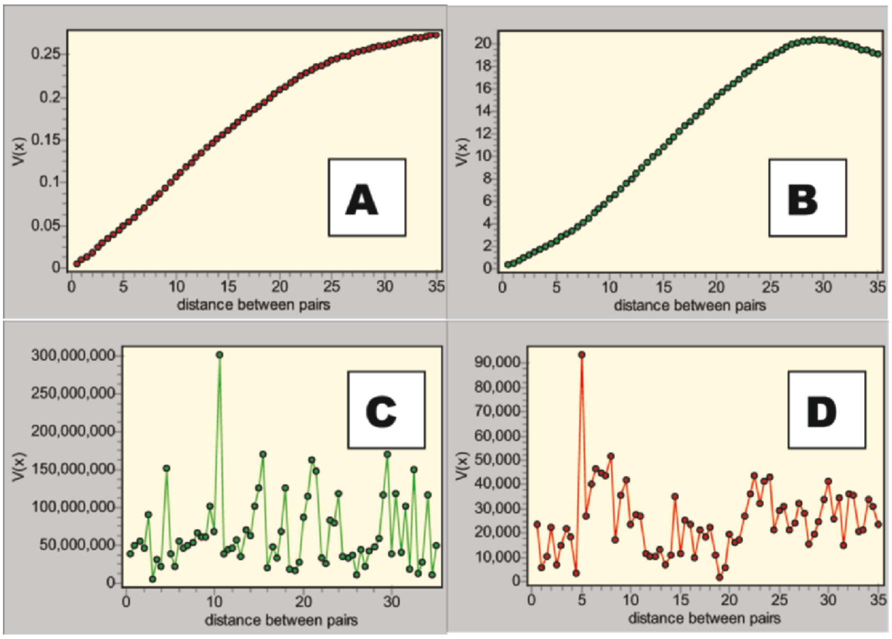


Figure 5. Omnidirectional semivariograms (moments estimator) with lag of 0.5 degrees, over 0.5-35 degrees extent. A) MARA/ARMA index of climatic suitability for *P. falciparum* transmission in four consecutive months; B) Number of consecutive months with a MARA/ARMA index of climatic suitability for *P. falciparum* transmission of p Σ0.9 in each month; C) biting rate; D) entomological inoculation rate

In this context, an interesting approach is proposed by Root and Schneider (1995): the so-called Strategic Cyclical Scaling (SCS) method. This method involves continuous cycling between large- and small-scale assessments. Such an iterative scaling procedure implies that a specific global model is disaggregated and adjusted for a specific region or country. The new insights are then used to improve the global version, after which implementation for another region or country follows. In malaria modelling some progress has been made (Lindsay and Martens 1998). This SCS method can also be used for conceptual validation of models.

The trend in current modelling is to move toward greater and greater disaggregation, assuming that this yields better models (Rotmans and Van Asselt 2000). In general, it is difficult to know when to stop building more detail into an IA model. Past decades of model building have shown that small and transparent models are often superior in that they provide similar results to large models faster and offer ease of use. In this respect, it is useful to distinguish between *complicated* and *complex* models. Complicated models are models that include a variety of processes, many of which may be interlinked. If incremental changes in these processes generally lead to incremental changes in model output, one can conclude that the dynamics of the model are almost linear and not complex at all. The more complicated the model, the higher the possibility of errors and bugs. It requires thorough testing to pick up most if not all errors and bugs, an activity which is, unfortunately, heavily underrated. Complex models, however, contain relatively few processes, but incremental changes in these processes may result in considerable changes in the results of the overall model. This non-linear behaviour, due to the inclusion of feedbacks, adaptation, self-learning and chaotic behaviour, is often unpredictable.

Practically speaking, this means that disaggregation of models has profound consequences for the dynamics of the model. Breaking down a global model into various regions requires that the regional dynamics be dealt with in an adequate manner. Current regional models use grid cells or classes for representing geographical differences and heterogeneities in regional models. They do not capture, however, the regional dynamics with regard to population growth and health, economic development, resource use and environmental degradation, let alone regional interactions through migration and trade.

The way ahead

As the *full* complexity of the interactions between global developments and human health cannot be satisfactorily reduced to modelling, what is the role of such modelling? Despite the difficulties and limitations of the modelling process, models first of all draw attention to the potential health impact of these global changes. Second, they may indicate the relative importance of the factors that influence these outcomes. This enhances public discussion, education and policy-making. However, even more important is the role modelling plays in the systematic linkage of multiple cause-and-effect relationships based on available knowledge and reasoned guesses. This should increase our understanding of the health impacts of global changes, and identify key gaps in data and knowledge needed to improve the analysis of these effects.

References

Anderson, R.M. and May, R.M., 1991. *Infectious diseases of humans: dynamics and control*. Oxford University Press, Oxford.

Aron, J.L. and Patz, J.A. (eds.), 2001. *Ecosystem change and public health: a global perspective*. The Johns Hopkins University Press, Baltimore.

Craig, M.H., Snow, R.W. and Le Sueur, D., 1999. A climate-based distribution model of malaria transmission in sub-Saharan Africa. *Parasitology Today,* 15 (3), 105-111.

Davis, A.J., Jenkinson, L.S., Lawton, J.H., et al., 1998. Making mistakes when predicting shifts in species range in response to global warming. *Nature,* 391 (6669), 783-786.

Flowerdew, R., Geddes, A. and Green, M., 2001. Behaviour of regression models under random aggregation. *In:* Tate, N.J. and Atkinson, P.M. eds. *Modelling scale in geographical information science*. Wiley, Chichester, 89-104.

Gallup, J.L. and Sachs, L.D., 2001. *The economic burden of malaria*. Center for International Development, Harvard University, Cambridge. CMH Working Paper Series no. WG1:10. [http://www.cmhealth.org/docs/wg1_paper10.pdf]

Hay, S.I., Cox, J., Rogers, D.J., et al., 2002. Climate change: regional warming and malaria resurgence-reply. *Nature,* 420 (6916), 628.

Hay, S.I., Rogers, D.J., Toomer, J.F., et al., 2000. Annual *Plasmodium falciparum* entomological inoculation rates (EIR) across Africa: literature survey, internet access and review. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 94 (2), 113-127.

Hay, S.I., Tucker, C.J., Rogers, D.J., et al., 1996. Remotely sensed surrogates of meteorological data for the study of the distribution and abundance of arthropod vectors of disease. *Annals of Tropical Medicine and Parasitology,* 90 (1), 1-19.

Hulme, M. (ed.) 1996. *Climate change and Southern Africa: an exploration of some potential impacts and implications for the SADC region*. University of East Anglia, Norwich.

Lindsay, S.W. and Martens, W.J., 1998. Malaria in the African highlands: past, present and future. *Bulletin of the World Health Organization,* 76 (1), 33-45.

Lindsay, S.W., Parson, L. and Thomas, C.J., 1998. Mapping the ranges and relative abundance of the two principal African malaria vectors, *Anopheles gambiae* sensu stricto and *An. arabiensis*, using climate data. *Proceedings of the Royal Society of London. Series B. Biological Sciences,* 265 (1399), 847-854.

Martens, P., 1998. *Health and climate change: modelling the impacts of global warming and ozone depletion*. Earthscan, London.

Martens, P., 1999. *MIASMA: Modelling framework for the health Impact Assessment of Man-induced Atmospheric changes (CD-ROM)*. Electronic Series on Integrated Assessment Modeling (ESIAM) no. 2.

Martens, P., Kovats, R.S., Nijhof, S., et al., 1999. Climate change and future populations at risk of malaria. *Global Environmental Change. Part A. Human and Policy Dimensions,* 9 (1), S89-S107.

Martens, P. and McMichael, A.J., 2001. Vector-borne diseases, development and climate change: an editorial comment. *Integrated Assessment,* 2 (4), 171-172.

Martens, P. and McMichael, A.J. (eds.), 2002. *Environmental change, climate and health: issues and research methods*. Cambridge University Press, Cambridge.

Martens, W.J., 1995a. Climate change and malaria: exploring the risks. *Medicine and War,* 11 (4), 202-213.

Martens, W.J., Niessen, L.W., Rotmans, J., et al., 1995. Potential impact of global climate change on malaria risk. *Environmental Health Perspectives,* 103 (5), 458-464.

Martens, W.J.M., 1995b. *Modelling the effect of global warming on the prevalence of schistosomiasis*. National Institute of Public Health and the Environment RIVM, Bilthoven. RIVM Rapport no. 461502010.

Martin, P.H. and Lefebvre, M.G., 1995. Malaria and climate: sensitivity of malaria potential transmission to climate. *Ambio,* 24 (4), 200-207.

Oliver, M.A., 2001. Determining the spatial scale of variation in environmental properties using the variogram. *In:* Tate, N.J. and Atkinson, P.M. eds. *Modelling scale in geographical information science*. Wiley, Chichester.

Openshaw, S., 1984. *The modifiable areal unit problem*. GeoBooks, Norwich. Concepts and Techniques in Modern Geography no. 38.

Patz, J.A., Hulme, M., Rosenzweig, C., et al., 2002. Climate change: regional warming and malaria resurgence. *Nature,* 420 (6916), 627-628.

Rogers, D.J. and Randolph, S.E., 2000. The global spread of malaria in a future, warmer world. *Science,* 289 (5485), 1763-1766.

Root, T.L. and Schneider, S.H., 1995. Ecology and climate: research strategies and implications. *Science,* 269 (52), 334-341.

Rotmans, J. and Van Asselt, M.B.A., 2000. Integrated assessment modelling. *In:* Martens, P. and Rotmans, J. eds. *Climate change: an integrated perspective*. 239-275. Advances in Global Change Research no. 1.

Sutherst, R.W., 1998. Implications of global change and climate variability for vector-borne diseases: generic approaches to impact assessments. *International Journal of Parasitology,* 28 (6), 935-945.

Sutherst, R.W., Maywald, G.F. and Skarratt, D.B., 1995. Predicting insect distributions in a changed climate. *In:* Harrington, R. and Stork, N.E. eds. *Insects in a changing environment: 17th symposium of the Royal Entomological Society of London, 7-10 September 1993 at Rothamsted Experimental Station, Harpenden*. Academic Press, London, 60-91.

Tol, R.S.J. and Dowlatabadi, H., 2001. Vector-borne diseases, development and climate change. *Integrated Assessment,* 2 (4), 173-181.

3

Global environmental change and health: integrating knowledge from natural, socioeconomic and medical sciences

Rik Leemans [#]

Abstract

Environmental problems, such as air quality, pollution and toxicity, have historically strongly been linked with health issues. The earliest environmental policies were targeted to negate health impacts. This focus has become less obvious during the last decades when environmental problems became more diffuse and covered larger areas and regions. Nowadays, degradation of natural resources, climate change and the decline in biodiversity are the major environmental problems. To deal effectively with these problem international conventions and national policies strongly relate also to developmental issues, equity and improved human well-being.

The Millennium Ecosystem Assessment (MA; www.millenniumassessment.org), a four-year international work programme designed to meet the needs of decision-makers for scientific information on ecosystem change, has taken up the challenge to comprehensively assess the consequences of environmental change for ecosystems, ecosystems services and human well-being. The MA focuses on how changes in ecosystem services have affected human well-being, how ecosystem changes may affect people in future decades, and what types of responses can be adopted at local, national or global scales to improve ecosystem management and thereby contribute to human well-being and poverty alleviation. Health is one of the central themes in the Millennium Assessment.

Keywords: ecosystems; ecosystem services; integrated assessment; human well-being; global change; UN conventions; Millennium Ecosystem Assessment

Introduction

Environmental problems, such as air quality, pollution and toxicity, have historically strongly been linked with health issues. The earliest environmental policies were actually targeted to negate health impacts. For example, in the early days of industrialization, the burning of coal in small local furnaces caused severe pollution in cities. Newspaper headlines clearly linked smog events to death incidences. This led to respiratory diseases and adversely impacted health. In the middle of the last century, the causal relationships between air-pollution and health were clearly understood. This led to a series of diverse policies. In general smoke stacks were raised, improved furnaces and, in some cases, transitions to other fuels

---

[#] Environmental Systems Analysis Group, Wageningen Univ., P.O. Box 47, 6700 AA Wageningen, The Netherlands. E-mail: rik.leemans@wur.nl

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 15-26.

were implemented. Health concerns were the prime reason for the revolutionary shift from coal to natural gas in The Netherlands. In a military-like campaign, 90% of all households were coupled to the natural gas grid in less than 7 years, after large amounts of natural gas were discovered close to the village of Slochteren. Simultaneously, the Dutch coal mines were closed. This event rapidly improved air quality in The Netherlands. Also many became aware of the immediate threat of toxic substances that were cumulating in the environment and food chains. Carson's book 'Silent Spring' (1962) is widely recognized as the onset of increasing awareness of environmental threats and the urgency to mitigate them.

However, many of the measures taken did not really reduce pollution levels but merely diluted them. The immediate health effects were much less obvious and could only be assessed by detailed and long-term epidemiological research. Acidification, for example, became a regional problem because high smoke stacks allowed for long-distance spreads and caused problems thousands of kilometers away. Acidification only became obvious when the quality of remote poorly buffered lakes in Scandinavia and Canada rapidly deteriorated. Whole ecosystems were killed and the water was crystal-clear (or almost dead). Such regional or continental environmental problems did not have direct health effects but only cumulative effects of long-term exposures to relatively low doses. The need for policy development was not governed by health concern any more but by valuable and vulnerable (eco)systems. Critical load assessments are a nice example of this change (Alcamo et al. 1987). In these days, environmental problems also more and more became resource problems (e.g. Meadows et al. 1972), which also shifted the focus of environmental problems away from health issues.

In the 1980s the link between health and the environment became stronger again for a short period after the ozone hole over Antarctica was discovered. This hole and the thinning of the ozone layer elsewhere cause an increase in UV radiation with again serious health impacts (e.g. skin cancer). When the problem was fully understood, international policy agreements rapidly supported a reduction and later a complete ban of substances that destroy the ozone layer. Nowadays, the ozone layer is recovering.

The destruction of the ozone layer was the first global environmental problem. In the late 1980s and '90s many more followed. First, deforestation and the global decline in biodiversity were seen as a large threat to the many ecosystems of the world. Then, climate warming as a consequence of increased atmospheric concentrations of greenhouse gases was identified as a major emerging problem. Impacts on ecosystems, floods, droughts, agriculture and sea level rise were seen as major impacts, which argued for mitigation. IPCC's first assessment (McG. Tegart, Sheldon and Griffiths 1990), however, already provides a comprehensive account for the impacts on human health. They already highlight the health consequences of reduced food production, heat waves, vector-borne diseases and others, but little was done with this information. Only in the 3rd assessment report (McCarthy et al. 2001), health was again assessed more prominently. Only after the extremely warm European summer of 2003, in which many thousands of people died due to access heat, health and the environment was again at the front pages of all newspapers.

The international conventions that resulted from the 1972 and 1992 Environmental conferences in, respectively, Stockholm and Rio de Janeiro established and re-emphasized the environment as a major policy issue. In between, environmental issues and resource use were regarded as finite. The publication of the Bruntland report (1987) marked a milestone in our understanding and emphasized sustainable development. This was reiterated in the World Development Goals and later also Millennium Development Goals from the Summit on Sustainable Development in 2001 in Johannesburg. All these conventions and internationally accepted policy targets have nowadays one thing in common: they link the environment to development, poverty reduction, improvement of equity, education and sustainability and, more generally to the improvement of human well-being. Although health is not often explicitly mentioned, health is regarded as a major constituent of human well-being.

This paper presents an ongoing effort, the Millennium Ecosystem Assessment, to assess the relationship between ecosystems, ecosystem services and human well-being and how environmental change has affected this. The aim is to discuss the possibilities to link health issues more comprehensively with environmental issues.

The Millennium Ecosystem Assessment

The MA is a four-year international work programme, which was launched by United Nations Secretary-General Kofi Annan in June 2001, designed to meet the needs of decision-makers for scientific information on the links between ecosystem change and human well-being. The MA focuses on how changes in ecosystem services have affected human well-being, how ecosystem changes may affect people in future decades, and what types of responses can be adopted at local, national or global scale to improve ecosystem management and thereby contribute to human well-being and poverty alleviation. Human development is thus about creating the conditions in which people can develop their full potential while conserving essential ecosystems and providing ample ecosystem services. Development is thus about expanding the choices people have to lead lives that they value.

Parties to the Convention on Biological Diversity (CBD; http://www.biodiv.org), the Convention to Combat Desertification (CCD; http://www.unccd.int), the Ramsar Convention on Wetlands (http://www.ramsar.org) and the Conservation of Migratory Species of Wild Animals (CMS or Bonn Convention; http://www.wcmc.org.uk/cms) have asked the MA to provide scientific information to assist in the implementation of these treaties. The MA will also address the needs of other stakeholders, including national governments, the private sector, organizations of indigenous peoples and other non-governmental organizations (NGOs). The MA is closely coordinated with other international assessments that focus in greater depth on particular sectors or drivers of change, such as the Intergovernmental Panel on Climate Change (IPCC; http://www.ipcc.ch), the Global International Waters Assessment (GIWA; http://www.giwa.net) and the Land Degradation Assessment (LADA; http://www.fao.org/ag/agl/agll/lada/default.stm). This improves the political legitimacy of the assessment.

The MA follows a similar rigour in its assessment as the IPCC. Such scientific assessments apply the judgment of experts to existing knowledge to provide scientifically credible answers to policy-relevant questions. Included material must therefore be published in the peer-reviewed literature. In the MA, each chapter is reviewed twice by individual experts and representatives of the conventions and national governments. Authors must respond adequately to each comment. The whole review process is overseen by a dedicated review board. This process guarantees scientific rigour. At the start of the assessment, all conventions that requested the MA, were requested to provide their ‘user needs’. These needs were updated regularly. Additionally, frequent progress reports are made to the major Conferences of Parties of each convention. These outreach activities will enhance the utility of the MA. The final reports, which are due in 2005, will be approved by the MA board, with representatives of all the conventions, international organizations, the private sector and national governments.

During the design phase of the MA, it also became apparent that a comprehensive presentation of underlying definitions, concepts and theories must be developed first. A writing team was established, which resulted in the Millennium Ecosystem Assessment's Ecosystem and Human Well-being: a Framework for Assessment (2003). This publication has further directed the assessment of the different working groups.

The MA conceptual framework

Ecosystem services are the benefits people obtain from ecosystems (Millennium Ecosystem Assessment 2003). Provisioning, regulating, supporting and cultural services are distinguished (Figure 1). Ecosystem services include products such as food, fuel and fibre; regulating services such as climate regulation and disease control; and non-material benefits such as spiritual or aesthetic benefits. Health is strongly linked to both provisioning services such as food production and regulating services, including those that influence the distribution of disease-transmitting insects and of irritants and pathogens in water and air. Health can also be linked to cultural services through recreational and spiritual benefits.

Human well-being has also multiple constituents, including the basic material for a good life, freedom and choice, health, good social relations, security, and peace of mind and spiritual experience (Figure 1). How well-being, ill-being or poverty are experienced and expressed depends on context and situation, reflecting local physical, social and personal factors such as geography, environment, age, gender and culture. In all contexts, however, ecosystems are essential for human well-being through their provisioning, regulating, cultural and supporting services.

Human intervention in ecosystems can amplify the benefits to human society. However, evidence in recent decades of escalating human impacts on ecological systems worldwide raises concerns about the spatial and temporal consequences of ecosystem changes detrimental to human well-being.

Changes in ecosystem services affect human well-being in many ways. The MA conceptual framework (Figure 2) assumes that a dynamic interaction exists between people and ecosystems, with the changing human condition serving to drive change in ecosystems both directly and indirectly and with changes in ecosystems causing changes in human well-being. At the same time, many other factors independent of the environment change the human condition, and many natural forces are influencing ecosystems.

The problem posed by the growing demand for ecosystem services is compounded by increasingly serious degradation of the capability of ecosystems to provide these services. In many parts of the world, this degradation of ecosystem services is exacerbated by the associated loss of the knowledge and understanding held by local communities – knowledge that sometimes could help to ensure the sustainable use of the ecosystem.

This combination of growing demands being placed on increasingly degraded ecosystems could seriously diminish the prospects for sustainable development. Human well-being is affected not just by gaps between ecosystem-service supply and demand but also by the increased vulnerability of individuals, communities and nations. Productive ecosystems, with their array of services, provide people and communities with resources and options they can use as insurance in the face of natural catastrophes or social upheaval. While well-managed ecosystems reduce risks and vulnerability, poorly managed systems can exacerbate them by increasing risks of flood, drought, crop failure or disease.

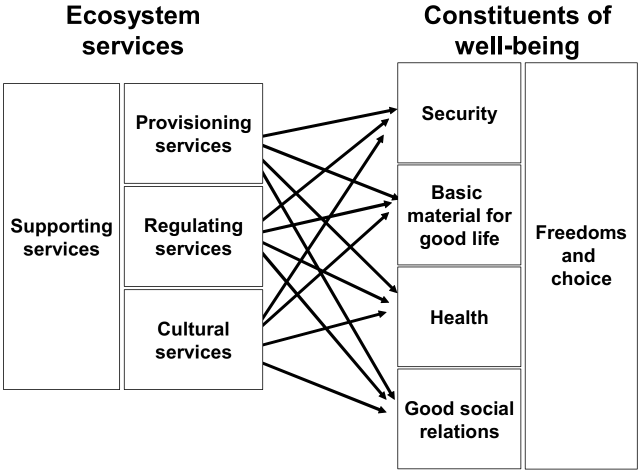


Figure 1. The different ecosystem services and constituents of human well-being and their linkages

In recent decades the world has witnessed not just dramatic changes to ecosystems but equally profound changes to social systems that shape both the pressures on ecosystems and the opportunities to respond. The relative influence of individual nation states has diminished with the growth of power and influence of a far more complex array of institutions, including regional governments, multinational companies, the United Nations, and civil-society organizations. Stakeholders have become more involved in decision-making. Given the multiple actors whose decisions now strongly influence ecosystems, the challenge of providing information to decision-makers has grown. At the same time, the new institutional landscape may provide an unprecedented opportunity for information concerning ecosystems to make a major difference. Improvements in ecosystem management to enhance human well-being will require new institutional and policy arrangements and changes in rights and access to resources that may be more possible today under these conditions of rapid social change than they have ever been before.

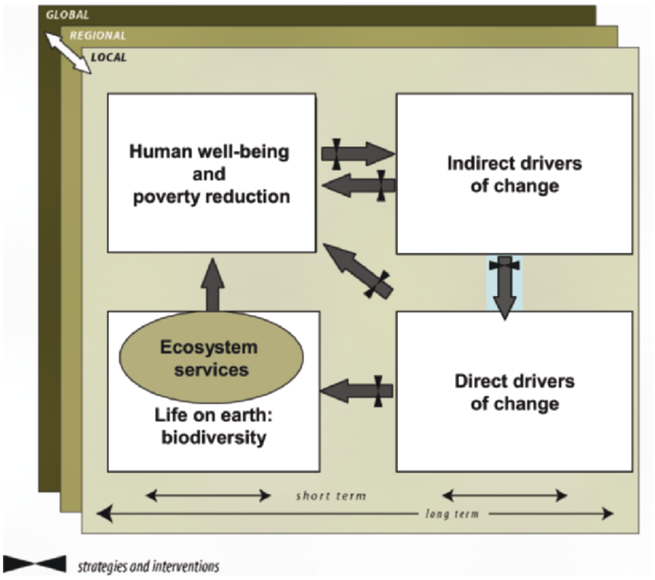


Figure 2. The conceptual framework of the Millennium Ecosystem Assessment

A full assessment of the interactions between people and ecosystems requires a multi-scale approach because it better reflects the multi-scale nature of decision-making, allows the examination of driving forces that may be exogenous to particular regions, and provides a means of examining the differential impact of ecosystem changes and policy responses on different regions and groups within regions. Additionally, in the more local assessment, local and indigenous knowledge can more easily be incorporated into the assessment.

Health is in many respects a strong integrative component of human well-being, since changes in economic, social, political, residential and behavioural circumstances all have health consequences. These factors also strongly influence ecosystems. There is more evidence that changes in ecosystems and in ecosystem services affect livelihood, income and migration and could well lead to political conflicts (e.g. Biggs et al. 2004), than there is on the direct consequences of ecosystem changes for human health. Therefore health in the Millennium Assessment is treated somewhat separately from the other components of well-being (Figure 3) and is addressed in the assessment report in dedicated chapters (e.g. the health synthesis chapter of the responses working group) and in a dedicated summarizing synthesis volume (also with strong contributions of WHO).

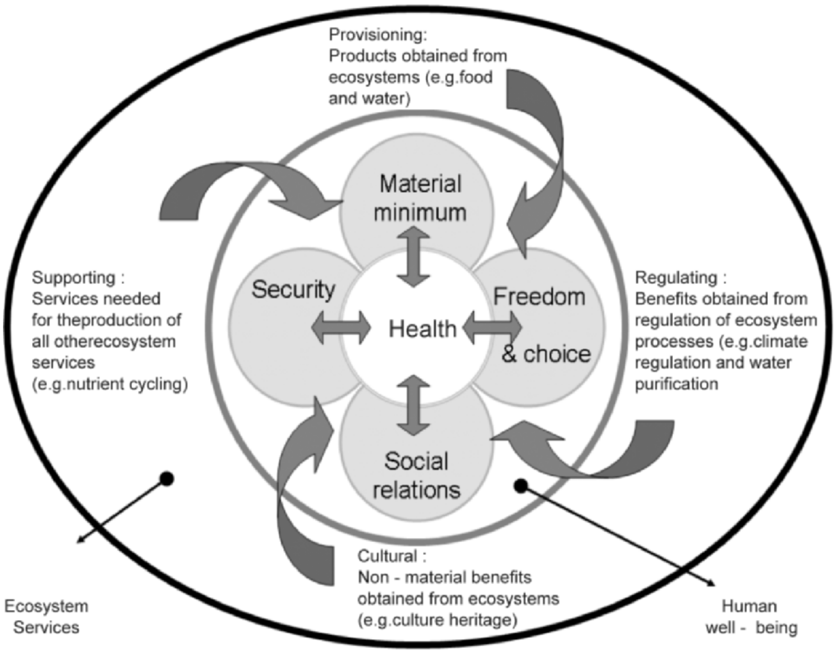


Figure 3. Health as in integral part of human well-being

The assessment process

The assessment process occurs at different levels. Each sub-regional assessment includes health elements, especially focusing on local conditions and knowledge. Wherever possible indigenous knowledge is included in these assessments as well. All the information, however, accumulates in the different global assessments. The assessment process should provide proper baseline data from series of reliable sources. We will make a large effort to make all these datasets available. This will help the peer review process and increase transparency.

Controversial issues must be discussed. If a uniting view cannot be established, opposing views with their arguments must be provided. For example, the value of an almost extinct species ranges from minus (the construction company that wants to build on the species' habitat), zero (direct use value) to infinite (the conservationist) and all values in between (lawyers, tourists, farmers, geneticists, etc). All their arguments are valid for certain conditions but are impossible to reconcile. The assessment must be sensitive to such controversies and must not produce opinionated or policy-prescriptive statements.

With respect to health and other impacts, IPCC (McCarthy et al. 2001) has taken a very sequential approach. Energy scholars used highly aggregated global models to define different future emissions paths. Carbon-cycle modellers and atmospheric chemists used that as input to their models to calculate the resulting atmospheric concentrations, which in turn were used by climate modellers to estimate patterns of climate change. Impact assessors used these climate-change scenarios to estimate impact levels. Many impact models do not produce real impacts but estimate the changes in relative risk of specific threats, such as diseases. The output is then converted to single indicators, such as

Disability-Adjusted Life Year (DALY), which is the only quantitative indicator of disease burden that reflects the total amount of healthy life lost, to all causes during a period of time (World Bank 2002).

The Millennium Assessment tries to improve on this linear approach by closely following the interactions and linkages in its conceptual framework (Figure 2). The steps involved in the assessment are the following:

1. **Identify systems.** The Millennium Assessment selected a series of major systems. These are cultivated land, drylands, forests and woodlands, urban areas, inland water, coastal regions, marine ecosystems, polar regions, mountains and islands. Selection criteria were based upon the uniqueness of these systems themselves and/or the inimitability of its problems (or drivers).
2. **Identify services**. The Millennium Assessment classified all possible ecosystems services into provisioning services, which include all goods produced or provided by ecosystems, regulating services, which include all the benefits obtained from regulation of ecosystem processes, cultural services, which include the non-material benefits obtained from ecosystems, and the supporting ecosystems, which underlay all other services and maintain the conditions for life on earth. Biodiversity is not considered to be a specific ecosystems service because it is related to all others.
3. **Identify drivers**. Indirect drivers that operate at a distance, such as demography, economy and technology, and direct drivers, such as land-use change and pollution, are distinguished. All these drivers operate at different scales. Some cannot be influenced by local decision-makers (i.e. exogenous drivers) but only by national decision-makers (i.e. endogenous drivers). Changing scales also means that different sets of drivers have to be addressed.
4. **Identify the links to and interactions with human well-being** (cf. Figure 1). Not all the links are equally important. Some act directly, others act indirectly. Drivers that impact ecosystems often only indirectly affect human health.
5. **Select appropriate indicators to depict change**. Indicators should be representative for the component or process that they describe; they should be sensitive to changes; they should be reliable and acceptable for a larger user community.
6. **Assess status and trends, using these indicators and baseline data**. Here the analysis must include a description of the conditions before and after changes in drivers. Such changes should be communicated with the appropriate indicators. Figure 4 illustrates this with a hypothetical example of conversion of forest to grassland.

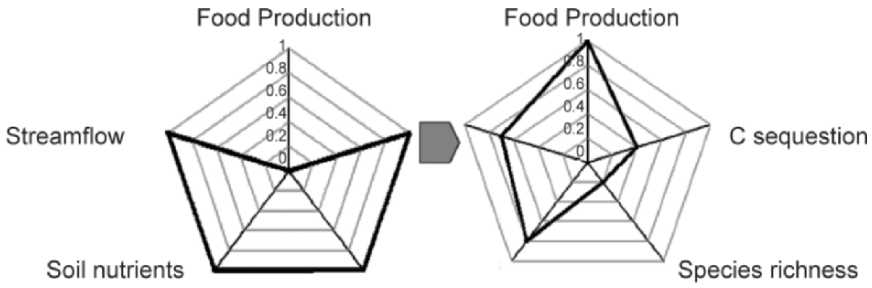
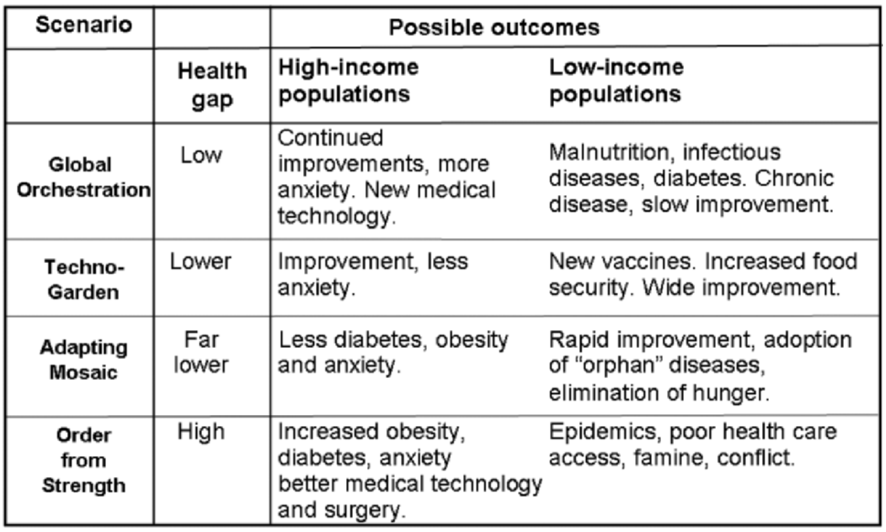


Figure 4. Changes in different indicators for a conversion of natural forest to cropland

7. **Develop scenarios for different non-implausible narratives.** The scenario working-group of the Millennium Assessment has developed four narrative scenarios that depict plausible alternative futures and illustrate a range of possible trajectories. Table 1 characterizes some of the aspects of these scenarios. The strengths of these scenarios are: they blend qualitative and quantitative aspects; they make trade-offs clear; they highlight surprises; and they illustrate effects of alternative policies successful in other sectors. One of the main objectives of these scenarios is to answer the question “how might ecosystems change in the future and what would the health implication of these changes be?”.
   The four scenarios are:
   Global Orchestration: This scenario emphasizes the production of manufactured and human capital. There is a strong belief that market deregulation will improve social and economic well-being and, in the long run, ecological conditions. Ecosystem problems are dealt with reactively. The under-estimation of environmental concerns increases the risks of ecological surprises, including emerging infectious diseases.
   Technogarden: Technology and market-orientated institutional reforms are used to achieve solutions to environmental problems. Technological improvements are combined with better ecological engineering to optimize ecosystem services. It is assumed that ecological engineering is fairly successful and produces few adverse ecological surprises, and that the ability of societies to cope with these surprises is high.
   Order from Strength: The world is progressively compartmentalized as better-off populations focus inwardly in response to perceived threats. Limited benefits are provided for allied poor countries. The environment is seen as secondary, and there is a belief that technology can solve most environmental challenges. Parts of the developing world experience constant low-level violence, with periodic frank conflict.
   Adapting Mosaic: Society emphasizes the flexible management of socio-ecological systems, and the balancing of human with manufactured and natural capital. A mix of optimism and humility leads to the preparation for adverse ecological surprises. Political and economic power devolves, but, eventually, the focus on local governance leads to failures in managing the global commons. In response, communities develop ecologically-centred networks.
8. **Evaluate response options and strategies** and their context to understand what works where and why. There are two routes to avoiding disease and injury caused by ecosystem change. One is to prevent or limit environmental damage; the other way is to make whatever changes will protect individuals and populations from the consequences of ecosystem change. Both are assessed. One of the major preliminary finding is that policies and actions to reduce vulnerability to disease and injury have much in common with the steps that need to be taken to promote sustainable use of ecosystems.
9. **Use integrated assessment tools to identify and understand trade-offs and synergies** between different policy options. Where there are trade-offs, it is important for decision-makers and the public to understand the health consequences so that they can be included alongside economic or other costs when prioritizing decisions. Major trade-offs, for example, exist between infectious-disease risk and some development projects geared to food production, electrical power and economic gain.

Table 1. Health issues in the scenarios of the Millennium Assessment



Scenario		Possible outcomes	
	Health gap	High-income populations	Low-income populations
Global Orchestration	Low	Continued improvements, more anxiety. New medical technology.	Malnutrition, infectious diseases, diabetes. Chronic disease, slow improvement.
Techno-Garden	Lower	Improvement, less anxiety.	New vaccines. Increased food security. Wide improvement.
Adapting Mosaic	Far lower	Less diabetes, obesity and anxiety.	Rapid improvement, adoption of "orphan" diseases, elimination of hunger.
Order from Strength	High	Increased obesity, diabetes, anxiety better medical technology and surgery.	Epidemics, poor health care access, famine, conflict.

10. **Identify major uncertainties** in the baseline scenarios and response options. There are unavoidable uncertainties about the impacts of environmental changes on human health. These include the potential magnitude, timing and effects of environmental change; the sensitivity of health and other ecosystem services; the effectiveness of different courses of action to address the potential impacts; and the shape of future societies. Traditional epidemiological methods are not well-suited to such issues, as they are designed to test the influence of discrete risk factors on well-defined health outcomes (e.g. the effect of smoking on lung cancer), and emphasize avoiding an incorrect identification of a harmful effect. In contrast, environmental change has diverse and wide-ranging rather than discrete effects on individuals or small areas, an absence of control groups, and may be difficult or impossible to reverse, so that false negative effects are equally as important as false positives. Still, other approaches, such as scenario analysis, have to be developed to be able to communicate uncertainty to decision-makers and so comprehensively addressing their needs.
11. **Develop the assessment reports** and communicate major findings to the user community. Well-written technical summaries, summaries for decision-makers and synthesis reports for specific audiences, such as each convention or the private sector, all with clear illustrations, are needed to communicate the findings of the assessment. The Millennium Assessment has already appointed an outreach officer and is planning for an effective communication strategy (see also www.millenniumassessment.org).

One of the current outcomes of the health chapters of the millennium assessment is a risk assessment for health impacts of different ecosystems services (Figure 5). Here the direct effects of, e.g., water and food scarcity are listed. Also the direct physical impacts of sudden events such as gales and floods stand out. Changes in climate and decline of biodiversity are much more diffuse.

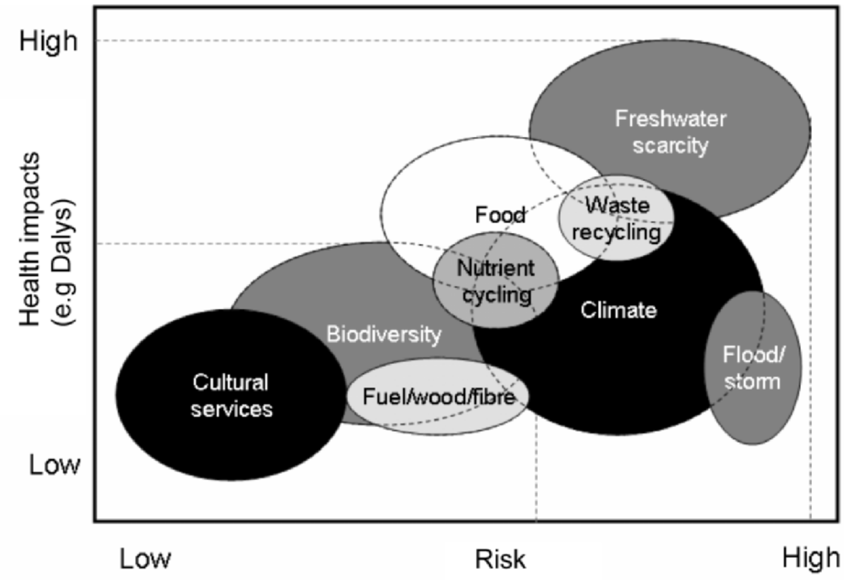


Figure 5. A simple risk assessment of health impacts and different types of environmental change

Concluding remarks

The Millennium Ecosystem Assessment differs form assessments like the IPCC in that it comprehensively looks at multiple drivers and multiple impacts. It more strongly bridges between the natural and social sciences and tries to understand the systemic interactions between ecosystems, ecosystem services and human well-being. One of the main findings is that a lot of the science needed to do this is still immature. The Millennium Assessment will therefore probably not provide ultimate answers to the entire user needs but will, at least, provide a foundation for further integrative research.

The Earth Systems Science Partnership of all the global-change research programmes is already picking up this challenge by developing a joint project on global environmental change and human health. Here frameworks for improved vulnerability and adaptation assessments will be developed together with a better understanding of all the environment–health relations. The objective is to understand better the multi-faceted and complex linkages between global change (including climate change, land- and sea-use changes, global biodiversity loss and changes, global socio-economic changes) and human health. This project is also strongly supported by the World Health Organization. In the coming decade much advancement in understanding will surely be made in this research area. When available, decision-makers and the broader public will surely gain from these achievements.

References

Alcamo, J., Amann, M., Hettelingh, J.-P., et al., 1987. Acidification in Europe: a simulation model for evaluating control strategies. *Ambio,* 16 (5), 232-245.

Biggs, R., Bohensky, E., Desanker, P.V., et al., 2004. *Nature supporting people: the southern African Millennium Ecosystem Assessment*. Council for Scientific and Industrial Research, Pretoria.

Brundtland, G.H. (ed.) 1987. *Our common future*. Oxford University Press, Oxford.

Carson, R., 1962. *Silent spring*. The Riverside Press, Cambridge.

McCarthy, J.J., Canziani, O.F., Leary, N., et al. (eds.), 2001. *Climate change 2001: impacts, adaptation and vulnerability*. Cambridge University Press, Cambridge. [http://www.grida.no/climate/ipcc_tar/wg2/index.htm]

McG. Tegart, W.J., Sheldon, G.W. and Griffiths, D.C. (eds.), 1990. *Climate change: the IPCC impacts assessment*. Australian Government Publishing Service, Canberra.

Meadows, D.H., Meadows, D.L., Randers, J., et al., 1972. *The limits to growth: a report for the Club of Rome's project on the predicament of mankind*. Universe Books, New York.

Millennium Ecosystem Assessment, 2003. *Ecosystems and human well-being: a framework for assessment*. Island Press, Washington. [http://pdf.wri.org/ecosystems_human_wellbeing.pdf]

World Bank, 2002. *World development report 2003: sustainable development in a dynamic world: transforming institutions, growth, and quality of life*. Oxford University Press, New York. [http://econ.worldbank.org/wdr/wdr2003/text-17926/]

4

Application of geographic information systems to the study of the ecology of mosquitoes and mosquito-borne diseases

John E. Gimnig [#]*, Allen W. Hightower, William A. Hawley*

Abstract

Geographic information systems (GIS) are powerful computer mapping and analysis systems for studying spatial patterns and processes; they are applicable to numerous disciplines, including the study of mosquito ecology. The distribution of mosquitoes is largely dependent upon the spatial distribution of their larval breeding sites, their flight range and the spatial distribution of their preferred hosts. These are all heterogeneous in space and time and GIS therefore has many potential applications to the study of mosquitoes and the diseases they transmit. GIS may be used to map and analyse the spatial distribution of mosquitoes and to assess the ecological factors that contribute to observed distributions. A detailed understanding of what drives heterogeneities in the distribution of mosquitoes and mosquito-borne diseases can help to design better, more efficient control programmes that maximize the use of limited resources.

Keywords: geographic information systems; remote sensing; mosquitoes; malaria

Introduction

Geographic information systems (GIS) are computerized systems capable of integrating, displaying and analysing large quantities of spatial data (Vine, Degnan and Hanchette 1997). A GIS is a powerful tool for elucidating spatial patterns and processes. In addition, GIS is able to link spatial and non-spatial data, allowing for a wide range of display and analysis capabilities. GIS has applications in numerous fields of study, including marketing, agriculture, forestry, animal ecology, transportation planning and public heath (Clarke, McLafferty and Tempalski 1996). Applications in public health include the estimation of spatial variation of disease, determination of risk factors of disease, and improved delivery of health services (Briggs and Elliott 1995; Tanser and Le Sueur 2002; Vine, Degnan and Hanchette 1997).

The use of GIS has increased dramatically in recent years due to several factors. One is the recognition of its application to a wide range of disciplines. However, its widespread appeal was made possible mainly by increasing technological developments. The advent of powerful, inexpensive personal computers and the development of easy to use, menu-driven GIS software made it possible for persons with little or no expertise to design and conduct spatial studies. Lastly, the acquisition of spatial data has become easier. Global positioning systems (GPS)

[#] John E. Gimnig, Centers for Disease Control and Prevention, Division of Parasitic Diseases, Mailstop F-22, 4770 Buford Highway, Atlanta, GA 30341, USA. E-mail: JGimnig@cdc.gov

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 27-39.

have become less expensive and easier to use with increased capabilities for rapidly collecting both spatial and non-spatial data. For many applications, spatial data already exist and public-domain digital maps can be downloaded from the Internet (Clarke, McLafferty and Tempalski 1996; Moore and Carpenter 1999).

GIS has many applications to the study of vector-borne diseases, as many of the underlying processes influencing the distribution of insect vectors of disease are spatially heterogeneous. Mosquitoes require pools of water in which to breed and the short flight range of many species limits the adult populations to areas surrounding their breeding sites. Recently, there has been interest in applying GIS to study the continental and global distribution of malaria and the mosquitoes that transmit malaria (Coetzee, Craig and Le Sueur 2000; Craig, Snow and Le Sueur 1999; Omumbo et al. 1998). These continent-scale studies have also been used to estimate the impact of global warming on the distribution of mosquitoes and malaria.

On a smaller scale, GIS has several applications to the study of mosquito biology and ecology. In many cases, GIS is the best or the only available method to answer questions regarding mosquito ecology. Studies of risk as a function of distance from known breeding sites are one common application of GIS. This is particularly useful in areas with a small number of discrete breeding sites around urban or highland areas where mosquitoes exhibit strong spatial patterns over short distances. Using knowledge of the distribution of adult mosquitoes and the distribution of larval breeding sites, average flight distances of malaria vectors may be inferred using GIS. GIS, in combination with remote-sensing (RS) technology, has also been employed to predict areas of high productivity of mosquitoes and potential malaria epidemics based on the detection of proxy ecological variables (Hay et al. 2000; Thomson et al. 1996). Other factors affecting the distribution of mosquitoes, such as the distribution of available hosts, have been investigated with GIS. The rapid decline of adult mosquitoes at the onset of the dry season and the rapid increase at the onset of the rains has puzzled mosquito biologists. Various hypotheses to explain the rapid changes in adult numbers include aestivation of adults through gonotrophic dissociation, extended survival of eggs and larvae on wet or damp soil, or survival in focal refugia where breeding may occur year-round. Through repeated measures of mosquito abundance over time, GIS may be applied to identify the location of potential dry-season refugia of mosquitoes. GIS has been applied to estimate the impact of insecticide-treated nets (ITNs) on the spatial distribution of malaria vectors. The results suggest that ITNs derive some of their benefit from an area-wide impact on adult mosquito populations and that this benefit may extend into areas where ITNs are not used. Lastly, GIS has application in the design and implementation of control activities that target the vectors of disease. In this paper we describe the development and application of GIS technology to the study of mosquitoes and malaria.

Development of a GIS

The development and application of a GIS includes 3 components: data acquisition and management, visual presentation and statistical analysis. The first factor to take into consideration is the scale that is relevant to the questions being addressed (Clarke et al. 2002; Moore and Carpenter 1999). The selection of scale is critically important as biologically relevant spatial patterns may be masked if the scale is not appropriate. The scale should take into consideration the question being addressed and the biological processes underlying the topic under study. Continental- or regional-scale models may help further define the relationship between climate and the risk of malaria, better quantify risk over large geographic regions and assess the potential impact of climate change on malaria distribution. However, these models mask local-scale variation. For studies of mosquito ecology, the appropriate scale is likely just a few kilometres as the relevant underlying biological process (flight range) is usually less than 1 kilometre.

The acquisition of spatial data may be done by several means. First, existing maps or aerial photographs may be digitized and imported into a spatial database. This has already been done for many areas and public-domain maps may be available on the Internet for many areas of developed countries (Clarke et al. 2002; Moore and Carpenter 1999). In addition to Cartesian coordinates, other geo-referenced information such as postal codes or even specific addresses may be available in these countries. Unfortunately, reliable maps, aerial photos and other geo-referenced information often are not available in developing countries. Also, for the study of mosquito ecology, it is often necessary to map features that do not appear on existing maps (e.g. small bodies of water). In these cases, one may develop maps using GPS technology. Simple hand-held GPS units have become increasingly affordable and easy to use and may be employed to rapidly generate accurate maps. Many GPS units even allow for data entry so that non-spatial data, linked to a geographical feature, may be recorded at the same time as the geographical position. Simple GPS is often adequate for many spatial studies as there are many sources of error that may reduce its accuracy. If more accurate readings are desired, differential GPS may be employed. This approach can generate positional data that are accurate to within one metre (Hightower et al. 1998). Additional, non-spatial data may also be linked with positional data for incorporation into statistical models.

Numerous software packages make presentation and simple analysis of spatial data easier than ever. The use of maps showing spatial patterns may be regarded as a simple, straightforward approach to data analysis as many spatial patterns are evident when simply presented on a map. Spatial patterns may be presented using contours, sized symbols and shading. In addition, a GIS can estimate distances, conduct buffer analysis, perform a spatial query on data from multiple sources and perform polygon overlay analysis. While simple visual presentation is often sufficient to discern spatial patterns, it is often necessary to perform formal data analysis. Data analysis methods for spatial data are numerous and varied. Detailed description of spatial-data analysis methods is beyond the scope of this paper (for more detailed discussion, see Moore and Carpenter 1999), however, they may be grouped into exploratory analysis and modelling. Exploratory analytic techniques are generally used to identify clusters and determine whether these occur by chance. Many of these methods do not account for underlying distribution of populations but are a quick way to assess ‘hot spots’ that may deserve further investigation. Other exploratory techniques include kriging and Bayes methods for data smoothing and interpolation. Results can easily be presented in the form of surface maps employing colour shading to indicate areas of high or low risk. Overlaying these interpolated maps on other geographic features is an informal approach to identifying potential risk factors. More formal data analysis can also be done by modelling, integrating GIS data with standard statistical models. Unfortunately, many entry-level GIS software packages do not allow for advanced analytic techniques but these may usually be done in existing statistical packages.

Chapter 4

Applications in mosquito ecology

GIS has many applications to the study of mosquitoes and mosquito-borne diseases. The distribution and abundance of mosquitoes and other vectors of human disease are often determined by factors that exhibit clear spatial heterogeneity. The most obvious factor influencing the distribution of mosquitoes is the distribution of breeding sites. The distribution of available hosts and the distribution of vector-control interventions may also affect mosquito abundance and distribution. Below, we review some of the applications of GIS technology to the study of malaria vectors, with an emphasis on the vectors in sub-Saharan Africa.

Mosquito abundance and distance from breeding sites

There have been numerous studies demonstrating the spatial distribution of malaria vectors as a function of distance from known or suspected breeding sources. Larval mosquitoes are usually highly aggregated in pools of waters with specific characteristics. The distribution of adults is largely dependent upon the distribution of these larval habitats and the flight range of the adults. Using this information it is possible to estimate and even predict the risk of exposure (i.e. infectious bites) based upon the distance to known breeding sites.

Smith et al. (1995) described the small-scale spatial and temporal variation in the abundance of malaria vectors in a single village near Ifakara, Tanzania. They mapped the houses in the village using GPS and performed CDC light-trap collections from a subset of houses every two weeks for one year. Mosquito abundance was modelled using several statistical methods to adjust for spatial and temporal effects as well as the effect of non-spatial variables such as the presence of windows or animal sheds. Contour maps were generated based upon the models and overlaid on maps of the study area. Areas of high mosquito abundance within houses tended to correlate with low-lying areas near streams and rice fields. However, after accounting for housing density, it was observed that the average number of *Anopheles gambiae s.l.* per hectare was highest on densely populated ridges at the centre of the village. This demonstrates that the underlying distribution of houses may affect apparent spatial patterns and that the unit of measure (number per house vs. number per hectare) must be selected carefully. For ecological studies assessing overall population densities, the number of mosquitoes per hectare may be the more appropriate unit of measure. However, studies of malaria epidemiology are usually interested in estimating the exposure of individual persons and the number of mosquitoes per house may be the more appropriate unit of measure for these studies. This effect of different units of measure was less pronounced in *An. funestus*, which had the highest density per house and the highest density per hectare in the low-lying areas of the village.

Ribeiro et al. (1996) studied the distribution of malaria vectors in a single village in Ethiopia. Existing maps of the village were digitized and converted to Cartesian coordinates for data analysis. Mosquitoes were collected monthly by mouth aspiration or pyrethrum spray catch. An average of 54 houses were sampled by mouth aspiration each month. Aggregation of mosquitoes was estimated using Taylor's power regression plot and Iwao's mean crowding plots. In addition, kriging was performed to estimate the number of mosquitoes throughout the village for each month. Mosquitoes were highly aggregated, particularly during the dry season. For most months, fewer than 20% of houses accounted for 50% of all collected mosquitoes. Maps based upon kriging analysis showed that clusters of mosquitoes tended to segregate around the edges of villages. It was hypothesized that the distribution of mosquitoes was largely affected by the distribution of breeding sites around the village. It was also suggested that selective targeting of areas of high mosquito abundance could maximize the effectiveness of vector control, particularly when mosquito densities are low.

Two studies in urban areas clearly demonstrate the strong effect of distance to breeding sites on adult mosquito populations and the risk of malaria infection. In Dakar, Senegal, the dispersion of adult mosquitoes (*An. arabiensis*) from a permanent swamp and the prevalence of antibodies to *Plasmodium falciparum* in children residing near the swamp were investigated (Trape et al. 1992). Mosquito abundance within houses varied by distance from the swamp. In the rainy season, there were an average of 414 *An. arabiensis* per house within 160 m of the swamp while there were only 21 per house at distances 785-910 m from the swamp. During the dry season the effect of distance was even more pronounced. The average number of *An. arabiensis* was 84 per house at distances <160 m from the swamp, 40 per house at distances of 160-285 m from the swamp and <10 per house at distances >285 m from the swamp. There was also a decrease in proportion of children with antibodies to *P. falciparum* at increasing distances from the swamp. The prevalence of children without antibodies rose from 17% in children residing within 160 m of the swamp to 73% in children residing 785-910 m from the swamp. Similar observations were made in Maputo, Mozambique (Thompson et al. 1997). Entomological inoculation rates (EIR), malaria prevalence and clinical malaria were observed over 2.5 years in a suburb of Maputo adjacent to mosquito breeding-sites. Malaria prevalence in areas adjacent to the breeding sites ranged from 40 to 60% but was as low as 5-11% just 500 m from the breeding sites. The risk of clinical malaria was estimated to be 6.2 times higher in individuals living within 200 m of the breeding site compared to persons living >500 m away. EIRs were estimated to be as high as 20 infectious bites per person per year in areas adjacent to the breeding site but were too low to measure in areas more distant from the breeding site.

Clarke et al. (2002) studied the relationship between distance from mosquito breeding-sites and entomological and clinical malaria indices in 48 villages along the River Gambia in West Africa. Distances from villages to the nearest edge of the alluvial plain of the River Gambia were estimated from 1:50,000 maps. Mosquitoes were collected every 2 weeks throughout the transmission season from 2 houses in each of the 48 villages. A cross-sectional survey was conducted in 1996 in which children from sentinel houses and their neighbours were tested for malaria and anaemia. EIRs, the prevalence of parasitaemia and the prevalence of enlarged spleens were all lower in villages $\geq$3 km away from main breeding sites along the river. However, among infected children, rates of high-density parasitaemia, fever and anaemia were all higher in villages $\geq$3 km from the breeding sites. Furthermore, older children in these villages did not experience a decline in clinical illness. These data suggest that the lower transmission in villages further from mosquito breeding-sites results in a reduced acquisition of natural immunity to *P. falciparum*. In a similar study in the same area, Thomas and Lindsay (2000) correlated exposure to adult mosquitoes in 10 villages with distance to breeding sites. Using multispectral SPOT satellite imagery with 20 m resolution to detect larval breeding sites within 2 km of a village, they were able to estimate the exposure to adult mosquitoes in 26 villages where clinical surveys had been conducted but entomological data were unavailable. Similar to the study of Clarke et al. (2002), the estimated exposure rates for each village were positively correlated with parasite prevalence and negatively correlated with high density parasitaemia and splenomegaly.

The use of RS in conjunction with GIS to predict areas of high mosquito density is illustrated in several studies from Central America. Rejmankova et al. (1995) used RS to estimate land-cover elements in Belize and then predict areas with high/low densities of *An. albimanus*. Land cover was classified using SPOT satellite imagery with a resolution of 20 m x 20 m. Areas identified as contact zones between the fresh water and the sparse emergent-vegetation zones on the SPOT image were considered predictors of *An. albimanus* densities. Villages within 500 m of a larval habitat were predicted to be high-risk villages while villages located >1500 m from a larval habitat were predicted to be low-risk villages. The SPOT classification was verified by human landing catches made for one night during the dry season in each of 16 villages. Villages were defined as having high mosquito densities if there were $\geq$0.5 mosquitoes/human/minute; villages with <0.5 mosquitoes/human/minute were considered to have low mosquito densities. There was good agreement between densities predicted by the SPOT image and those observed in the human-landing collections. All sites predicted to have low densities had landing rates <0.5 mosquitoes/human/minute while one village predicted to have high densities by SPOT imagery was found to have low densities in the human-landing collections. Similar studies with *An. albimanus* have been done in other areas of Central America. Beck et al. (1994) used SPOT imagery to classify land cover and then used a GIS to create 1-km buffers around 40 villages in southern Mexico. The proportion of each land-cover classification was estimated within the 1-km buffer surrounding each village. Vector abundance was measured using light traps in each village over 4 months in 1992. Discriminant function and linear regression analyses both showed *An. albimanus* densities to be correlated with the proportion of land cover surrounding villages classified as transitional swamp or unmanaged pasture. Additional studies using SPOT imagery have been used with somewhat less accuracy to predict areas with high densities of *An. psuedopunctipennis* (Roberts et al. 1996) and the larval breeding sites of *An. vestitipennis* (Rejmankova et al. 1998).

Spatial distribution of hosts and mosquito community structure

Many mosquito species feed on a restricted range of available hosts. Members of the *An. gambiae* complex in East Africa exhibit distinct host-choice behaviour with *An. gambiae* being strongly anthropophilic and *An. arabiensis* usually being strongly zoophilic. It is well known that the location of sampling of adult females will strongly affect the proportion of each of these sibling species. Recent studies suggest that the spatial distribution of hosts may also affect the spatial distribution of the larvae of these species. Charlwood and Edoh (1996) and Minakawa et al. (1999) both found that *An. gambiae* larvae were more prevalent near human habitation while *An. arabiensis* larvae were more common near animals. Several studies have shown little or no discriminating physical or chemical characteristics between habitats with *An. gambiae* vs. those with *An. arabiensis* (Minakawa et al. 1999; Gimnig et al. 2001). In the study by Minakawa et al. (1999), the only variable that was predictive of *An. gambiae* and *An. arabiensis* was proximity to human habitation.

To expand on this finding, Minakawa, Seda and Yan (2002) used a GIS to compare the proportions of *An. gambiae* and *An. arabiensis* larvae in relation to proximity to human and animal habitation in western Kenya. Surveys of larval habitats were conducted in the early and late rainy season of 1999. Anopheline larvae were collected and preserved in ethanol for identification by polymerase chain reaction. All houses, cowsheds and larval habitats were mapped by GPS and distances from larval habitats to the nearest house and cowshed were calculated. The densities of humans and cattle around each larval habitat were estimated by taking the average numbers of humans and cattle in the 5 nearest houses and cowsheds. The ratio of human density to cow density and the ratio of the distance from larval habitats to houses and from larval habitats to cowsheds were modelled using linear regression to assess their effect on the proportion of *An. gambiae* in each larval habitat. Both measures indicated that the proportion of *An. gambiae* was higher in habitats near houses while the proportion of *An. arabiensis* was higher near cowsheds. Analysis of adult densities in houses in the study area indicated that only proximity to larval habitats was a significant predictor of adult densities – the densities of humans and cows and the distance to the nearest cowshed were not significantly associated with adult *An. gambiae* or *An. arabiensis* densities within houses. This study highlights the importance of the availability of hosts on the spatial distribution of larval mosquitoes and the community structure within larval habitats. Additional research employing GIS is necessary to further assess how the spatial distribution of human hosts within villages may affect the spatial distribution of adult mosquitoes.

Identification of dry-season refugia

In areas of sub-Saharan Africa with highly seasonal transmission, malaria vectors are often absent for much of the year. How mosquitoes survive dry periods has been a subject of conjecture. It has been hypothesized that mosquitoes may aestivate through some form of gonotrophic dissociation, that eggs or larvae may survive on damp or even dry soil for short periods (Beier et al. 1990; Minakawa et al. 2001), or that mosquito populations persist year-round in localized refugia. By applying a GIS over time, seasonal foci of mosquitoes may be identified that would suggest refugia where mosquito breeding continues during extended dry periods.

Evidence from a study in western Kenya suggested that malaria vectors in this region survive dry seasons by retreating to refugia around the beds of streams and rivers (Hightower et al. 1998). The entire 70-km^2 study area in western Kenya was mapped by differential GPS. Geographic features mapped included hospitals, clinics, medicine shops, major shopping centres, schools, churches, boreholes, burrow pits and all 1,169 compounds (clusters of houses belonging to one family). Also mapped were roads, streams and the shore of lake Victoria, which bordered the study area. Mosquitoes were collected from a subset of houses in June and September of 1995, representing the end of the rainy season and the dry season, respectively. Bed-net trap collections were made from 394 houses in June and from 416 houses in September. At least 3 collections were made for each house and were averaged for each month. Linear regression was used to assess the relationship between mosquito density and the distance from potential larval habitats, defined as the lakeshore, streams and burrow pits.

For *An. gambiae*, average density decreased with increasing distance from potential larval habitats during the dry season (P=0.0039). This relationship was not evident during the rainy season (p=0.153). These results were interpreted to indicate that *An. gambiae* breeding continues year round, but is restricted to areas around streams and the lakeshore where receding waters likely leave pools of water that are suitable for developing larvae. For *An. funestus*, the average number of adults actually increased with increasing distance from larval habitats during the rainy season (p=0.0191) but not the dry season (p=0.6608). The somewhat surprising results observed for *An. funestus* highlight our lack of knowledge of *An. funestus* breeding habits.

This study demonstrates how a GIS may be used to identify areas where mosquitoes may survive extended dry periods. This is not definitive proof that these areas act as refugia. Nor does it exclude the possibility that other survival mechanisms contributed to the dry-season survival of *An. gambiae*, particularly in other regions of Africa. However, as is often the case, GIS may generate hypotheses or indicate additional avenues of research. In this case, surveys of larval mosquitoes during the dry season may provide further evidence that *An. gambiae* is breeding in isolated areas during the dry season. The poor correlation between distance from suspected breeding sites and the abundance of *An. funestus* adults indicates additional research is necessary to characterize the larval habitats of this mosquito properly.

Spatial impact of vector control interventions

Insecticide-treated mosquito nets and curtains (ITNs) have been shown to reduce malaria morbidity and all-cause mortality (Snow et al. 1988; Phillips-Howard et al. 2003) in sub-Saharan Africa, and the World Health Organization's Roll Back Malaria Initiative has advocated their use for the prevention of malaria. Despite their obvious benefits, one concern about ITNs has been that pyrethroid insecticides have strong excito-repellent properties and that incomplete coverage will result in diversion of mosquitoes from households with nets to those without nets (Lines, Myamba and Curtis 1987). This could result in even higher exposure to infected mosquitoes among persons who do not own nets. This is a particular concern as most ITN distribution programmes in Africa rely on private markets or partially subsidized, targeted distribution through the public sector. If diversion of malaria vectors does occur, current distribution systems are likely to increase malaria exposure among the poorest and most vulnerable populations.

We tested the hypothesis that widespread distribution of ITNs affects the spatial distribution of malaria vectors as part of a large-scale trial of ITNs conducted in western Kenya (Gimnig et al. 2003). The study area, west of Kisumu along the shores of Lake Victoria, had been mapped previously using differential GPS (Hightower et al. 1998). The 19 villages located in the southern part of the study area were included in the entomological evaluation. Weekly bed-net trap collections were conducted in households where children had been enrolled in a study of malaria epidemiology and the development of natural immunity since 1992. Nine of the 19 villages were randomly allocated to receive ITNs, and in December of 1996, ITNs were distributed to cover all the sleeping spaces (beds and mats) in the intervention villages.

Entomological collections continued through October of 1997 in the control villages only. These data provided an opportunity to determine whether ITNs in the intervention villages affected the distribution of malaria vectors in the control villages. Control households were categorized by distance to the nearest intervention village as 0-299 m, 300-599 m, 600-899 m or ≥900 m. The effect of distance from the intervention village on the number of mosquitoes collected was modelled by Poisson regression. Distance to intervention villages was included in the models either as a categorical variable or as a continuous categorical variable to test for trends. Models were constructed for *An. gambiae s.l.* and *An. Funestus* and each model controlled for pre-intervention trends. Other variables controlled for in the models were rainfall, temperature and distance to the lakeshore. For *An. gambiae*, there was a pre-existing trend of increasing numbers with increasing distance from the intervention area (p=0.027). However, this trend was exacerbated in the intervention year (p=0.002) and the difference between years was statistically significant (p=0.05). For *An. funestus*, no trend was observed in the pre-intervention year (p=0.373), while a strong trend of increasing numbers with increasing distance from intervention villages was observed after the introduction of ITNs (p=0.014). Categorical analysis indicated that the effect on *An. gambiae* could be detected up to 600 m from an intervention village. For *An. funestus*, the effect was strongest within 300 m from an intervention village and was not statistically significant at distances further than 300 m. These results indicated that populations of *An. gambiae* and *An. funestus* were depressed in the areas surrounding ITNs and suggested that high coverage of ITNs has a community-wide impact on these malaria vectors.

These results were confirmed by spatial analysis of clinical indicators of malaria (Hawley et al. 2003). Malaria-specific indicators were measured in 2 cross-sectional surveys conducted in 60 villages located north of the entomological study area. The surveys were conducted in February-March of 1997 and November-December of 1998. Approximately 900 children under 3 years of age were examined in each cross-sectional survey for malaria parasitaemia, high-density parasitaemia, clinical malaria and anaemia. Logistic regression was used to assess the effect of distance to the nearest intervention or control village for each health indicator. The distance variable included 8 categories. For ITN villages, distances to control villages were categorized as 0-299 m, 300-599 m, 600-899 m. and >900m. For control villages, distances to intervention villages were categorized using the same distance categories. Models controlled for age, sex, weight for age, cross-sectional number and distance to nearest health clinic. For all malaria-specific outcomes, the spatial patterns were similar. Children residing in intervention villages experienced a protective effect for malaria-specific disease outcomes compared to children in control villages. This protective effect extended into adjacent control villages with children residing within 300 m of the intervention villages receiving a similar protective effect as children residing within the intervention villages. Analysis of the spatial pattern of child mortality within the whole of the study area yielded similar results. The spatial pattern of geohelminth infections, which should not be affected by ITNs, was also modelled. No apparent pattern of geohelminth infections was observed indicating that the results for malaria-specific outcomes were not the result of study/model design.

Additional models were constructed to assess what proportion of households must be covered with ITNs to observe this community effect. Three-hundred-metre buffers were created around each household in the control villages and coverage – defined as the proportion of households using ITNs within the 300-m buffer zone – was calculated for each household. The effect of coverage on malaria-specific indicators was modelled using logistic regression with households in areas of 0% coverage used as the reference group. Rates of high-density parasitaemia and anaemia decreased with increasing coverage of ITNs surrounding a control household. Children living in control households in areas where coverage with ITNs was $\geq$50% were significantly less likely to have high-density parasitaemia or anaemia compared to children living in areas where coverage with ITNs was 0%.

These studies, employing GIS, indicated that the spatial distribution of ITNs affects the spatial distribution of malaria vectors as well as the spatial pattern of clinical illness. These findings are in agreement with other studies that suggest that high coverage of ITNs may reduce morbidity (Howard et al. 2000) and mortality (Binka, Indome and Smith 1998) among neighbours who do not own ITNs. One drawback in these studies is that the distribution of ITNs was artificial, with villages having either very high or very low coverage. In practice, the distribution of ITNs will be more random. The effect of incomplete coverage in these situations may be evaluated using the buffer analysis approach described above.

Designing vector control interventions with GIS

Given the spatial heterogeneity in the distribution of anopheline vectors of malaria, GIS has potential applications in designing and monitoring interventions. Studies demonstrating the rapid decline in vector abundance and malaria prevalence at increasing distances from known vector breeding-sites suggest that spatial targeting of interventions to areas nearest breeding sites could have a substantial impact upon malaria prevalence in communities, at least in certain situations. A targeted approach would be a more cost-effective use of limited resources than complete coverage when malaria risk varies substantially and predictably within a community. RS could also be used as a tool for rapidly identifying potential vector breeding-sites to supplement a GIS approach to targeted vector control.

The use of GIS has been already been applied for surveillance for malaria as well as targeting of vector control interventions for malaria prevention. In Israel, a national database of vector breeding-sites and population centres was created (Kitron et al. 1994). Distances between breeding sites and population centres were calculated and the risk of malaria transmission was estimated based upon different vector species, their vector capacity and their flight ranges. Although malaria is not endemic to Israel, the surveillance system ensures that localized epidemics can rapidly be associated with probable vector species, likely breeding sites and potential human source of infection. Appropriate control measures can then be rapidly implemented.

In South Africa, GIS was used to better define malaria risk in two districts within Mpumalanga province (Booman et al. 2000). The reporting system for malaria was strengthened and modified to include address in case reports. Data collected from 1995 through 1999 were used to estimate the incidence of malaria in each village and town in Barberton and Nkomazi districts and the data were analysed visually by creating thematic maps displaying malaria risk throughout the two districts. A clear decline in malaria incidence was observed from west to east, with the highest rates in villages and towns along the border with Mozambique. Statistical analysis indicated that persons living within 5 km of the Mozambique border had a 4-fold higher risk of malaria compared with persons residing in villages more distant. This finding allowed district managers and the Mpumalanga Malaria Control Programme managers to limit indoor residual spraying to villages closer to the Mozambique border.

Targeting of vector control interventions requires detailed knowledge of vector biology and ecology, particularly breeding habits and flight range. While targeting can greatly increase the effectiveness of interventions, exclusion of locations where transmission occurs may cause targeted interventions to fail. Furthermore, the level of transmission may also determine whether spatially targeted interventions are appropriate (Carter, Mendis and Roberts 2000). In areas of low to moderate transmission, spatial aggregation of vectors and malaria cases is common and spatial targeting may be appropriate. In areas of high transmission, spatial aggregation in the level of transmission still occurs but low-level transmission likely occurs throughout much of these areas. In addition, the high prevalence of asymptomatic carriers makes it difficult to identify spatial clustering. However, spatial variation in malaria risk among the young may still exist and targeted interventions may have some roll to play in high-transmission areas.

Summary

GIS has numerous applications to the study of the ecology of mosquitoes and malaria. GIS is useful for studying the spatial distribution of mosquitoes and the factors that contribute to heterogeneities in their distribution. It has been used in the past to investigate the relationship between the distribution of larval habitats and the density of adult mosquitoes in houses. These studies contribute to our understanding of the biology of adult mosquitoes (i.e. flight ranges) and suggest targeted approaches to the control of mosquitoes and the diseases they transmit. Other studies demonstrate the importance of host availability and control measures in determining the distribution of both larval and adult mosquitoes. Studies employing GIS indicate that the population dynamics of strongly anthropophilic (or zoophilic) mosquitoes is partly driven by access to the preferred hosts. Additional areas where GIS technology may contribute to the study of mosquitoes and mosquito-borne disease include studies of landscape architecture to assess how elevation, slope and land-use patterns influence the formation of larval breeding sites and the generation of interpolated measures of transmission as predictors to understand better the relationship between malaria transmission and disease outcomes. Further studies using RS in conjunction with GIS will help identify gaps in our knowledge of the characteristics of larval biology and may even be used as a predictor of areas of high disease transmission. As GIS technology becomes more affordable and more user-friendly, it will also have increasing applications in designing control and surveillance programmes for malaria and other diseases in developing countries.

References

Beck, L.R., Rodriguez, M.H., Dister, S.W., et al., 1994. Remote sensing as a landscape epidemiologic tool to identify villages at high risk for malaria transmission. *American Journal of Tropical Medicine and Hygiene,* 51 (3), 271-280.

Beier, J.C., Copeland, R., Oyaro, C., et al., 1990. *Anopheles gambiae* complex egg-stage survival in dry soil from larval development sites in western Kenya. *Journal of the American Mosquito Control Association,* 6 (1), 105-109.

Binka, F.N., Indome, F. and Smith, T., 1998. Impact of spatial distribution of permethrin-impregnated bed nets on child mortality in rural northern Ghana. *American Journal of Tropical Medicine and Hygiene,* 59 (1), 80-85.

Booman, M., Durrheim, D.N., La Grange, K., et al., 2000. Using a geographical information system to plan a malaria control programme in South Africa. *Bulletin of the World Health Organization,* 78 (12), 1438-1444.

Briggs, D.J. and Elliott, P., 1995. The use of geographical information systems in studies on environment and health. *World Health Statistics Quarterly,* 48 (2), 85-94.

Carter, R., Mendis, K.N. and Roberts, D., 2000. Spatial targeting of interventions against malaria. *Bulletin of the World Health Organization,* 78 (12), 1401-1411.

Charlwood, J.D. and Edoh, D., 1996. Polymerase chain reaction used to describe larval habitat use by *Anopheles gambiae* complex (Diptera: Culicidae) in the environs of Ifakara, Tanzania. *Journal of Medical Entomology,* 33 (2), 202-204.

Clarke, K.C., McLafferty, S.L. and Tempalski, B.J., 1996. On epidemiology and geographic information systems: a review and discussion of future directions. *Emerging Infectious Diseases,* 2 (2), 85-92.

Clarke, S.E., Bøgh, C., Brown, R.C., et al., 2002. Risk of malaria attacks in Gambian children is greater away from malaria vector breeding sites. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 96 (5), 499-506.

Coetzee, M., Craig, M. and Le Sueur, D., 2000. Distribution of African malaria mosquitoes belonging to the *Anopheles gambiae* complex. *Parasitology Today,* 16 (2), 74-77.

Craig, M.H., Snow, R.W. and Le Sueur, D., 1999. A climate-based distribution model of malaria transmission in sub-Saharan Africa. *Parasitology Today,* 15 (3), 105-111.

Gimnig, J.E., Kolczak, M.S., Hightower, A.W., et al., 2003. Effect of permethrin-treated bed nets on the spatial distribution of malaria vectors in western Kenya. *American Journal of Tropical Medicine and Hygiene,* 68 (4 Suppl.), 115-120.

Gimnig, J.E., Ombok, M., Kamau, L., et al., 2001. Characteristics of larval anopheline (Diptera: Culicidae) habitats in Western Kenya. *Journal of Medical Entomology,* 38 (2), 282-288.

Hawley, W.A., Phillips-Howard, P.A., Ter Kuile, F.O., et al., 2003. Community-wide effects of permethrin-treated bed nets on child mortality and malaria morbidity in western Kenya. *American Journal of Tropical Medicine and Hygiene,* 68 (4 Suppl.), 121-127.

Hay, S.I., Omumbo, J.A., Craig, M.H., et al., 2000. Earth observation, geographic information systems and *Plasmodium falciparum* malaria in sub-Saharan Africa. *In:* Hay, S.I., Randolph, S.E., Rogers, D.J., et al. eds. *Remote sensing and geographical information systems in epidemiology*. Academic Press, San Diego, 173-215. Advances in Parasitology no. 47.

Hightower, A.W., Ombok, M., Otieno, R., et al., 1998. A geographic information system applied to a malaria field study in western Kenya. *American Journal of Tropical Medicine and Hygiene,* 58 (3), 266-272.

Howard, S.C., Omumbo, J., Nevill, C., et al., 2000. Evidence for a mass community effect of insecticide-treated bednets on the incidence of malaria on the Kenyan coast. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 94 (4), 357-360.

Kitron, U., Pener, H., Costin, C., et al., 1994. Geographic information system in malaria surveillance: mosquito breeding and imported cases in Israel, 1992. *American Journal of Tropical Medicine and Hygiene,* 50 (5), 550-556.

Lines, J.D., Myamba, J. and Curtis, C.F., 1987. Experimental hut trials of permethrin-impregnated mosquito nets and eave curtains against malaria vectors in Tanzania. *Medical and Veterinary Entomology,* 1 (1), 37-51.

Minakawa, N., Githure, J.I., Beier, J.C., et al., 2001. Anopheline mosquito survival strategies during the dry period in western Kenya. *Journal of Medical Entomology,* 38 (3), 388-392.

Minakawa, N., Mutero, C.M., Githure, J.I., et al., 1999. Spatial distribution and habitat characterization of anopheline mosquito larvae in Western Kenya. *American Journal of Tropical Medicine and Hygiene,* 61 (6), 1010-1016.

Minakawa, N., Seda, P. and Yan, G., 2002. Influence of host and larval habitat distribution on the abundance of African malaria vectors in western Kenya. *American Journal of Tropical Medicine and Hygiene,* 67 (1), 32-38.

Moore, D.A. and Carpenter, T.E., 1999. Spatial analytical methods and geographic information systems: use in health research and epidemiology. *Epidemiologic Reviews,* 21 (2), 143-161.

Omumbo, J., Ouma, J., Rapuoda, B., et al., 1998. Mapping malaria transmission intensity using geographical information systems (GIS): an example from Kenya. *Annals of Tropical Medicine and Parasitology,* 92 (1), 7-21.

Phillips-Howard, P.A., Nahlen, B.L., Kolczak, M.S., et al., 2003. Efficacy of permethrin-treated bed nets in the prevention of mortality in young children in an area of high perennial malaria transmission in western Kenya. *American Journal of Tropical Medicine and Hygiene,* 68 (4 Suppl.), 23-29.

Rejmankova, E., Pope, K.O., Roberts, D.R., et al., 1998. Characterization and detection of *Anopheles vestitipennis* and *Anopheles punctimacula* (Diptera: Culicidae) larval habitats in Belize with field survey and SPOT satellite imagery. *Journal of Vector Ecology,* 23 (1), 74-88.

Rejmankova, E., Roberts, D.R., Pawley, A., et al., 1995. Predictions of adult *Anopheles albimanus* densities in villages based on distances to remotely sensed larval habitats. *American Journal of Tropical Medicine and Hygiene,* 53 (5), 482-488.

Ribeiro, J.M., Seulu, F., Abose, T., et al., 1996. Temporal and spatial distribution of anopheline mosquitos in an Ethiopian village: implications for malaria control strategies. *Bulletin of the World Health Organization,* 74 (3), 299-305.

Roberts, D.R., Paris, J.F., Manguin, S., et al., 1996. Predictions of malaria vector distribution in Belize based on multispectral satellite data. *American Journal of Tropical Medicine and Hygiene,* 54 (3), 304-308.

Smith, T., Charlwood, J.D., Takken, W., et al., 1995. Mapping the densities of malaria vectors within a single village. *Acta Tropica,* 59 (1), 1-18.

Snow, R.W., Lindsay, S.W., Hayes, R.J., et al., 1988. Permethrin-treated bed nets (mosquito nets) prevent malaria in Gambian children. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 82 (6), 838-842.

Tanser, F.C. and Le Sueur, D., 2002. The application of geographical information systems to important public health problems in Africa. *International Journal of Health Geographics,* 1 (1), 4.

Thomas, C.J. and Lindsay, S.W., 2000. Local-scale variation in malaria infection amongst rural Gambian children estimated by satellite remote sensing. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 94 (2), 159-163.

Thompson, R., Begtrup, K., Cuamba, N., et al., 1997. The Matola malaria project: a temporal and spatial study of malaria transmission and disease in a suburban area of Maputo, Mozambique. *American Journal of Tropical Medicine and Hygiene,* 57 (5), 550-9.

Thomson, M.C., Connor, S.J., Milligan, P.J., et al., 1996. The ecology of malaria-as seen from Earth-observation satellites. *Annals of Tropical Medicine and Parasitology,* 90 (3), 243-264.

Trape, J.F., Lefebvre-Zante, E., Legros, F., et al., 1992. Vector density gradients and the epidemiology of urban malaria in Dakar, Senegal. *American Journal of Tropical Medicine and Hygiene,* 47 (2), 181-189.

Vine, M.F., Degnan, D. and Hanchette, C., 1997. Geographic information systems: their use in environmental epidemiologic research. *Environmental Health Perspectives,* 105 (6), 598-605.

5

A model structure for estimating malaria risk

M.B. Hoshen [#] *and A.P. Morse* [##]

Abstract

Malaria is one of the leading causes of death in the developing world today. While prevention and treatment methods are available, their large-scale usage is a major drain on governmental budgets, and not applied whenever necessary. For this reason, understanding the endemicity of a region will allow the efficient implementation of suitable prevention methods. More importantly, the prediction of extraordinary malaria outbreaks will allow the recruitment of emergency facilities before transmission becomes widespread. In addition, climate change may influence the endemicity pattern of a region, causing malaria incidence to rise in areas in which it was non-existent or controlled. For all these purposes, a seasonal to decadal malaria forecast is needed. A novel approach has been attempted, using dynamic mathematical biological modelling. There has been initial work on the prediction of malaria epidemic based on seasonal climate forecasts, in areas of unstable transmission, which may be used to provide early warning. Here we describe a mathematical biological model of the weather-dependent parasite transmission dynamics, within-host and within-vector. The biological structure and the mathematic formulation permit computer simulation of infection patterns under various climatic and control conditions. Here we present the model structure and results at a local scale using reanalysis weather data. We then discuss the role of different aspects of the impact of unusual climatological effects and their potential implications, as well as further developments in the simulation structure and outline pathways for future progress. We also suggest further aspects of biological research, required for model improvement.

Keywords: malaria transmission; dynamic modelling; mathematical model; endemicity; Africa

Introduction

Malaria is one of the major causes of global mortality and morbidity. With an unknown number of 1 - 2.7 million patients dying annually and hundreds of millions afflicted, the need for containment and for reduction of the health burden is obvious. But due to the scarcity of resources, and the lack of a clear policy of their distribution, this control is not attained. Even though the aetiology of the disease has been known for a century (Ross 1911), the full application of this knowledge requires a practical model for a decision-making process. This model must be either robust enough to

---

[#] Virtual Population Laboratory, Physics Department, University of Liverpool, Liverpool L69 7ZE, UK. E-mail: hoshen@liv.ac.uk

[##] Geography Department, University of Liverpool, Liverpool L69 7ZT, UK. E-mail: morse@liv.ac.uk

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 41-50.

reflect all conditions or, preferably perhaps, flexible enough to be adaptable to local conditions. The development of such a model, and the training of the model to local conditions which can be applied to changing conditions, is a formidable task. Such a model must attempt to combine various sources of data regarding different aspects of the disease dynamics and link these aspects with external causes or covariates, which serve as driving forces or as surrogates for such forces. Due to the constant increase in empirical knowledge regarding malaria, given the international interest being drawn lately to the disease, the model should be developed in a way in which new segments of knowledge may be added into the modelling structure. Hence a modular structure is required, allowing for evaluation and updating of sub-processes, which may be defined, measured and tested in laboratory or field settings. Parameter values may thus be introduced empirically, and may be amended to reflect changes due to trends or to human intervention.

The principal malaria transmission models to date are of a few general forms. There are statistical models, which compare malaria transmission variables (such as the entomological inoculation rate, EIR) with local conditions (Killeen et al. 2000). There are rules-based models, which determine the regions in which malaria transmission is possible (Snow et al. 1998). In addition there are dynamic models relating malaria transmission to constant climate conditions (Bailey 1982). Hitherto there do not seem to have been models relating malaria transmission to changing weather, and which hence may serve for decision-making based on weather forecasts, nor in the evaluation of the impact of public-health effects on transmission dynamics in a varying climate.

The present report wishes to fill part of the niche with some of the basic groundwork towards a complete numerical model for the weather-based epidemiology of *falciparum* malaria. The report will present a simple model of malaria transmission dynamics, and then present the results of variation of model values to determine the robustness of the structure. It will then suggest various ways of evaluating the impact of intervention policies, and some simple pictures of minor climate change and potential impact on clinical incidence.

Materials and methods

The basic structure of the model and its mathematical formulation will be published elsewhere (Hoshen and Morse 2004) and will only be highlighted here. The model is based on the full dynamics of the host–vector–parasite triangle depicted graphically in Figure 1.

We must differentiate between human (hepatic and erythrocytic stages) and mosquito infection (sporogonic cycle) dynamics, while the mosquito life (gonotrophic) cycle must also be taken into consideration. The human life cycle is less important as human life expectancy is many times longer than the duration of infection. Human malaria-related mortality is rarely a significant fraction of the total population.

The parasite life cycle, with human asexual and vector sexual sections, is presented in Figure 2. Both humans and mosquitoes may be infected by parasites. The human infection is transmitted by anophelean mosquito bites and the mosquito infection transmitted by biting of humans. No direct transmission is possible between mosquitoes or between humans.

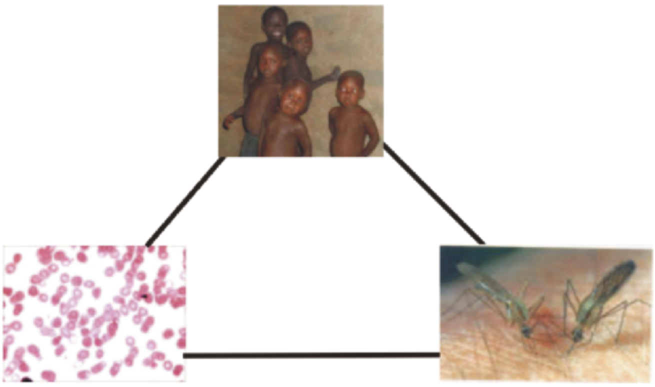


Figure 1. The disease interaction triangle: human host, *Anopheles* vector and *Plasmidum* parasite (shown in human blood sample)

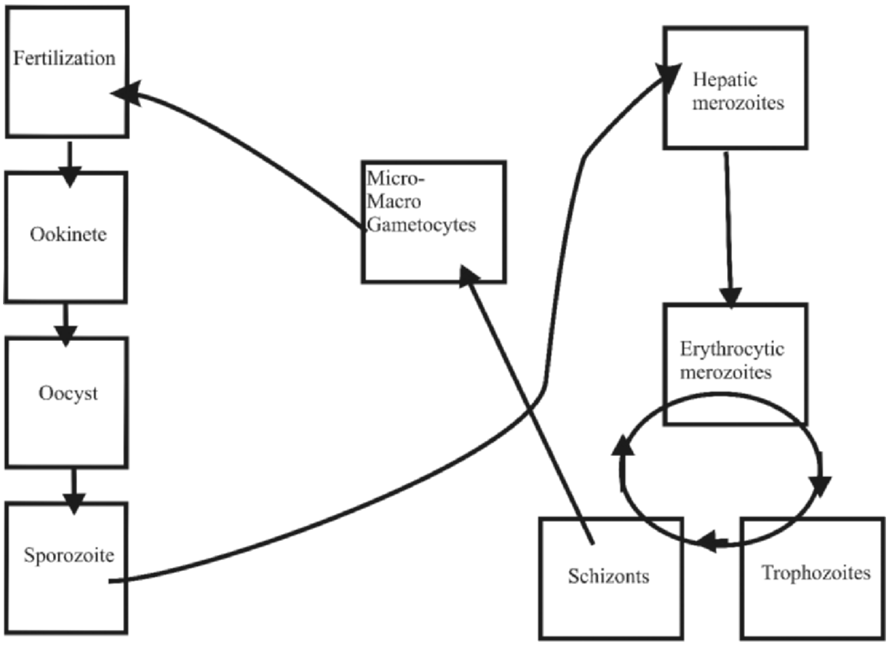


Figure 2. The parasite life cycle. The sexual (vector) stage is depicted on the left side, while the asexual (human) stage is on the right side. For intra-organism development time direction is downwards. The erythrocyte stage is cyclic multiplication

Human clearance of infection is a slow process, which may last a year. It is assumed to be a first-order process. Infectious mosquitoes never clear their infection until death. Both human and vector infections take time to develop into an infectious status. The indigenous mosquito does not seem to be harmed by the infection, but non-immune humans may die or be severely sick. The impact of immunity on severity of human infection is complex. In many cases, such as when infection is constant, the infection is asymptomatic (thus 'healthy' individuals may be carriers), while in cases when the infection pressure is reduced, such as after a sustained low-transmission season, morbidity and mortality increase. While the within-host parasite dynamics are weather-independent, the within-vector parasite dynamics, as well as the mosquito's life cycle (Figure 3), are weather-dependent. Both the development of the parasite within the vector (sporogonic cycle) and the progress of the gonotrophic cycle (process of biting, development of eggs and oviposition) have been modelled by the usage of degree-day dynamics (Detinova 1962). Thus the length of either cycle may be expressed as $L_C=1+D_d/(T-T_c)$, where D_d is the length of the cycle in degree days, T_c the threshold for development and T the daily average temperature. D_d is 37 and 111 degree day, and T_c is 7.7 and 18°C for the gonotrophic and sporogonic cycles, respectively.

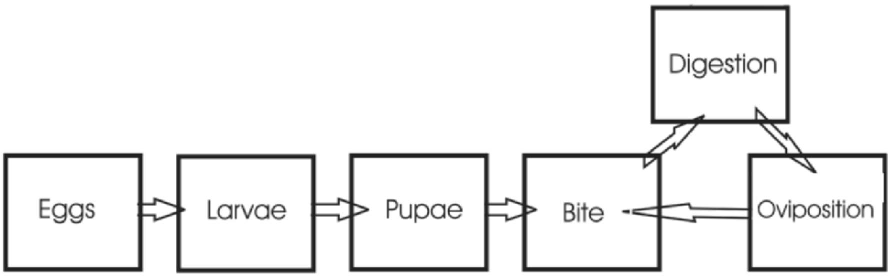


Figure 3. Schematic representation of vector development. Pre-gravid development is towards the right. Mature dynamics are cyclic

Numerous issues are still contestable in the model. Some sub-models have not been created with full empirical evidence. Some have been based on partial evidence, while in some cases we have tried to rule between two possibilities. Here we would like to investigate the sensitivity of these model processes to changes in values of parameters which seem to be crucial to the modelling of the transmission process. New field research is now underway to measure the values of these parameters in natural settings.

The daily survival of the adult *Anopheles gambiae (s.l.)* vector is temperature-dependent. It is not clear whether the survival per gonotrophic cycle is constant, save extremely high lethal temperatures, and hence the daily survival is dependent on the length of the gonotrophic cycle, with the death rate being a constant for all weather conditions (Hitherto Lindsay-Birley model, LB) (Lindsay and Birley 1996), or whether survival decreases more smoothly for higher temperatures (Martens model, MM) (Martens et al. 1995). Thus we test the output with both models, and for varying values of the LB per cycle survival α. The default value was 0.44.

For other parameters we start with values which seem to be realistic, being within empirical ranges (when determined) and producing results which are consistent with clinical reports. We then vary a single parameter at a time to establish the range that causes little change in the output. This will allow a determination of those parameters whose values have to be measured with greater accuracy.

Our model includes the following parameters (default values in brackets):

InoculationEfficiency (IE=0.9): the probability that a carrier mosquito will infect a bitten healthy human. This probability includes the probability of the inverse process. The probability of an uninfected human becoming infected is thus the number of biting infectious mosquitoes, multiplied by IE.

Host infection survival rate (0.9716). This is the daily probability that an infected human will not clear his/her infection. The default value reflects a probability of roughly 90% of an individual clearing an untreated infection within 80 days. This is consistent with reports of malariotherapy.

As oviposition is dependent on the existence of waterbodies, and *An. gambiae* usually oviposit in temporary waterbodies, such as puddles, hoofprints etc., oviposition rate is related to recent rainfall. It is, in principle, also related through evapotranspiration to temperature and humidity, and to soil type by absorption. Due to lack of data on the suitable water-balance dynamics we simplified the relation to a fixed ratio between per-mosquito per cycle oviposition to the decadal rainfall by rate constant β (1.0). This will be improved when analysis of measurements being performed now becomes available.

The Detinova model attributes different values of the gonotrophic cycle degree-day values to different humidity conditions. As we found the humidity value in our dataset was not reliable, we chose rainfall to be a surrogate for humidity. We used a single value as a threshold for transition between humid and dry conditions. In Detinova's data there are actually three different ranges of humidity, but as the intermediate and dry values are almost identical, we have elected using only two, the humid and dry conditions. The transition between them serves as a threshold (5mm).

One of the early discoveries in the modelling of malaria was the problem of the low probability of survival of mosquitoes (and hence infections) from year to year in a region of seasonal transmission. A long dry season, long hot or cold seasons can all eliminate the mosquito populations. There have been numerous discoveries which allow for the mosquito survival, either by aestivation/over-wintering in secluded hibernation locations, by delay in the maturation of eggs or mosquito long-range migration. All these processes may contribute to the re-establishment of malaria transmission. The continuation of infection dynamics in a numerical setting, when infected mosquitoes are not surviving, is enabled by the continuous influx of new infected mosquitoes, presumed waking from a period of aestivation, or new migrants. They are released into the population at a constant rate (1.00/10 days). This number is far too small to sustain malaria, except when favourable conditions for mosquito viability prevail.

Another source of reinstallation of the disease could be the arrival of new sick patients into the population (transient workers, soldiers etc.). To model this value we allow for the import of a set number (0.0) of new cases per 100 persons in the population, every 4 days.

Mosquitoes may bite both humans and cattle. This tendency is a combination of the relative abundance of cattle and the strain specific tendency. This value (0.5) is measured entomologically. As far as the model is concerned, these are wasted bites, which do not allow transmission in either direction, as cattle are not a host for *falciparum*.

As a coarse evaluation of the possible effects of climate change we varied the temperature by raising and lowering the reported temperature. We experimented with temperature changes in 1^{o}C step from -5^{o}C to +5 ^{o}C from the reanalysis data. In addition we experimented with changing rainfall patterns by multiplying the rainfall values by a constant varying from 0.5 to 1.5 of the reanalysis daily rainfall.

To compare with the numerically varied weather, we have used also spatial variation, comparing with data from adjacent grid points (17.5^{o}S and 20.0^{o}S, 22.5^{o}E, 25.0^{o}E, 27.5^{o}E and 30.0^{o}E).

The purpose is to establish whether projected climate change is greater or less than spatial variation, as a determinant of malaria outbreaks.

The data is being reported graphically here. A form of numerical analysis will be developed in the future.

Results

Early 1996 and 1997 were epidemic years in the region, as a result of the heavy rains in the rain season beginning November. We would thus expect of the model prediction of high incidence. This we do indeed find in almost all runs as displayed. We would like to compare however the behaviour as determined by the various values of the parameters. To begin with, in Figure 4 we compare the Lindsay-Birley and Martens models. During rainy years the Martens-model incidence was usually proportional to the annual rainfall. In drier years, the model could not show support for incidence. The dependence on rainfall is far less clear on the various realizations of the LB model. This seems to be true for all values of the gonotrophic-cycle survival rate. In Figure 5 (see Colour pages elsewhere in this book) we compare the values given by the model using different inoculation-efficiency parameters. Perhaps not surprisingly, when the number of mosquitoes is very large (1996-9), the precise value is less important, but, when there are fewer mosquitoes (years 2000 and early 2001), transmission is highly dependent on the efficiency of the individual vector.

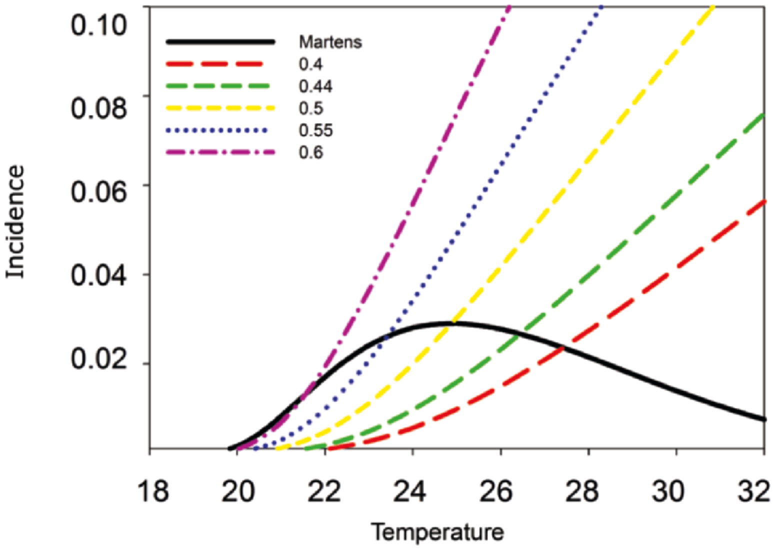


Figure 4. Comparison of Martens and Birley-Lindsay models of predicted incidence for various average temperature values. Different values of gonotrophic-cycle survival are simulated

In Figure 6 we examine the importance of the interaction between mosquito and environment. The gonotrophic-cycle length is dependent on humidity. The major importance of this parameter is in years in which the rainfall is heavy and with a double peak (1996-7 and 2000), requiring a continuation of mosquito population between rainy seasons.

In Figure 7 (see Colour pages elsewhere in this book) we compare the importance of the immune system to the dynamics of incidence. For years in which infection levels are extremely high (1999) the entire population is constantly infected, independent of the clearance rate, but in other years the clearance rate is a major determinant of the incidence rate, as the prevalence, and hence the mosquito infection rate is dependent on this parameter.

In Figure 8 we display incidence according to the model when varying the temperature by a constant shift, in this case a warming or a cooling by 1°C.

In Figure 9 we present the variation of the incidence pattern for the region 17.5-20°S by 22.5-30.0 °E, for gridpoints at 2.5° spacing.

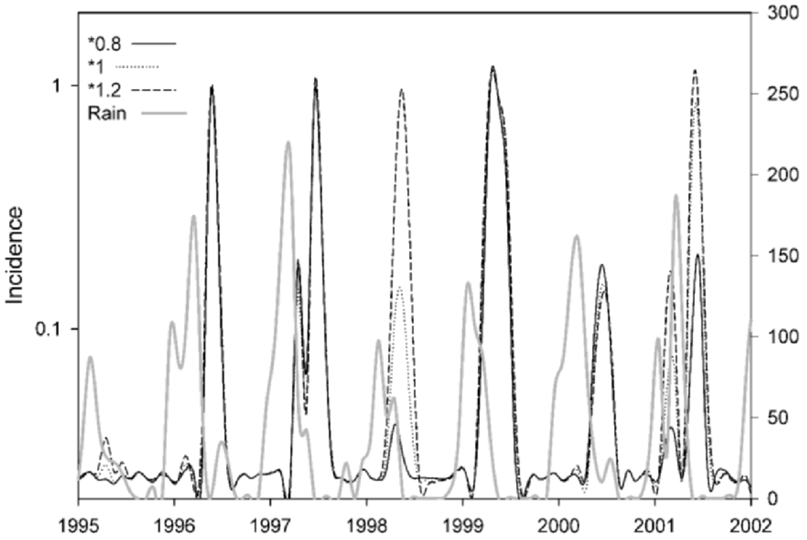


Figure 6. Sensitivity of simulated incidence to variation in rain for 17.5°S 25.0°E using ERA-40 weather. Calculated rainfall is multiplied by a constant (0.8, 1, 1.2) for the entire simulation

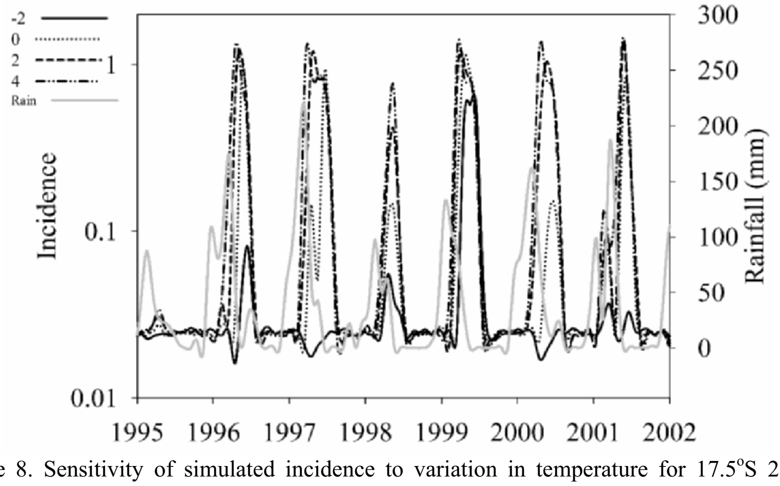


Figure 8. Sensitivity of simulated incidence to variation in temperature for 17.5°S 25.0°E using ERA-40 weather. Calculated temperature varied by an additive constant (-2, 0,2 ,4) for the entire simulation

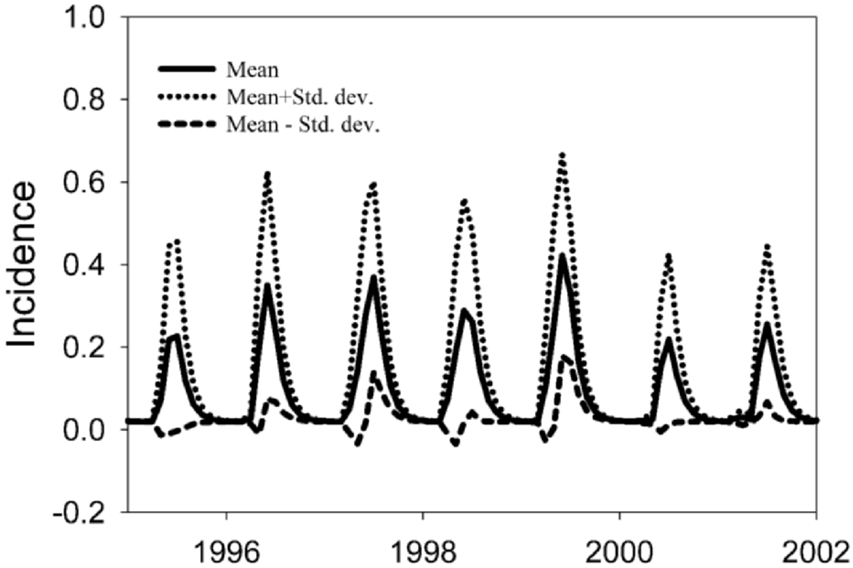


Figure 9. Variation of simulated incidence between ERA-40 grid-points. Solid line: mean of 8 grid-points. Dotted lines: mean ± standard deviation

Discussion

It seems that the complexity of the model entails the combination of many separate sub-models, each with its own parameterization. This process is obviously far from desirable, as the numerous parameters could potentially create larger variation than the weather driving force, and indeed the output of a forecast by the malaria model is dependent on the choice of model parameters. Nevertheless, if the model parameters can be optimally set, the variation is limited, and the influence of weather will be predictable. When this obstacle has been surmounted, we may utilize weather forecasts for malaria prediction.

This modelling process has a few benefits, as opposed to other methodologies, such as a scenario-based, statistical modelling method. The first is the ability to apply the method in cases substantially different from those tested. This is a special boon when attempting to establish the importance of changing climate or of the influence of extraordinary weather conditions (such as after heavy rains). Another benefit of the mathematical-biological methodology is the ability to simulate changes to entomological, parasitological or immunological aspects of the system. Thus such methods are suitable for calculating the impact of intervention policies, and thus for weighting the costs of alternative health policies, such as deciding on the cost-effectiveness of the utilization of spraying. The impact of the increased malaria prevalence in a highland area affected by global warming may be mitigated by the increased immune status. A mathematical model can readily apply such processes.

There are two possible methodologies in the usage of complex mathematical models, which are actually complimentary. One approach is to analyse the influence of a single variable (or possibly a combination) in the model output. Then we may compare the output of the entire model with clinical malaria reports. The alternative is to form a set of small experiments, each testing a single factor, in comparison with a standard set of values. This latter was the alternative we chose. A set of experiments to establish the values of the parameters in a single setting is under way.

We find that the values of the parameters are indeed causing sizable variations in the heights and shapes of the peaks. We do find, however, that the seasonality is unchanged with variations in parameters. Weather is still the principal driver.

Weather variations can increase or reduce inter-annual variation. The fairly low temperatures at the beginning of year 2000 did not allow the development of a sizable incidence that year, independent of variations in rainfall. However, an increase of 2°C is sufficient to result in an epidemic year. Variation of rainfall did not create as large variations in incidence as did temperature variation, with a clear exception in year 2001, where the first peak of the dual-peak epidemic was highly sensitive to rainfall. This leads us to understand that in this region, in which malaria is driven by the rainy season, the actual size of the epidemic is mainly determined by temperature, as the temperature is close to the development threshold.

Malaria is an environmentally driven disease and as such is highly dependent on variation in local conditions. This can be seen when we compare the conditions across Southern Africa. The inter-grid point variation in incidence is very large, as the standard variation is as large as the mean. Nevertheless, the seasonal pattern of all locations is similar. In addition, the interannual variation of the mean is similar to that of the inter-gridpoint standard deviation, reflecting the general persistence of interannual variability over the large region. Thus we find that the epidemic structure may be understood using only macro-scale information. This is quite important as climate change models work only at this scale.

We may hence conclude that the interannual variation of malaria incidence in Southern Africa is determined by both rainfall and temperature variation. The variation of temperature is of greatest importance. Thus in the case of a uniform heating of the region, we could expect the area to move from its present epidemic structure to seasonal endemicity. Unless rainfall patterns change considerably, there will be no significant change in the seasonal structure of the epidemic seasons.

Conclusion

In this short report we have presented a weather-based model of malaria transmission. We have investigated the sensitivity of the model to variations in both parameter values and weather. We have demonstrated that the interannual variation is determined by both temperature and rainfall, and that this dependence is robust to variations in parameter values. We have shown that in spite of inter-gridpoint variations, the model gives time patterns which are representative of whole regions, allowing it to serve as a basis for large-scale climate models. We have also shown that small changes in baseline temperatures will significantly increase the incidence in some otherwise non-epidemic years, an effect not found with rainfall variations.

References

Bailey, N.T.J., 1982. *The biomathematics of malaria.* Griffin, London. Biomathematics of Diseases no. 1.

Detinova, T.S., 1962. *Age-grouping methods in Diptera of medical importance: with special reference to some vectors of malaria.* World Health Organization, Geneva. World Health Organization Monograph Series no. 47.

Hoshen, M.B. and Morse, A.P., 2004. A weather-driven model of malaria transmission. *Malaria Journal,* 3 (1), 32. [http://www.malariajournal.com/content/3/1/32]

Killeen, G.F., McKenzie, F.E., Foy, B.D., et al., 2000. A simplified model for predicting malaria entomologic inoculation rates based on entomologic and parasitologic parameters relevant to control. *American Journal of Tropical Medicine and Hygiene,* 62 (5), 535-544.

Lindsay, S.W. and Birley, M.H., 1996. Climate change and malaria transmission. *Annals of Tropical Medicine and Parasitology,* 90 (6), 573-588.

Martens, W.J., Niessen, L.W., Rotmans, J., et al., 1995. Potential impact of global climate change on malaria risk. *Environmental Health Perspectives,* 103 (5), 458-464.

Ross, R., 1911. *The prevention of malaria*. John Murray, London.

Snow, R.W., Gouws, E., Omumbo, J., et al., 1998. Models to predict the intensity of *Plasmodium falciparum* transmission: applications to the burden of disease in Kenya. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 92 (6), 601-606.

6

Rapid assessment of malaria risk using entomological techniques: taking an epidemiological snapshot

P.F. Billingsley[1], *J.D. Charlwood*[2] *and B.G.J. Knols* [3,4]

Abstract

The pivotal role of mosquitoes in malaria epidemiology means that in practice, control efforts against the disease must include sustainable control of the vectors. This has fostered many careful and complex longitudinal studies designed to estimate the entomological inoculation rate (EIR) as a measure of risk of exposure to infection. Alternatives to this estimate – anti-circumsporozoite protein antibodies, conversion rates in non-immunes or re-infection rates – require sampling of blood from patients and have associated compliance and interpretation issues. Here, we describe how entomological techniques, which provide information on mosquito population densities, age structures and infection characteristics, allied with mapping and modelling approaches can provide a relative estimate of EIR within a few days of fieldwork. The information could be used to decide upon and track intervention measures, as well as to monitor disease outbreaks. Standardizing the techniques used for rapid assessment could enable comparison of malaria risk in different ecological and epidemiological settings.

Keywords: malaria; mosquito; epidemiology; entomological infection rate, rapid assessment, transmission

Introduction

Time spent in reconnaissance is never wasted – this is as true for a great general such as Napoleon as for those involved in infectious disease control, and so the gathering of reliable information on exposure risk is a central facet of malaria control programmes. Reduction of exposure to the vectors, either by controlling mosquitoes or avoiding their bites, is still a major element in malaria control policies. However, local resources are usually severely restricted and administrators often have to make decisions based on limited information. Not only administrators but communities, families and individuals affected by the disease all need adequate information to decide where, when and what they should do to reduce the risk of infection.

In many ways malaria transmission patterns are like the fractals seen in chaos theory. The so-called '80/20 rule' encapsulates the idea that most malaria transmission

---

[1] School of Biological Sciences, University of Aberdeen, Tillydrone Avenue, Aberdeen AB24 2TZ, UK. E-mail: p.billingsley@abdn.ac.uk

[2] Entomology Unit, Agency's Laboratories Seibersdorf, International Atomic Energy Agency, A-1400 Vienna, Austria

[3] Entomology Unit, Agency's Laboratories Seibersdorf, International Atomic Energy Agency, A-1400 Vienna, Austria

[4] Laboratory of Entomology, Wageningen University, PO Box 8031, 6700 EH Wageningen, The Netherlands

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 51-68.

is concentrated in a small fraction of the population (Woolhouse et al. 1997). Thus, heterogeneous patterns of transmission rates are reproduced at differing levels of scale. For example, even within a high-transmission district some villages will have a greater amount of transmission than others. Within those villages most of the transmission will be restricted to a small number of hamlets, within hamlets to some houses and even within houses to some individuals (Smith et al. 1995).

Rapid assessment (RA) techniques aim to provide information at any or all of these different scales to identify areas where transmission is concentrated, enabling the optimal use of limited resources for control. Although RA cannot provide the same depth and breadth of data as longitudinal studies, the scope and reliability of the data it provides will increase with use and so its utility to health-planning operations should also grow. Before this happens, however, RA must become accepted as a viable addition, rather than alternative, to the classic longitudinal survey. In malaria epidemiology, longitudinal studies are commonly regarded as the essential prerequisite to planned intervention trials. Short-term studies are often decried because they may represent only a single transmission cycle, a single season or a single year, or have no local comparative data. Longitudinal studies can sometimes ignore the spatial variation of transmission within a study area (Thompson et al. 1997; Smith et al. 1995) and take a long time to provide answers. Thus, they become cumbersome and inappropriate when and where responsive control is needed in the face of changing malaria patterns or epidemic malaria emergence. For example, in refugee situations sometimes large numbers of people, from different epidemiological (immunological) backgrounds, set up temporary homes in areas where there may be a significant risk of transmission. In such a scenario, a protracted assessment would be unethical, but implementing a control programme without any assessment would have potential for not solving the problem.

Models for malaria transmission place great emphasis on the mosquito (Killeen et al. 2000b; Koella 1991), so information gathered about the vector is crucial. Gathering vector data is also less dependent upon human compliance. In this article we will demonstrate how information from mosquito collections and dissections might be considered sufficient to estimate relative exposure to malaria and hence provide estimates of malaria risk in different malaria epidemiological settings.

Measuring risk

There are a number of ways of estimating the risk to a non-immune or semi-immune individual of acquiring a malaria infection. The best indicator, and the only one suitable for use in high transmission areas, is the entomological inoculation rate (EIR), which is classically calculated from the number of mosquitoes biting an 'average' human host and the proportion of these that contain (infective) sporozoites (Garrett-Jones 1964). At low transmission rates, the measurement of anti-CSP antibodies in human hosts (Wijesundera et al. 1990) or of conversion rates (Gupta and Snow 1996) provides two alternatives to EIR estimations. However, when transmission rates increase above a threshold, correlations between these three parameters can be lost (Kilombero Malaria Project 1992). Where existing parasites have been cleared, the conversion rates have been considered an indicator of malaria risk (Trigg et al. 1997), but without the application of PCR-based techniques it is impossible to differentiate between re-infections and recrudescence of parasites suppressed by drugs or the immune system. It is usually argued that the best way of obtaining a picture of the epidemiology of malaria in a new setting is to conduct a cross-sectional parasite prevalence survey and for such surveys, dipstick assays can provide immediate results. While entomological and parasitological surveys can be performed simultaneously, in areas of high transmission it is likely that parasitaemias will be saturated and information on spatial distribution of risk of infection rather than parasites will not be obtainable from parasitological data alone.

There is a need to identify relative as well as absolute risk of infection. Using RA to decide upon suitable interventions may seem questionable since control efforts are not likely to be directed solely at the few high-density houses in a study site. We would argue however that, whilst not ignoring the rest of the area, interventions should initially be directed at or include such areas, be they houses in a village or villages in a district. Often the most exposed households are those in the more remote areas. Given the 80/20 rule, if these households are ignored or not identified prior to implementation, control will be incomplete and ineffective despite what might otherwise seem to be a good coverage. Thus, one purpose of the RA is to identify transmission ‘hot spots’ that should be prioritized for interventions. For example, in the Ifakara region of Tanzania, although the ‘average’ villagers may receive a mean of 300 infective bites per year, some villagers receive 10 times less than that and some, who live in the more remote areas, 10 times more, this heterogeneity being a direct consequence of variation in mosquito biting-rates (Figure 1) (Charlwood et al. 1995a; 1995b).

Rapid assessment: snapshot epidemiology?

The pros and cons of rapid assessment

A good RA will provide information about relative and perhaps absolute risk in a short time. It is likely to be most effective when deployed over a wide area, giving a series of ‘snapshots’ or stills from what can be considered a longitudinal ‘film’. Increases in absolute (and sometimes relative) oocyst and sporozoite infections are the inevitable presages of malaria outbreaks. Where these can be identified prior to epidemics of human infection, and the risk of infection determined with some degree of accuracy, then pre-epidemic intervention is a conceivable outcome of RA. This holds true for a range of settings including epidemics in migrant or refugee populations, seasonal malaria transmission, where land use is changing, and where drug or insecticide resistance is developing. The general approach outlined below and in Figure 2 is applicable to any vector-borne disease where trapping, collecting and analysis of vectors are suitably advanced.

There are critical requirements for RA protocols that underpin any adaptations to the local situation. RA should be capable of collecting, processing and analysing the bulk of the necessary samples and data in the field, and thereby provide an acceptable and accurate estimate of the malaria risk. Like any assay, entomology-led RA needs to be sensitive, since assessments might be undertaken at low mosquito population densities. Nevertheless, there will be some sites and times of year when vector populations are so small that RA of mosquito populations, particularly adults, is just not feasible. While accepting these caveats’ broad applicability, flexibility and ease of use will be important in the acceptance of RA. With field data collected and analysed

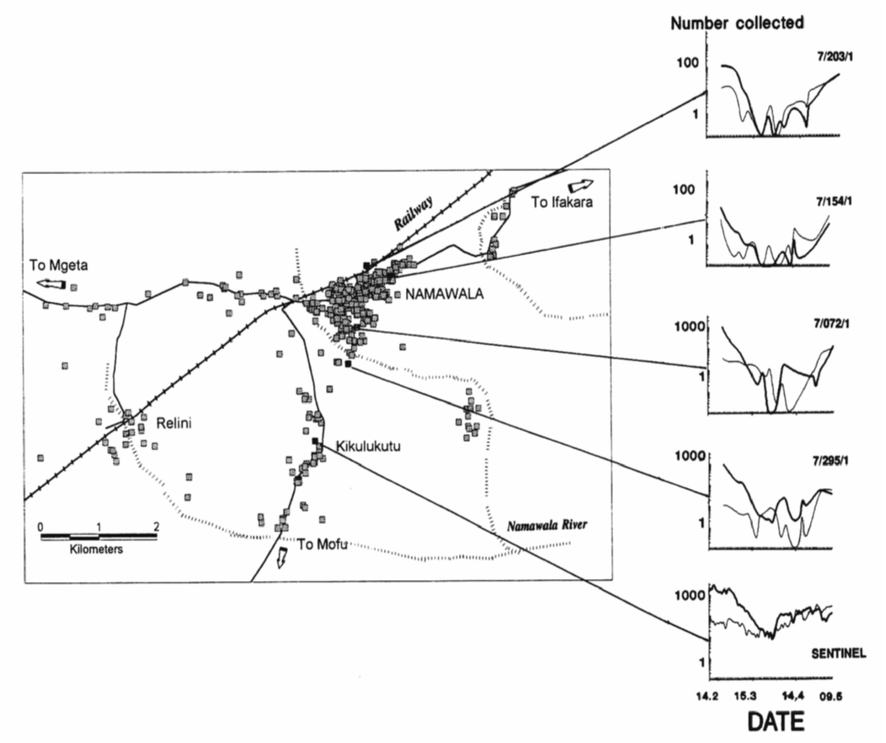


Figure 1. Spatial heterogeneity of mosquito numbers in an African village. CDC light traps were used to collect *Anopheles gambiae s.l.* (heavy lines) and *An. funestus* (thin lines) in houses in and around the village of Namawala, Tanzania in February to May 1991. The map shows the relative positions of the houses, and the graphs show that, although absolute numbers are different at each site, the ratio of each species between houses stays relatively constant. Using a sentinel light trap in an area of high mosquito density allows immediate mapping and comparison of spatially heterogeneous data. Reprinted from Charlwood et al. (1995a; 1995b) with permission from CABI publishing

in consistent and comparable ways, there is also the exciting possibility that information can be collated from diverse ecological and epidemiological settings, contributing the much-needed fine-scale resolution for national-, regional- and continental-scale estimates of malaria risk (such as Mapping Malaria Risk in Africa) (Le Sueur et al. 1997).

Background information

Although there are few malaria-endemic regions where mosquito species and populations have not been described, priming on local species complexes, transmission rates, exo- or endophilic mosquito behaviour, and presence of each *Plasmodium* species will be essential. On-line databases can provide time-saving and

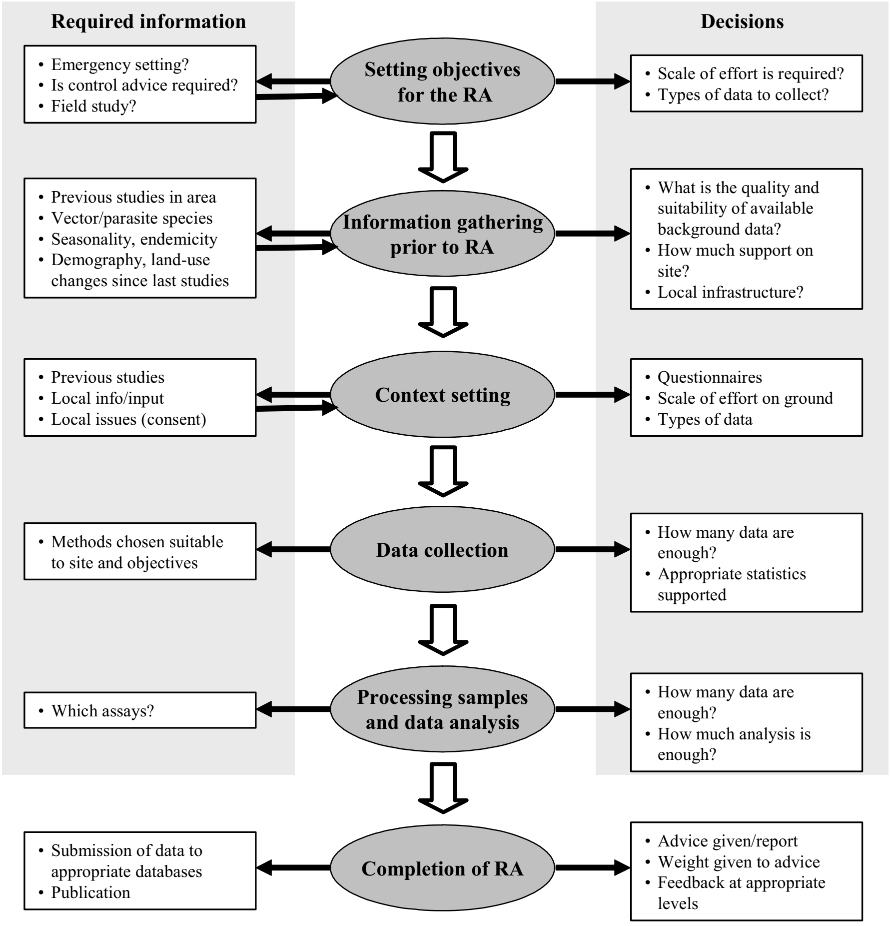


Figure 2. Proposed outline for rapid assessment of malaria. The process for the RA from inception to completion is shown in the shaded boxes (centre column). The process requires input of information and its modification to suit the local situation at all stages of the RA (left shaded area). Similarly, there is a series of rational decisions to be made that will influence the scale, start and end of the RA (right shaded column). The completed RA report will vary to suit the sponsors and the objectives they have set, but in all cases a clear weighting should be given to the completed RA

decision-enhancing information. Amongst these, the normalized vegetation index (NDVI) can allow the presence of members of a species complex to be predicted with some accuracy (Figure 3a) (Lindsay, Parson and Thomas 1998). This is clearly demonstrable for the *Anopheles gambiae s.s.* and *An. arabiensis* species where, if NDVI predicts high proportion of either species, the accuracy of that prediction is very high (Figure 3b).

However, the local microepidemiology is likely to differ from regional descriptions, and the RA team should be prepared for such eventualities. Setting the RA into a seasonal context is important since rainfall or NDVI may also be good

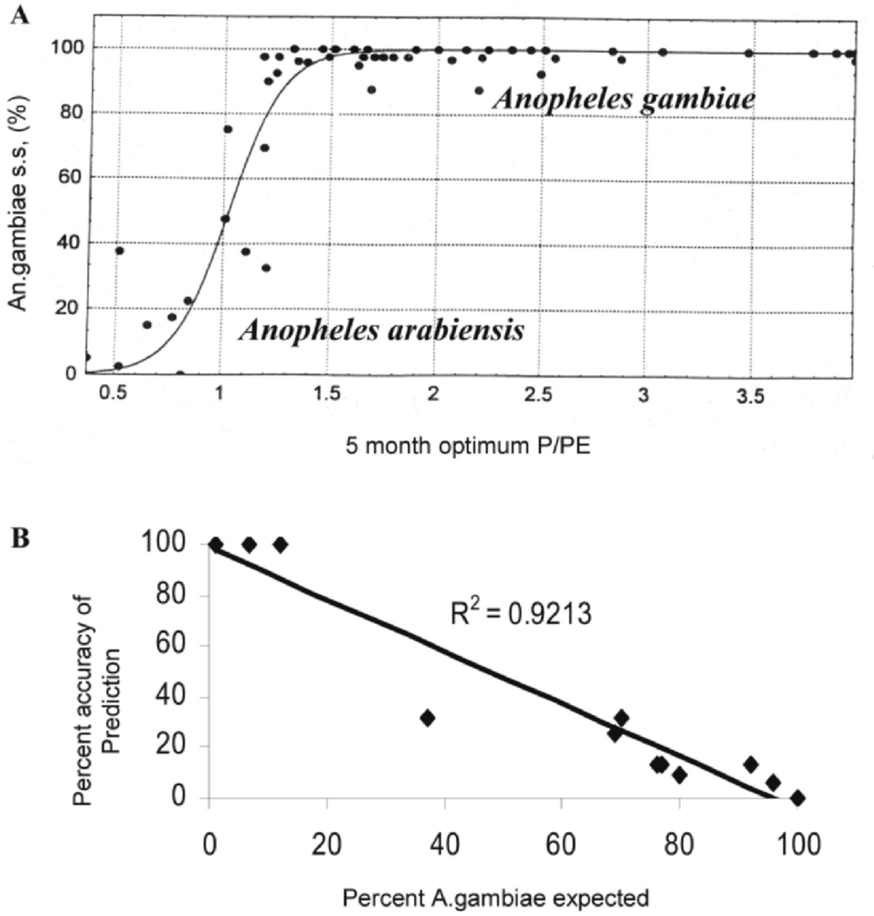


Figure 3. Prediction of relative *Anopheles gambiae s.s.* and *Anopheles arabiensis* based upon climate data. Measures of humidity (P/PE) were plotted against the proportion of each species at sites in Africa (A). *An. gambiae s.s.* and *An. arabiensis* separated based upon high (P/PE>1.2) or low (P/PE< 0.8) humidity, respectively (courtesy of Prof. S. Lindsay, University of Durham, UK). The fitted line was used to predict the proportion of *An. gambiae* at other sites with good accuracy (B) especially at the extremes where populations of only one species would be expected (based on data in Lindsay, Parson and Thomas 1998)

predictors of mosquito numbers (Thomson et al. 1996; 1997) and population structures (Figure 4). At the start of the RA, non-entomological background data can be gained quickly. These can include information about human populations, living conditions and agricultural practices (most notably animal husbandry and those that favour vector breeding). Use of anti-mosquito measures such as bednets, mosquito coils, insecticides and repellents – all of which may be seasonally influenced (Charlwood et al. 1995b) – should be recorded. Simple questionnaires can also provide useful indicators on such things as anti-malarial drug usage, where people perceive mosquito populations to be high and of the presence of standing water (Teuscher 1992; Minja et al. 2001). In addition, recruitment of local expertise into the RA should excite local interest and provide opportunities for health education.

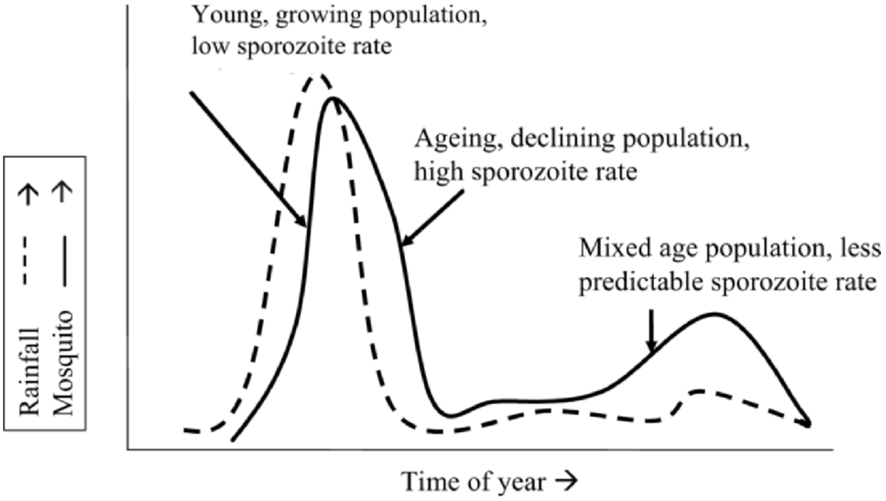
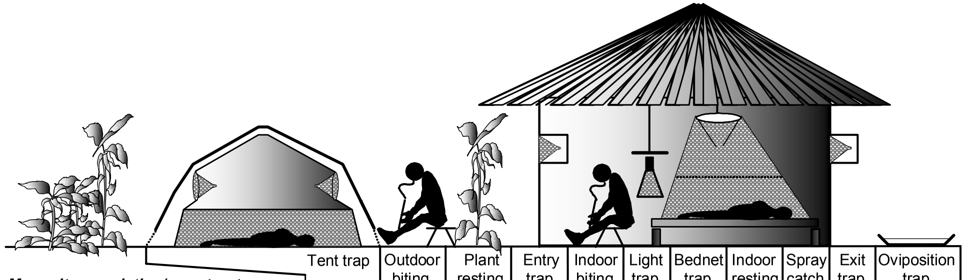


Figure 4. Effects of season on mosquito populations and malaria transmission. Mosquito populations typically lag slightly behind rainfall, such that rainfall increases are often followed by a peak in mosquito numbers (see also Figure 1). Leading up to the peak, mosquito populations are undergoing huge recruitment, will be relatively young and therefore have low salivary-gland infection rates with *Plasmodium* sporozoites. As the population declines, the ageing mosquito population has few if any new recruits and will have an increasingly high sporozoite rate. During periods where the mosquito populations are more stable (short rains for example), the age of the mosquito population can be very mixed and the sporozoite infection rate hard to predict. RA undertaken at any of these times must account for the differences in mosquito population characteristics as well as densities that seasonality will induce

What type of data and how many?

The RA will have specific objectives to address that may be determined by outside agencies prior to fieldwork. Mosquitoes possibly represent the most captured insect group in the world, and many methods to catch them have been devised (Figure 5), from which several can be selected that best answer the specific questions. For example, if the aim is to determine spatial variations in the EIR, then adult mosquitoes from light traps, tent or bednet traps (Mathenge et al. 2002; 2004), or landing or resting catches will suffice. If parasitaemias or human to mosquito transmission are of interest then mosquitoes with blood meals need to be collected. Where mosquito feeding-strategies and population structure are of interest in relation to control measures such as bednet introduction, then live mosquitoes from diverse collections are most appropriate. If the purpose is to incriminate a vector, then the RA must be able to identify local mosquitoes and collect numbers sufficient for parasite identification possibly at low prevalences (Hii et al. 2000). Here, too, the seasonal timing of the RA will be important. Mosquito populations differ not only in density



Mosquito population/age structure	Tent trap	Outdoor biting	Plant resting	Entry trap	Indoor biting	Light trap	Bednet trap	Indoor resting	Spray catch	Exit trap	Oviposition trap
• Density of biting population	■	■	■	■	■	■	■	■	■	■	■
• Ovarian development (% young females)	■	■	■	■	■	■	■	■	■	■	
• Parity status (survival rate, distance to oviposition site)	■	■	■	■	■	■	■	■		■	
• Mating plug (% young females, breeding)	■	■	■	■	■	■	■	■		■	
• Hydracine mites (% nulliparous)	■	■	■	■	■	■	■	■	■	■	
Mosquito behaviour											
• Indoor feeding (degree of endophagy)	■			■	■	■	■	■	■	■	
• Indoor resting (degree of endophily)								■	■		
• Outdoor feeding (degree of exophagy)		■									
• Outdoor resting (degree of exophily)										■	
• Blood from midgut (Human Blood Index)								■	■	■	
Malaria											
• Midgut (within 1 day) - *Plasmodium* in blood meal								■	■	■	
• Midgut (4-5 days) - delayed oocyst rate								■	■	■	
• Midgut (oocyst rate)	■	■	■	■	■	■	■	■	■	■	
• Salivary glands (sporozoite rate)	■	■	■	■	■	■	■	■	■	■	
• Risk of infection for collector		■			■						

Figure 5. Mosquito-trapping methods and their application. Trapping techniques can gather information required for determining the EIR. Each trapping or collecting method and subsequent handling of the mosquitoes can be used to sample a definable subpopulation of the local mosquitoes (left column), and these are selected according the specific aims of the RA. For example, indoor resting catches will provide the full range of information necessary to assess mosquito population structure, association with human hosts, and essential malaria information, and up to six of these collections could be performed by a field worker per day

but also in age structure, depending upon the season, and the RA should take into account the possibility that a population is stable, recruiting or in decline (Figure 1) as this greatly influences the sporozoite rate and EIR (Figure 4) (Charlwood et al. 1995a).

The more difficult decisions associated with RA are concerned with sampling effort – how many data are enough? When mosquito numbers are high, the job of the RA entomologist is much more straightforward. Mosquito densities will be collected and mapped quickly and with low effort, and estimating risk will be relatively routine for an experienced person. At low mosquito densities, decisions concerning the sampling effort will be crucial in determining the sensitivity of the RA. If several houses are sampled fruitlessly for mosquitoes, how is it possible to estimate risk? Lindblade, Walker and Wilson (2000) have addressed this question by comparing different sampling approaches and subsequent analyses to obtain estimates of risk of a malaria epidemic. If one uses a statistical approach driven by confidence intervals, then clearly the reliability of the data increases with sampling effort (20% error in risk estimation for 102 houses sampled increasing to 50% error for 16 houses). A useful alternative is a sequential approach that essentially devolves the decision-making process about sampling effort to the entomologist in the field. The relationship between number of households sampled and number of mosquitoes found can be considered a measure of risk at low densities (Figure 6), and as sampling proceeds, the decision can be taken that sufficient households with mosquitoes have been identified (or not) to advise on control measures. Obviously it takes more sampling effort to determine no risk (50 households) than placing a site above a risk threshold (20 houses). Another measure that may prove useful is to estimate the probability of finding a mosquito within a certain sampling effort. For the low mosquito numbers sampled by Lindblade, Walker and Wilson (2000), there was a 95% probability of finding a female *An. gambiae* in every seven houses sampled. However, the usefulness of these approaches remains largely untested, and the feasibility of their use in the field in control decision-making needs further consideration. Conversely, the over-dispersed pattern of oocyst infections in mosquitoes (Medley et al. 1993) has enabled the definition of a recognized minimum sampling effort (ca. 30 mosquitoes per sample) to estimate oocyst infection rates within predefined degrees of confidence (Billingsley et al. 1994).

An alternative and powerful approach is to exploit one or more of the many epidemiological models for malaria as an advisory tool for sampling strategies and effort. For example, the ratio of human to mosquito population densities, mosquito lifetime infectiousness and human infectious reservoir can be used in a relatively simple model for estimating EIR and the impacts of control measures upon it (Killeen et al. 2000b; 2000a). All of these parameters are measurable in the described RA approach. A still more powerful approach is the exploitation of less well-related datasets within a Bayesian statistical modelling approach (Smith et al. 1995). Bayesian modelling has been used to predict accurately (86%) the number of villages in an Amazonian region at high risk of *Onchocerca volvulus* infections, and thereby offer advice on control efforts (Carabin et al. 2003). The flexibility of the Bayesian method and its ability to incorporate diverse data into a predictive, testable model make this a powerful approach that remains underused. We anticipate that it will become an integral part of RA.

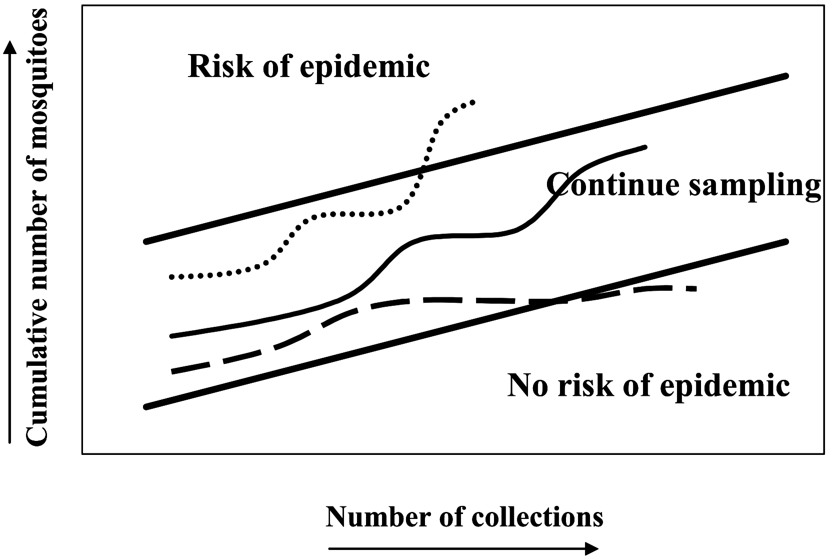


Figure 6. Trapping effort and outcome for malaria. The amount of effort that must be put into sampling has been modelled (Lindblade, Walker and Wilson 2000). The effort required is a combination of the required decision and the population densities of mosquitoes. As the number of samples accumulates, then the rate at which mosquitoes are found will help decide upon the risk to the community of a malaria epidemic. If sufficient mosquitoes are found with relatively low sampling effort (··········), then epidemic risk can be considered high; where most samples do not contain mosquitoes (– – –) risk is low and sampling can stop. Otherwise, more sampling is required (———) in order to reach a decision about risk and therefore control. This open-ended approach is especially sensitive in areas where mosquito numbers are low and malaria is unstable

Sample- and data-processing

Exploiting spatial information

The spatial heterogeneity of mosquito populations can be used by RA to provide relative-risk maps of the sampled area (Ribeiro et al. 1996). The important first is the production of physical maps of the assessment area. Maps can be produced, and houses numbered, using a variety of techniques. Simple sketch maps can be used to localize each mosquito collection site and provide crude reference points. The integration of RA maps into a larger frame of reference requires at least two geopositions obtained either from 1:10,000 maps or from hand-held Global Positioning Satellite (GPS) devices. Well-produced maps are useful investments for future reference and therefore must incorporate physical markers (trees, roads and railways) that outlive the average house. Within a few days of collection, maps showing relative mosquito densities can be produced by superimposing mosquito data onto the physical map. Gradients of mosquito numbers can be determined along sample transects or according to points on the map, and compared to human population densities to describe the heterogeneity in EIR.

The problems of non-temporal data

Temporal variation in mosquito numbers and species composition is an inherent problem to RA because of its snapshot nature. Nevertheless, relative gradients in mosquito densities between areas do not change overmuch (Figure 1) and ratios between collection sites at any one time will reflect all other collections. When coupled to meteorological data and compared to published material, it should be possible to place the RA ‘snapshot’ into a reasonably predictable temporal context (Charlwood et al. 1995a).

Malaria in the mosquito

Parasites can be identified in the mosquito by a range of simple or sophisticated techniques. Asexual and early sexual stages are easily identified in the blood meals of recently fed females, and their prevalence is proportional to parasite prevalence in human blood samples (Figure 7, Gare and Billingsley unpublished). Oocysts on the dissected midgut of unfed and gravid females can be observed through a compound microscope or, with care, a good dissecting microscope. The proportion of parous mosquitoes with oocysts provides an indication of the proportion of feeds infective to mosquitoes (the infectious reservoir) (Haji et al. 1996; Charlwood et al. 1997; Graves et al. 1988; Muirhead-Thomson 1954). Sporozoite identification by microscopy is labour-intensive, and does not identify *Plasmodium* species, although this is not a problem where only one parasite species is present, and ELISA or PCR on stored mosquitoes requires time and cost investment. A recently introduced dipstick assay offers an important field tool for RA, providing the first method to identify salivary gland sporozoites to species that is not laboratory-based and reliant upon equipment (Ryan et al. 2002).

Age structure of mosquito population

Depending on the type of collection the abdominal condition of mosquitoes provides an indication of the age structure of the population and their degree of endophily (Figure 5). For example, if a similar number of gravid and recently fed mosquitoes are collected resting from inside houses this indicates that the species is endophilic and probably susceptible to control by residual insecticides. Conversely, if there are many blood-fed and few gravid mosquitoes in a collection then the species is largely exophilic. The relative proportions of blood-fed, semi-gravid and gravid insects also provide an indication of the duration of the oviposition cycle length (Gillies 1956). Not all collection methods sample the same fraction of the population. The indoor resting sample, for example, tends to under-sample recently emerged insects and cannot therefore be used to determine recruitment (Takken et al. 1998).

Recruitment can be assessed by dissection of the ovaries. Depending on the dispersal pattern of the species, one might expect a large number of young insects close to breeding sites and fewer but older insects at a distance. In an RA, simple dissections can provide estimates of comparative potential risk in space as well as time. In assessing risk at any particular time it is also important to know if the vector population(s) are increasing, declining or stable (Figure 3). This can be determined by dissection of unfed mosquitoes (Figure 2) for the presence of a mating plug, the ovarian stage and parity status. Plugs are found only in young females and suggest localized breeding (Gillies 1956; Charlwood, Vij and Billingsley 2000) and young females with early stage ovarioles also indicate breeding taking place. The presence of ovariolar sacs in parous females indicates that the mosquitoes returned to feed shortly

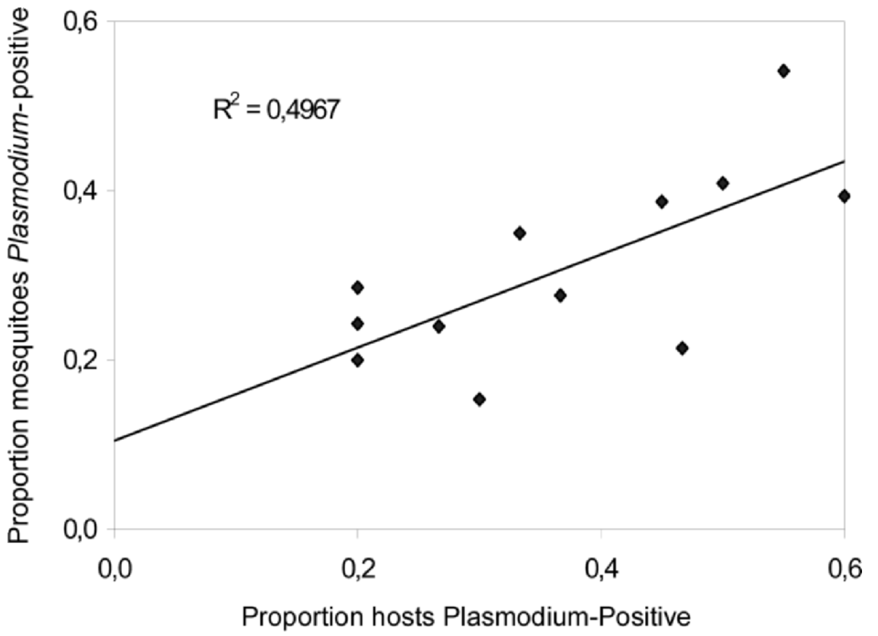


Figure 7. Relationship between *Plasmodium falciparum* asexual-stage intensities in human blood smears and mosquito blood meals. For a limited period after feeding, mosquito blood meals contain all components of the host blood, including asexual and sexual stages of the malaria parasites. The proportion of blood meals containing parasites has a direct relationship with the proportion of infected individuals within a household, and can be used as an indicator of parasite prevalence. Each point on the graph represents samples taken from households of different numbers of individuals, the infected proportion of which varied. For each household, blood meals from at least 30 mosquitoes were sampled (Gare and Billingsley unpublished)

after oviposition and therefore oviposition sites are likely to be close to the feeding site. The relative proportions of parous females with and without sacs can be used to determine mean ovipostion cycle length.

Survival-rate estimation is an important epidemiological parameter that has received the attention of entomologists for many years. Estimates of survival rate from parity rates of samples collected over a short period of time are only applicable if the population is in a steady state (i.e. when recruitment and death rates are equal) (Charlwood et al. 1995a) and here, setting the RA into a temporal context is important. Alternatives to parous-rate estimations (e.g. time series analysis) all require longitudinal collections, placing them outside the RA remit, and have generally proven inapplicable to mosquito studies (Charlwood 1986; Charlwood, Vij and Billingsley 2000).

Whilst the proportion of a population parous may vary due to rapid changes in recruitment, the infection rate in parous insects changes more slowly. Combined parous and oocyst rates provide a suitable estimate of the proportion of feeds infectious to the mosquito (Charlwood, Vij and Billingsley 2000); by further including sporozoite rate, mosquito survival can also be estimated (Charlwood et al. 1995a; Beier and Koros 1991). Estimates of sporozoite rates are a needed for EIR determination and are therefore likely to be included in any RA protocol. The relative proportion of parous mosquitoes with oocysts and sporozoites provides an indication of survival rate, age structure and vector potential. A comparison of actual and potential sporozoite rate (determined by survival rate of the mosquito) indicates the potential for amplified transmission. Under steady-state conditions the relative proportion of each age group, as defined by parity status and sac stage (of parous females), is an indicator of mosquito survival rate. Large imbalances in any age category imply that the population is growing recruiting or ageing, or that representative samples of the different age groups are not being obtained.

Mosquito behaviour

The feeding behaviour, in particular the human-biting rate, is an important component of EIR estimation. Abdomens of blood-fed females dried onto filter paper can be used to identify host source by ELISA or dipstick ELISA (Savage et al. 1991; Charlwood et al. 2001), either of which can be performed under field conditions. By siting collections indoors or outdoors, the exophilic behaviour of mosquitoes can be determined, and coupled with knowledge of the biting cycle and local habits, used to refine risk assessment.

Data management

The availability and affordability of palmtop and laptop computers, and their great advantages in terms of accuracy and efficiency of data input (Forster and Snow 1992) places them as essential items in the RA repertoire. A core working practice can be envisaged that will serve several purposes. Spreadsheets or databases can be designed for manual and automated (e.g. GPS, data-logging devices, weather stations) data input, and simultaneous sample processing (through unique labelling). The spreadsheets on palmtops could then be processed into a complete database for full data analysis. Analysis would include EIR estimates, mapping, spatial and (limited) temporal variations in mosquito numbers, risk factors, mosquito species contributions to transmission, and best sites to target for control measures. Inputting data directly into computers allows immediate cross-checking of data and their rapid processing (Sutherst 1998). The outputs can be formulated to provide information for other projects (such as MARA), to be comparable with other studies, be tailored towards available software for such things as impact assessment (Hay, Snow and Rogers 1998), be used to validate statistical (Smith et al. 1995) or predictive (Lindsay, Parson and Thomas 1998) models, or improve the resolution of maps of vector abundance (Snow, Marsh and Le Sueur 1996) or transmission intensity (Graves et al. 1988). Finally, with standardized data gathering and input coupled to archived field material, an RA repository could provide stored samples and on-line databases for a range of collaborative studies.

It is also important, of course, to ensure that answers derived from an RA to a specific set of questions are used to improve control efforts. The utility of the data depends upon the scale of the RA, resources available and questions being addressed. At the larger scale RA may allow a focusing of resources, say to particular villages within a district. Even within ‘low-density’ villages the RA may identify foci of intense transmission appropriate for such targeted control strategies as house spraying or selective vaccination.

Rapid assessment: present and future

The RA techniques described here are often applied by entomologists with or without RA interests; the techniques are all available, but have yet to be packaged into an assessment protocol. Given the increased scope for networking and data exchange, uniform methodology can be developed and results compared between areas. For example, if CDC miniature light traps are used to collect indoor biting vectors it behoves entomologists to use them in the same way (Mbogo et al. 1993; Mboera et al. 1998; Snow, Marsh and Le Sueur 1996). Broad use of the same techniques should provide hitherto unavailable ecological information on a continental scale; in Africa, in particular, the absence of such information makes it difficult to assess ecological trends within the *An. gambiae* complex. Meta-analysis from a number of sites could provide information on such things as species-specific dispersal rates under different ecological conditions. The techniques are available and the entomologists are there; what is required for the 'present' of RA is communication, coordination and application.

Once RA is established, its future looks brighter still. Numerous techniques that were developed over the past years, some in areas not related to malaria, can impact upon field studies in general and RA in particular. More use could be made of the mosquito blood meal to identify anti-CSP antibodies (exposure index in the humans), proteinase activities (time post feeding and therefore biting cycle), and human-feeding rate by dipstick assays. *Plasmodium* species-specific CSP can be detected in live mosquitoes (Billingsley et al. 1991) and the technique should be adaptable to determine low sporozoite rates in large mosquito samples as an alternative to ELISA or population screening (Shen et al. 1998). With the exception of polytene chromosome examination, there is no reliable field-based assay for identification of mosquitoes within a species complex. PCR-based approaches (Paskewitz and Collins 1990) require a laboratory, and DNA squashes (Hill, Urwin and Crampton 1991) have not lived up to their promise. It is possible that such differences in mosquito biology as attraction to specific odours or desiccation resistance can be exploited to identify separate species in simple ways. The equipment-driven side of RA also has an interesting future. Combined with data from weather stations (portable or regionally sited), GIS (Geographic Information Systems) information could be extrapolated to locate oviposition sites and enhance or validate predictive models from satellite data. A clockwork electrical supply, currently used to drive transistor radios, could allow microscopes, light traps and computers to be taken to remote sites without the need for generators (same for solar-powered 12V battery packs). Identification of host odours can drastically improve the efficiency of mosquito traps as shown with CO_2 and 1-octen-3-ol in mosquito traps in Florida (Takken and Kline 1989).

An explicit mosquito-based RA of malaria in the field has yet to be attempted. With current methodologies we urge field entomologists and malariologists to attempt some of the approaches outlined here. Their success will help develop an approach to malaria assessment that will be broadly applicable and can be implemented with limited training of local entomologists within a health-care setting.

References

Beier, J.C. and Koros, J.K., 1991. Visual assessment of sporozoite and bloodmeal ELISA samples in malaria field studies. *Journal of Medical Entomology,* 28 (6), 805-808.

Billingsley, P.F., Hodivala, K.J., Winger, L.A., et al., 1991. Detection of mature malaria infections in live mosquitoes. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 85 (4), 450-453.

Billingsley, P.F., Medley, G.F., Charlwood, J.D., et al., 1994. Patterns of infection of *Plasmodium falciparum* in wild caught *Anopheles* mosquitoes. *American Journal of Tropical Medicine and Hygiene,* 51, 260-270.

Carabin, H., Escalona, M., Marshall, C., et al., 2003. Prediction of community prevalence of human onchocerciasis in the Amazonian onchocerciasis focus: Bayesian approach. *Bulletin of the World Health Organization,* 81 (7), 482-490.

Charlwood, J.D., 1986. Survival rate variation of *Anopheles farauti* (Diptera: Culicidae) between neighbouring villages in coastal Papua New Guinea. *Journal of Medical Entomology,* 23 (4), 361-365.

Charlwood, J.D., Kihonda, J., Sama, S., et al., 1995a. The rise and fall of *Anopheles arabiensis* (Diptera: Culicidae) in a Tanzanian village. *Bulletin of Entomological Research,* 85, 37-44.

Charlwood, J.D., Qassim, M., Elnsur, E.I., et al., 2001. The impact of indoor residual spraying with malathion on malaria in refugee camps in eastern Sudan. *Acta Tropica,* 80 (1), 1-8.

Charlwood, J.D., Smith, T., Billingsley, P.F., et al., 1997. Survival and infection probabilities of anthropophagic anophelines from an area of high prevalence of *Plasmodium falciparum* in humans. *Bulletin of Entomological Research,* 87 (5), 445-453. [http://pest.cabweb.org/PDF/BER/BER87-5/445.pdf]

Charlwood, J.D., Smith, T., Kihonda, J., et al., 1995b. Density independent feeding success of malaria vectors in Tanzania. *Bulletin of Entomological Research,* 85, 29-35.

Charlwood, J.D., Vij, R. and Billingsley, P.F., 2000. Dry season refugia of malaria-transmitting mosquitoes in a dry savannah zone of east Africa. *American Journal of Tropical Medicine and Hygiene,* 62 (6), 726-732.

Forster, D. and Snow, B., 1992. Using microcomputers for rapid data collection in developing countries. *Health Policy and Planning,* 7 (1), 67-71.

Garrett-Jones, C., 1964. Prognosis for interruption of malaria transmission through assessment of the mosquito's vectorial capacity. *Nature,* 204, 1173-1175.

Gillies, M.T., 1956. A new character for the recognition of nulliparous females of *Anopheles gambiae*. *Bulletin of the World Health Organization,* 15 (3/5), 451-459.

Graves, P.M., Burkot, T.R., Carter, R., et al., 1988. Measurement of malarial infectivity of human populations to mosquitoes in the Madang area, Papua, New Guinea. *Parasitology,* 96 (Part 2), 251-263.

Gupta, S. and Snow, R.W., 1996. How do bednets influence the transmissibility of *Plasmodium falciparum*? *Parasitology Today,* 12 (3), 89-90.

Haji, H., Smith, T., Meuwissen, J.T., et al., 1996. Estimation of the infectious reservoir of *Plasmodium falciparum* in natural vector populations based on oocyst size. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 90 (5), 494-497.

Hay, S.I., Snow, R.W. and Rogers, D.J., 1998. Predicting malaria seasons in Kenya using multitemporal meteorological satellite sensor data. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 92 (1), 12-20.

Hii, J.L., Smith, T., Mai, A., et al., 2000. Comparison between anopheline mosquitoes (Diptera: Culicidae) caught using different methods in a malaria endemic area of Papua New Guinea. *Bulletin of Entomological Research,* 90 (3), 211-219.

Hill, S.M., Urwin, R. and Crampton, J.M., 1991. A comparison of non-radioactive labeling and detection systems with synthetic oligonucleotide probes for the species identification of mosquitoes in the *Anopheles gambiae* complex. *American Journal of Tropical Medicine and Hygiene,* 44 (6), 609-622.

Killeen, G.F., McKenzie, F.E., Foy, B.D., et al., 2000a. The potential impact of integrated malaria transmission control on entomologic inoculation rate in highly endemic areas. *American Journal of Tropical Medicine and Hygiene,* 62 (5), 545-551.

Killeen, G.F., McKenzie, F.E., Foy, B.D., et al., 2000b. A simplified model for predicting malaria entomologic inoculation rates based on entomologic and parasitologic parameters relevant to control. *American Journal of Tropical Medicine and Hygiene,* 62 (5), 535-544.

Kilombero Malaria Project, 1992. The level of anti-sporozoite antibodies in a highly endemic malaria area and its relationship with exposure to mosquitoes. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 86 (5), 499-504.

Koella, J.C., 1991. On the use of mathematical models of malaria transmission. *Acta Tropica,* 49 (1), 1-25.

Le Sueur, D., Binka, F., Lengeler, C., et al., 1997. An atlas of malaria in Africa. *Africa Health,* 19 (2), 23-24.

Lindblade, K.A., Walker, E.D. and Wilson, M.L., 2000. Early warning of malaria epidemics in African highlands using *Anopheles* (Diptera: Culicidae) indoor resting density. *Journal of Medical Entomology,* 37 (5), 664-674.

Lindsay, S.W., Parson, L. and Thomas, C.J., 1998. Mapping the ranges and relative abundance of the two principal African malaria vectors, *Anopheles gambiae* sensu stricto and *An. arabiensis*, using climate data. *Proceedings of the Royal Society of London. Series B. Biological Sciences,* 265 (1399), 847-854.

Mathenge, E.M., Killeen, G.F., Oulo, D.O., et al., 2002. Development of an exposure-free bednet trap for sampling Afrotropical malaria vectors. *Medical and Veterinary Entomolgy,* 16 (1), 67-74.

Mathenge, E.M., Omweri, G.O., Irungu, L.W., et al., 2004. Comparative field evaluation of the Mbita trap, the Centers for Disease Control light trap, and the human landing catch for sampling of malaria vectors in western Kenya. *American Journal of Tropical Medicine and Hygiene,* 70 (1), 33-37.

Mboera, L.E., Kihonda, J., Braks, M.A., et al., 1998. Influence of centers for disease control light trap position, relative to a human-baited bed net, on catches of *Anopheles gambiae* and *Culex quinquefasciatus* in Tanzania. *American Journal of Tropical and Medical Hygiene,* 59 (4), 595-596.

Mbogo, C.N., Glass, G.E., Forster, D., et al., 1993. Evaluation of light traps for sampling anopheline mosquitoes in Kilifi, Kenya. *Journal of the American Mosquito Control Association,* 9 (3), 260-263.

Medley, G.F., Sinden, R.E., Fleck, S., et al., 1993. Heterogeneity in patterns of malarial oocyst infections in the mosquito vector. *Parasitology,* 106 (5), 441-449.

Minja, H., Schellenberg, J.A., Mukasa, O., et al., 2001. Introducing insecticide-treated nets in the Kilombero Valley, Tanzania: the relevance of local knowledge and practice for an information, education and communication (IEC) campaign. *Tropical Medicine and International Health,* 6 (8), 614-623.

Muirhead-Thomson, R.C., 1954. Factors determining the true reservoir of infection of *Plasmodium falciparum* and *Wuchereria bancrofti* in a West African village. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 48 (3), 208-225.

Paskewitz, S.M. and Collins, F.H., 1990. Use of the polymerase chain reaction to identify mosquito species of the *Anopheles gambiae* complex. *Medical and Veterinary Entomolgy,* 4 (4), 367-373.

Ribeiro, J.M., Seulu, F., Abose, T., et al., 1996. Temporal and spatial distribution of anopheline mosquitos in an Ethiopian village: implications for malaria control strategies. *Bulletin of the World Health Organization,* 74 (3), 299-305.

Ryan, J.R., Dave, K., Collins, K.M., et al., 2002. Extensive multiple test centre evaluation of the VecTest malaria antigen panel assay. *Medical and Veterinary Entomolgy,* 16 (3), 321-327.

Savage, H.M., Duncan, J.F., Roberts, D.R., et al., 1991. A dipstick ELISA for rapid detection of human blood meals in mosquitoes. *Journal of the American Mosquito Control Association,* 7 (1), 16-23.

Shen, J., Zhang, S., Xu, B., et al., 1998. Surveillance for low-level malaria. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 92 (1), 3-6.

Smith, T., Charlwood, J.D., Takken, W., et al., 1995. Mapping the densities of malaria vectors within a single village. *Acta Tropica,* 59 (1), 1-18.

Snow, R.W., Marsh, K. and Le Sueur, D., 1996. The need for maps of transmission intensity to guide malaria control in Africa. *Parasitology Today,* 12 (12), 455-457.

Sutherst, R.W., 1998. Implications of global change and climate variability for vector-borne diseases: generic approaches to impact assessments. *International Journal of Parasitology,* 28 (6), 935-945.

Takken, W., Charlwood, J.D., Billingsley, P.F., et al., 1998. Dispersal and survival of *Anopheles funestus* and *An. gambiae* s.l. (Diptera: Culicidae) during the rainy season in southeast Tanzania. *Bulletin of Entomological Research,* 88 (5), 561-566.

Takken, W. and Kline, D.L., 1989. Carbon dioxide and 1-octen-3-ol as mosquito attractants. *Journal of the American Mosquito Control Association,* 5 (3), 311-316.

Teuscher, T., 1992. Household-based malaria control in a highly endemic area of Africa (Tanzania): determinants of transmission and disease and indicators for monitoring-Kilombero Malaria Project. *Memorias Do Instituto Oswaldo Cruz,* 87 (Suppl. 3), 121-130.

Thompson, R., Begtrup, K., Cuamba, N., et al., 1997. The Matola malaria project: a temporal and spatial study of malaria transmission and disease in a suburban area of Maputo, Mozambique. *American Journal of Tropical Medicine and Hygiene,* 57 (5), 550-9.

Thomson, M.C., Connor, S.J., Milligan, P., et al., 1997. Mapping malaria risk in Africa: what can satellite data contribute? *Parasitology Today,* 8, 313-318.

Thomson, M.C., Connor, S.J., Milligan, P.J., et al., 1996. The ecology of malaria-as seen from Earth-observation satellites. *Annals of Tropical Medicine and Parasitology,* 90 (3), 243-264.

Trigg, J.K., Mbwana, H., Chambo, O., et al., 1997. Resistance to pyrimethamine/ sulfadoxine in *Plasmodium falciparum* in 12 villages in north east Tanzania and a test of chlorproguanil/dapsone. *Acta Tropica,* 63 (2/3), 185-189.

Wijesundera, M.D., Peiris, J.S., Ariyaratne, Y.G., et al., 1990. Antibodies to *Plasmodium falciparum* sporozoites following a malarial outbreak in a non-endemic area of Sri Lanka. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 84 (1), 35-39.

Woolhouse, M.E., Dye, C., Etard, J.F., et al., 1997. Heterogeneities in the transmission of infectious agents: implications for the design of control programs. *Proceedings of the National Academy of Sciences of the United States of America,* 94 (1), 338-342.

7

Malaria risk in the highlands of western Kenya: an entomological perspective

C.J.M. Koenraadt [#] *and A.K. Githeko* [##]

Abstract

Epidemics of malaria seem to occur more frequently in the highlands of eastern Africa. In western Kenya, for example, epidemics have spread from 3 to 15 districts. There is an increasing debate on the possible causes of this phenomenon, but detailed field studies are lacking to test a number of basic hypotheses. In this chapter, we review some of the results from a comparative field study on malaria risk in a highland and a lowland area in western Kenya. Questions that will be addressed in this chapter are: under which conditions may malaria epidemics occur in highland areas and to what extent is the situation in western Kenya comparable to other highland areas in the region?

Keywords: *Anopheles gambiae*; *Anopheles arabiensis*; malaria risk; Kenya; environmental change; highlands

Introduction

The intimate relationships between parasites or viruses, and their vectors, hosts and natural environment make this ecological web extremely sensitive to disturbances. Therefore, environmental and socio-economic changes, such as global warming, deforestation, commercial development and construction of water-control systems, are expected to exert a huge impact on the transmission of viral and parasitic diseases, such as Rift Valley fever, yellow fever, schistosomiasis, filariasis and malaria (Githeko et al. 2000; Martens, Slooff and Jackson 1997; Martens 1998; Patz and Reisen 2001; Patz et al. 2000). The diseases may spread to areas where they did not occur before or the current situation may aggravate in areas where the disease is already endemic.

Theoretically, one infective mosquito bite is enough to acquire an episode of malaria. Clinical symptoms may range from mild, such as fever, abdominal pains, nausea and vomiting, to severe and life-threatening, such as anaemia, renal disfunction and cerebral malaria (Warrell 1993). However, not everybody who gets an infection becomes seriously ill or dies, because this depends on the degree of immunity of the individual. A substantial level of immunity to malaria may already be acquired after one or two infective bites. The antigenic variation of *P. falciparum* (i.e. the variation in antigens expressed at the surface of the infected red blood cell) is thought to play an important role

---

[#] Laboratory of Entomology, Wageningen University, The Netherlands; present address: AFRIMS Entomology Laboratory, 2 soi 15, Rachdamnoen road 1, Nai Muang, Muang, Kamphaeng Phet 62000, Thailand. E-mail: cjmkoenraadt@ucdavis.edu

[##] Kenya Medical Research Institute, P.O. Box 1578, Kisumu, Kenya. E-mail: agitheko@kisian.mimcom.net

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 69-78.

in this (Day and Marsh 1991; Gupta et al. 1999; Roberts et al. 1993). During their first 3 to 6 months of life, infants have a protective immunity through antibodies they obtained from their mother. After this period, they will build up protective immunity, if regularly infected, and around their fourth year of life the severity of malaria attacks begins to decline. As evidenced from field studies, death among adults is rare in high-transmission areas, but the level of immunity may rapidly decrease when moving outside these areas (Marsh 1993).

From this follows that children up to the fifth year of life are at high risk of dying from malaria (if not appropriately treated). Also pregnant women deserve special attention, since malaria infection during pregnancy may lead to low birth weight of the infant, either through prematurity or intra-uterine growth retardation. Low birth weight, on its turn, may lead to infant mortality (Steketee et al. 2001). Furthermore, people living in areas where transmission is low or absent, such as the cool highland areas or areas at the northern and southern fringes of current malaria distribution, are also at high risk of getting severe malaria once infected.

Epidemic malaria

Historically, outbreaks of malaria have occurred in areas of unstable malaria transmission when environmental conditions were favourable (Garnham 1945; 1948). However, there is evidence that the number of outbreaks has increased during the past decades. In eastern Africa, many countries have suffered from serious epidemics with a high number of deaths (Malakooti, Biomndo and Shanks 1998; Etchegorry et al. 2001; Bonora et al. 2001; Lindblade et al. 1999). In western Kenya, malaria epidemics have spread from 3 to 15 districts during the past 13 years, often with devastating effects (Githeko and Ndegwa 2001). Some of these epidemics have been associated with extreme weather events, such as the El Niño Southern Oscillation event in 1997-1998, which caused heavy rainfall and flooding in eastern Africa (WMO 1999). Curiously, the same climatic event in Tanzania was associated with lower malaria incidence (Lindsay et al. 2000), suggesting that no clear-cut answer exists to what the effects of these extreme weather events are on malaria transmission.

Next to analysing single malaria outbreaks, researchers have attempted to relate historical patterns of malaria incidence to environmental changes. Increased malaria incidence over the past 30 years in the highland tea estates of western Kenya could not be explained by increased temperatures or a changed climate in general (Shanks et al. 2000; 2002). Similar observations were made for other East-African countries (Hay et al. 2002a), although a re-analysis of climatic data did show a warming trend for the same countries (Patz et al. 2002). This has led to a debate on the potential causes of malaria resurgence in eastern Africa, with global warming on the one hand and non-climatic events, such as the emergence of chloroquine resistance during the 1980s, on the other (Hay et al. 2002b; Patz et al. 2002). Although climatic changes may not be evident from the recent past, a warming climate in the near future, as predicted by various climate-change scenarios (IMAGE team 2001), may have severe consequences for malaria transmission.

With the advancement of satellite imagery and Geographical Information Systems (GIS), researchers have been able to integrate the different entomological, epidemiological and socio-economic components of malaria risk in ‘easy-to-handle’ data sets and ‘easy-to-interpret’ figures (see, e.g., MARA/ARMA 2002). This has resulted in a variety of models to forecast malaria outbreaks (so-called early-warning systems (Thomson and Connor 2001), study malaria transmission patterns and assess malaria risk in relation to climate change (Table 1).

Table 1. Examples of models developed to predict malaria epidemics and assess malaria risk in relation to environmental change. Input data and output parameters are given together with the area for which they were developed

Input	Output	Area	Goal	Reference
Rainfall and maximum temperature	Epidemic risk	Kenya	Early warning	Githeko and Ndegwa (2001)
Malaria vector density	Epidemic risk	Uganda	Early warning	Lindblade, Walker and Wilson (2000)
Number of presumptive malaria cases	Epidemic risk	Madagascar	Early warning	Albonico et al. (1999)
Normalized Difference Vegetation Index (NDVI)	Malaria seasonality	Kenya	Predicting malaria transmission seasonality	Hay, Snow and Rogers (1998)
Rainfall and temperature	Distribution of *An. gambiae s.s.* and *An. arabiensis*	Africa	Facilitating species-specific vector-control activities	Lindsay, Parson and Thomas (1998)
Temperature, NDVI, cold-cloud duration and elevation	Distribution of 5 sibling species of the *An. gambiae* complex	Africa	Forecasting malaria	Rogers et al. (2002)
Rainfall and temperature	Distribution of malaria transmission	Africa	Providing basis for predicting impact of climate change	Craig, Snow and Le Sueur (1999)
Rainfall, temperature and population data	Distribution of population exposed	Africa	Providing risk map for malaria mortality	Snow et al. (1999)[1]
Temperature and rainfall	Potential malaria risk	World	Assessing malaria risk in relation to climate change	Martens et al. (1995)

[1] Based on the model of Craig, Snow and Le Sueur (1999)

Most of these models have been developed to investigate malaria risk on the continental scale of Africa. Logically, these models are too crude to assess malaria risk on local and regional scales. They have rarely been validated with real data and make many assumptions and generalizations on malaria transmission. For example, the vector of malaria is often modelled as a generic species, whereas many differences exist in the transmission capability of the main malaria vectors. In addition, most models only consider the effects of ecological variables on the adult stage, while effects on the larval stages are often neglected. Furthermore, it is still unknown which ecological variables are responsible for the temporal and spatial dynamics in species abundance and how this affects malaria risk. Besides, it is not clear how malaria transmission is maintained in highland areas or how epidemics may occur here.

Vector biology and malaria risk on a local scale

A means of understanding the effects of environmental factors on malaria vector biology and malaria risk is to study these on different spatial and temporal scales. This is schematically presented in Figure 1. A comparative field study was undertaken in western Kenya to investigate vector population dynamics in relation to malaria risk (Koenraadt 2003). *Anopheles arabiensis* Patton and *Anopheles gambiae s.s.* Giles, both members of the *Anopheles gambiae* complex, and *Anopheles funestus* Giles are the main vectors involved in malaria transmission in this area. In addition, western Kenya is of particular interest, since on a relatively small spatial scale there is considerable variation in altitude, climatological conditions and land-use patterns. As a consequence, the epidemiological situation of malaria varies as well (Figure 2). Here, we briefly summarize some of the most important findings of this study for our understanding on malaria transmission in highland areas.

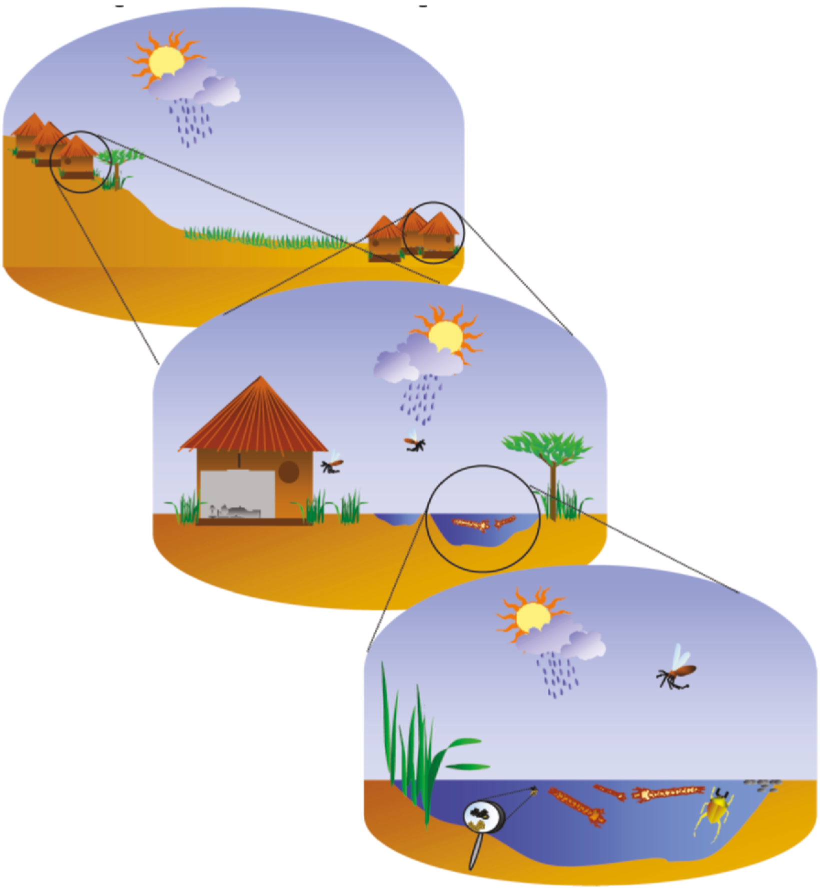


Figure 1. Schematic representation of the different scales when investigating the effect of environmental factors on vector biology and malaria risk

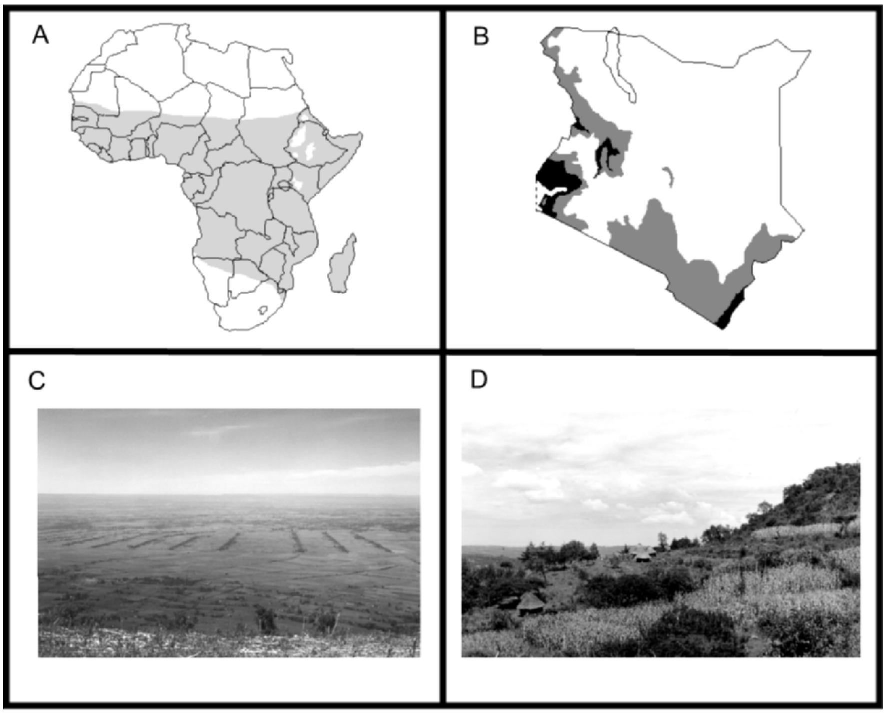


Figure 2. (A) Malaria distribution over Africa (drawn after WHO 1997); (B) epidemiological situation of malaria in Kenya. Black areas: endemic malaria; grey areas: epidemic malaria; white areas: no malaria (drawn after MARA/ARMA 2002); (C) picture of lowland area in western Kenya (approximately 1200 m altitude), characterized by the flat terrain and surrounded by large sugarcane plantations; (D) picture of highland area in western Kenya, 40 km south-east of the lowland area, characterized by a hilly landscape with mixed agriculture (approximately 1600 m altitude)

A striking result was that, despite the near absence of malaria vectors (5 malaria vectors were collected in 200 light-trap and 190 resting-catch collections spread over two years), malaria was transmitted throughout a two-year study period in a highland area of western Kenya (at 1600 m altitude). Malaria prevalence was relatively low, with a two year average of 10% among school children in the age of 5 - 10 years (minimum 0% and maximum 17% prevalence). Larval habitats of *An. gambiae s.l.* were present in the highland area, although their number was rather limited compared to a lowland area 40 km to the northwest (at 1200 m altitude). For example, only 7 *An. gambiae s.l.* breeding habitats were identified during a 4-month study within an area of approximately 4 km^2, whereas on a 1.7-km dirt road in a lowland area more than 100 *An. gambiae s.l.* breeding habitats could be identified on a single sampling occasion (Koenraadt, Githeko and Takken 2004). Interestingly, three of the seven identified breeding sites in the highland area were the result of human conduct: larvae were found in sites that were the result of leaking taps or in sites that were regularly filled by people for domestic purposes or to provide drinking water for cattle. All *An. gambiae s.l.* larvae were found in the presence of larvae of *An. christyi* Newstead & Carter. To what extent this association affected vector dynamics in the area, remains unclear. Experimental studies showed that larvae of *An. gambiae s.s.* and *An. arabiensis* did not survive the cool environmental temperatures in the highland area, whereas adults of both species (placed in cages) survived inside local houses in the same area (Koenraadt 2003). These studies also showed that adults of *An. gambiae s.s.* survived longer than *An. arabiensis* in the highland area, whereas the reverse was true for the lowland area. In addition, larvae of *An. arabiensis* developed faster to the pupal stage than *An. gambiae s.s.* in the lowland area, consistent with earlier findings under laboratory conditions (Schneider, Takken and McCall 2000). The combined experimental and field observations suggested that the contribution of a locally breeding vector population to malaria transmission in the highland area was negligible. More likely, the few infections among school children were caused by infected mosquitoes that immigrated from areas where environmental conditions are more favourable. Since children rarely moved out of the study area, we ruled out the possibility that their infections were obtained through visits to lower areas. Population-genetic studies on vectors collected in highland areas and in the nearby lowland areas may give more insight in the degree of gene flow and thus the amount of genetic divergence between highland and lowland mosquitoes (Wang, Kafatos and Zheng 1999; Lehmann et al. 1997, Lanzaro pers. comm.).

It should be emphasized that the transmission process described above may not be valid for all highland areas in eastern Africa. Local variation may arise as a result of differences in (i) geography, e.g. highland areas may be surrounded by steep escarpments or valley bottoms, and (ii) land cover/land use: suitability of the environment for mosquito survival and dispersal will differ between, for example, relatively bare highland areas, areas surrounded by marshes and areas with large-scale agriculture. Several studies have focussed on malaria transmission in high-altitude areas in Kenya, Tanzania and Uganda, and the role of vectors therein. However, these studies were limited to collections of the adult stages (Bødker 2000; Lindblade et al. 1999; 2000; Minakawa et al. 2002; Shililu et al. 1998). Therefore, most of these studies could not confirm the true existence of transmission by a local population or transmission by a population which immigrated from an adjacent area.

The insights obtained on malaria transmission in a highland area, allow us to speculate in more detail on the potential impact of environmental change on malaria risk. An increase in temperature in the near future, either as a result of global warming or land-use changes affecting microclimate, may enhance larval survival. As a result, local vector populations may establish in sufficient numbers to cause epidemics. This is supported by observations of Garnham (1945), who speculated that epidemics occurring at high altitudes may result from temporarily favourable climatic conditions that allow breeding of *An. gambiae*. On a larger time scale, it may be the more efficient vector *An. gambiae s.s.* settling first in highland areas, because this species survives better than *An. arabiensis* under present highland conditions.

Temperature and vector density have been used to develop early warning systems based on data from past epidemics (Githeko and Ndegwa 2001; Lindblade, Walker and Wilson 2000). Our results demonstrate that monitoring the larval stages may provide an additional means to assess the likelihood of outbreaks of malaria. For example, a warning based on increased environmental temperatures may be more confident if it is associated with high densities of local breeding sites in which larvae survive.

Final remarks

From our studies it became clear that many biological processes underlying the rise and fall of malaria vector populations are still poorly understood. Besides the mentioned differences in larval development and adult survival in response to different environmental conditions, other factors, such as competition among *An. gambiae s.l.* larvae occupying a site (Koenraadt and Takken 2003) and larval behaviour in response to drought (Koenraadt et al. 2003) may also play an important role in determining the size and species composition of vector populations. Although the evidence seems to point towards the establishment of vector populations in a highland area from nearby lower areas when environmental conditions are suitable, the degree of immigration remains to be studied. Finally, the phenomena observed in the highland area in western Kenya need to be evaluated for other areas in eastern Africa. Only then, local malaria risk models can be reliably upscaled to the regional and continental scale.

References

Albonico, M., De Giorgi, F., Razanakolona, J., et al., 1999. Control of epidemic malaria on the highlands of Madagascar. *Parassitologia,* 41 (1/3), 373-376.

Bødker, R., 2000. *Variation in malaria risk in the Usambara Mountains, Tanzania.* PhD Thesis University of Copenhagen, Copenhagen.

Bonora, S., De Rosa, F.G., Boffito, M., et al., 2001. Rising temperature and the malaria epidemic in Burundi. *Trends in Parasitology,* 17 (12), 572-573.

Craig, M.H., Snow, R.W. and Le Sueur, D., 1999. A climate-based distribution model of malaria transmission in sub-Saharan Africa. *Parasitology Today,* 15 (3), 105-111.

Day, K.P. and Marsh, K., 1991. Naturally acquired immunity to *Plasmodium falciparum*. *Immunology Today,* 12 (3), A68-A71.

Etchegorry, M.G., Matthys, F., Galinski, M., et al., 2001. Malaria epidemic in Burundi. *Lancet,* 357 (9261), 1046-1047.

Garnham, P.C.C., 1945. Malaria epidemics at exceptionally high altitudes in Kenya. *The British Medical Journal,* 11, 45-47.

Garnham, P.C.C., 1948. The incidence of malaria at high altitudes. *Journal of the National Malaria Society,* 7, 275-284.

Githeko, A.K., Lindsay, S.W., Confalonieri, U.E., et al., 2000. Climate change and vector-borne diseases: a regional analysis. *Bulletin of the World Health Organization,* 78 (9), 1136-1147.

Githeko, A.K. and Ndegwa, W., 2001. Predicting malaria epidemics in the Kenyan highlands using climate data: a tool for decision makers. *Global Change & Human Health,* 2 (1), 54-63. [http://www.ogp.noaa.gov/mpe/csi/esd/africa/fundproj/health/malaria_epidemic.pdf]

Gupta, S., Snow, R.W., Donnelly, C.A., et al., 1999. Immunity to non-cerebral severe malaria is acquired after one or two infections. *Nature Medicine,* 5 (3), 340-343.

Hay, S.I., Cox, J., Rogers, D.J., et al., 2002a. Climate change and the resurgence of malaria in the East African highlands. *Nature,* 415 (6874), 905-909.

Hay, S.I., Rogers, D.J., Randolph, S.E., et al., 2002b. Hot topic or hot air? Climate change and malaria resurgence in East African highlands. *Trends in Parasitology,* 18 (12), 530-534.

Hay, S.I., Snow, R.W. and Rogers, D.J., 1998. Predicting malaria seasons in Kenya using multitemporal meteorological satellite sensor data. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 92 (1), 12-20.

IMAGE team, 2001. *The IMAGE 2.2 implementation of the SRES scenarios: a comprehensive analysis of emissions, climate change and impacts in the 21st century*. RIVM, Bilthoven. RIVM Rapport no. 481508018.

Koenraadt, C.J., Githeko, A.K. and Takken, W., 2004. The effects of rainfall and evapotranspiration on the temporal dynamics of *Anopheles gambiae* s.s. and *Anopheles arabiensis* in a Kenyan village. *Acta Tropica,* 90 (2), 141-153.

Koenraadt, C.J., Paaijmans, K.P., Githeko, A.K., et al., 2003. Egg hatching, larval movement and larval survival of the malaria vector *Anopheles gambiae* in desiccating habitats. *Malaria Journal,* 2 (1), 20 p. [http://www.malariajournal.com/content/2/1/20]

Koenraadt, C.J. and Takken, W., 2003. Cannibalism and predation among larvae of the *Anopheles gambiae* complex. *Medical and Veterinary Entomology,* 17 (1), 61-66.

Koenraadt, C.J.M., 2003. *Mosquitoes, men and malaria in Kenya: a study on ecological factors affecting malaria risk*. PhD Thesis Wageningen University, Wageningen.

Lehmann, T., Besansky, N.J., Hawley, W.A., et al., 1997. Microgeographic structure of *Anopheles gambiae* in western Kenya based on mtDNA and microsatellite loci. *Molecular Ecology,* 6 (3), 243-253.

Lindblade, K.A., Walker, E.D., Onapa, A.W., et al., 1999. Highland malaria in Uganda: prospective analysis of an epidemic associated with El Niño. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 93 (5), 480-487.

Lindblade, K.A., Walker, E.D., Onapa, A.W., et al., 2000. Land use change alters malaria transmission parameters by modifying temperature in a highland area of Uganda. *Tropical Medicine and International Health,* 5 (4), 263-274.

Lindblade, K.A., Walker, E.D. and Wilson, M.L., 2000. Early warning of malaria epidemics in African highlands using *Anopheles* (Diptera: Culicidae) indoor resting density. *Journal of Medical Entomology,* 37 (5), 664-674.

Lindsay, S.W., Bødker, R., Malima, R., et al., 2000. Effect of 1997-98 El Niño on highland malaria in Tanzania. *Lancet,* 355 (9208), 989-990.

Lindsay, S.W., Parson, L. and Thomas, C.J., 1998. Mapping the ranges and relative abundance of the two principal African malaria vectors, *Anopheles gambiae* sensu stricto and *An. arabiensis*, using climate data. *Proceedings of the Royal Society of London. Series B. Biological Sciences,* 265 (1399), 847-854.

Malakooti, M.A., Biomndo, K. and Shanks, G.D., 1998. Reemergence of epidemic malaria in the highlands of western Kenya. *Emerging Infectious Diseases,* 4 (4), 671-676.

MARA/ARMA, 2002. *MARA LITe: Mapping Malaria Risk in Africa Low-end Information Tool*. South African Medical Research Council, Malaria Research Programme. [http://www.arma.org.za/lite.htm]

Marsh, K., 1993. Immunology of human malaria. *In:* Gilles, H.M., Warrell, D.A. and Bruce-Chwatt, L.J. eds. *Bruce-Chwatt's essential malariology*. Arnold, London, 60-77.

Martens, W.J., 1998. Health impacts of climate change and ozone depletion: an ecoepidemiologic modeling approach. *Environmental Health Perspectives,* 106 (Suppl. 1), 241-251.

Martens, W.J., Niessen, L.W., Rotmans, J., et al., 1995. Potential impact of global climate change on malaria risk. *Environmental Health Perspectives,* 103 (5), 458-464.

Martens, W.J., Slooff, R. and Jackson, E.K., 1997. Climate change, human health, and sustainable development. *Bulletin of the World Health Organization,* 75 (6), 583-588.

Minakawa, N., Sonye, G., Mogi, M., et al., 2002. The effects of climatic factors on the distribution and abundance of malaria vectors in Kenya. *Journal of Medical Entomology,* 39 (6), 833-841.

Patz, J.A., Graczyk, T.K., Geller, N., et al., 2000. Effects of environmental change on emerging parasitic diseases. *International Journal of Parasitology,* 30 (12/13), 1395-1405.

Patz, J.A., Hulme, M., Rosenzweig, C., et al., 2002. Climate change: regional warming and malaria resurgence. *Nature,* 420 (6916), 627-628; discussion 628.

Patz, J.A. and Reisen, W.K., 2001. Immunology, climate change and vector-borne diseases. *Trends in Immunology,* 22 (4), 171-172.

Roberts, D.J., Biggs, B.A., Brown, G., et al., 1993. Protection, pathogenesis and phenotypic plasticity in *Plasmodium falciparum* malaria. *Parasitology Today,* 9 (8), 281-286.

Rogers, D.J., Randolph, S.E., Snow, R.W., et al., 2002. Satellite imagery in the study and forecast of malaria. *Nature,* 415 (6872), 710-715.

Schneider, P., Takken, W. and McCall, P.J., 2000. Interspecific competition between sibling species larvae of *Anopheles arabiensis* and *An. gambiae*. *Medical and Veterinary Entomology,* 14 (2), 165-170.

Shanks, G.D., Biomndo, K., Hay, S.I., et al., 2000. Changing patterns of clinical malaria since 1965 among a tea estate population located in the Kenyan highlands. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 94 (3), 253-255.

Shanks, G.D., Hay, S.I., Stern, D.I., et al., 2002. Meteorologic influences on *Plasmodium falciparum* malaria in the Highland Tea Estates of Kericho, Western Kenya. *Emerging Infectious Diseases,* 8 (12), 1404-1408.

Shililu, J.I., Maier, W.A., Seitz, H.M., et al., 1998. Seasonal density, sporozoite rates and entomological inoculation rates of *Anopheles gambiae* and *Anopheles funestus* in a high-altitude sugarcane growing zone in Western Kenya. *Tropical Medicine and International Health,* 3 (9), 706-710.

Snow, R.W., Craig, M.H., Deichmann, U., et al., 1999. A preliminary continental risk map for malaria mortality among African children. *Parasitology Today,* 15 (3), 99-104.

Steketee, R.W., Nahlen, B.L., Parise, M.E., et al., 2001. The burden of malaria in pregnancy in malaria-endemic areas. *American Journal of Tropical Medicine and Hygiene,* 64 (1/2 Suppl.), 28-35.

Thomson, M.C. and Connor, S.J., 2001. The development of Malaria Early Warning Systems for Africa. *Trends in Parasitology,* 17 (9), 438-445.

Wang, R., Kafatos, F.C. and Zheng, L., 1999. Microsatellite markers and genotyping procedures for *Anopheles gambiae*. *Parasitology Today,* 15 (1), 33-37.

Warrell, D.A., 1993. Clinical features of malaria. *In:* Gilles, H.M., Warrell, D.A. and Bruce-Chwatt, L.J. eds. *Bruce-Chwatt's essential malariology*. Arnold, London, 35-49.

WHO, 1997. World malaria situation in 1994. *Weekly epidemiological record* (36), 269-276. [http://www.who.int/docstore/wer/pdf/1997/wer7236.pdf]

WMO, 1999. *The 1997-1998 El Niño event: a scientific and technical retrospective*. World Meteorological Organization. WMO Report no. 905. [http://www.wmo.ch/nino/WMO905-e.pdf]

8

Malaria risk scenarios for Kisumu, Kenya: blending qualitative and quantitative information

Michael van Lieshout [#]

Introduction

The processes in today's world – including socioeconomic change, demographic change and environmental change – oblige us to broaden our conception of the determinants of population health (Martens and Rotmans 2002). Although the speed and direction of these changes involve great uncertainty, they will for certain affect the future prevalence of all kinds of diseases that may pose a threat to the world's future prosperity. The continuous interaction between a number of factors and processes at different spatial- and temporal-scale levels per definition makes human health, and e.g. malaria, complex to analyse.

Integrated projections of the potential risks of malaria pose a difficult challenge due to a combination of a diversity of related global and local changes. The sensitivity and adaptive capacity amongst exposed populations vary considerably. Malaria prevalence depends on factors such as population density, level of economic and technological development, local environmental conditions, pre-existing health status, and the quality and availability of health care and public-health infrastructure.

The intricate relationships between malaria parasites, hosts and their vectors make the ecological web extremely sensitive to disturbances therein. It is expected that e.g. global climate and other environmental changes will have a significant impact on local malaria risk in the near future.

To explore possible futures of malaria risk and provide sound policy-relevant guidance for decision makers, the value of integrated scenarios has increasingly and widely been recognized. In contrast to many scenario studies, this study elaborates on malaria risk due to the mutual interplay of different simultaneous developments. Often the effects of separate developments have been considered (e.g. (Alene and Bennett 1996; Rogers and Randolph 2000; Craig, Snow and Le Sueur 1999), providing a less comprehensive view on the future of malaria.

CAMERA

The scenarios for malaria risk in Kisumu region have been developed as part of the CAMERA (Cellular Approach for Malaria Eco-epidemiological Risk Assessment) project. The main objective of this research project was to assess the impact of environmental and socioeconomic changes on the risk of vector-borne diseases, and more specific of malaria. Until now integrated future analyses of this region are disregarded.

[#] International Centre for Integrative Studies, University of Maastricht, The Netherlands

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 79-98.

The Kisumu study area (Figure 1, see Colour pages elsewhere in this book) is situated in southwest Kenya at the eastern shores of the Winam Gulf of Lake Victoria, and stretches from Kisumu town, on the Kano plains (1100 m altitude), to Kericho (2100 m), 80 km further east. Although the study area straddles the equator, its altitude allows for a relatively mild tropical climate. The climatic conditions make the area quite suitable for agriculture compared to other parts of Kenya. Consequently, due to the fertile grounds and the relatively mild climate, the southwest is amongst the most densely populated areas of Kenya.

The present vector and population density and poverty contribute to a high infection risk in the mainly rural areas. Except for the highland area above 1500 m and the urban areas like Kisumu town, the region can be considered a high-transmission-risk area.

This paper provides a next step towards an integrated ‘modelling’ framework to elaborate on scenarios for local malaria risk and a long time horizon. Based on a combination of possible images of the future of the area and on computer modelling, scenarios have been developed with regard to plausible changes in local malaria risk. The images give voice to important qualitative factors shaping development such as values, behaviours and institutions, providing a broader perspective than is possible from mathematical modelling alone. The quantitative analysis by means of the computer simulation model offers quantitative underpinning and spatial visualization of malaria risk in relation to the main environmental parameters. As part of the CAMERA project a field study (conducted by Wageningen University in cooperation with KEMRI) took place in Miwani at 1200 m altitude, Fort Ternan at 1500 m and Kericho at 2000 m. The paper continues with a description of the computer model developed to assess local malaria risk, after which the current malaria risk and the analysis of Kisumu region are described. Finally, sketches of possible futures are presented by means of the scenarios, blending qualitative and quantitative information.

Malaria in Kisumu: a local-risk model

A mutual interplay

The transmission of malaria is determined by the combined action of three components (Figure 2), viz., humans and animals serving as hosts, vectors transmitting the disease, and parasites or pathogens infecting both host and vector.

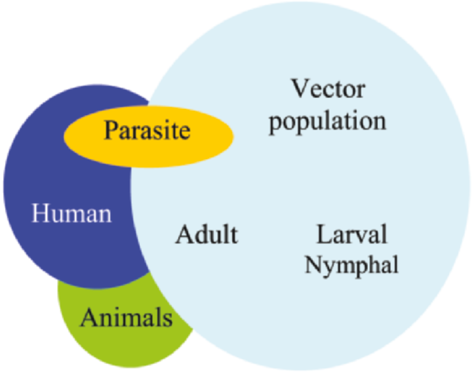


Figure 2. Three main components of malaria (Casman and Dowlatabadi 2002)

The composition, sensitivity, behaviour and adaptive capacity of these components together determine the malaria transmission risk and the mortality and morbidity rate amongst the human population. In turn, these main determinants are affected by a complex interplay of natural, social, economic and institutional aspects. While the basis of potential malaria outbreaks and endemicity lies within the ecological domain, the actual impact of the exposure on the local population is strongly influenced by socioeconomic factors. It is acknowledged that the status and development of these factors in the different domains are intertwined.

The role of computer modelling to elaborate current and future malaria risk has significantly increased in the past few years. Within the scope of this study a specific model has been developed to assess the impact of changes in a diversity of factors underlying malaria risk for Kisumu region. The LEMRA (Local Eco-epidemiological Malaria Risk Assessment) model integrates physical, environmental and partly social factors influencing malaria risk into one dynamic model at a high level of spatial detail (1x1 km^2) (Figure 3, see Colour pages elsewhere in this book).

Model parameters and risk classification

The model, built in a layered-grid-based format, determines for each of the layers the malaria risk based on a qualitative relation between risk and the grid-based input. The layers contain GIS information of temperature, land use, precipitation, infrastructure and population. The population layer was switched off, since the main aim of this study was not to elaborate on the different stages of development of the disease. Moreover, the importance of density and spread of population is taken into account in the qualitative analysis. The following paragraphs will describe in more detail the implemented mathematical relations for the main environmental factors: temperature, land use and precipitation, and infrastructure.

Temperature

The behaviour and survival probability of the vector and the development rate of the parasite are to a large extent determined by temperature. Although human (host) behaviour is also affected by temperature, this has not been taken into consideration explicitly. To assess the malaria risk with regard to temperature the transmission potential (TP), a derivative of the basic reproduction rate (R_0), has been applied. TP is the reciprocal of the critical mosquito density. TP is used here as a comparative index for estimating the impact of changes in ambient temperature patterns on the risk of malaria (Martens et al. 1999), assuming that all other relevant factors remain unchanged. A high TP indicates that, despite a smaller or, alternatively, a less efficient vector population, a certain degree of transmission may be maintained in a given area.

Based on the monthly mean temperature the TP has been derived for each cell. The model has implemented a minimum temperature of 16°C with respect to the development of the parasite, and a minimum temperature of 9.9°C with respect to feeding behaviour. Table 1 illustrates in what way TP has been implemented and translated to a risk classification (translation based on expert judgment; W. Takken personal communication). Drawback of this method is that the minimum temperature, related to the development of a stable vector population, is not taken into account.

Table 1. Malaria risk and transmission potential (TP)

Risk	TP	Classification
No	0	0
Low	0 < TP < 0.01	1
Medium	0.01 < TP < 0.03	2
High	0.03 <TP < 0.055	3
Very high	0.055 < TP	4

Land cover and precipitation

The combination of land cover and precipitation is used as a rough estimate for the suitability of breeding sites. The current model implements the rainfall – 'malaria risk' relation as a threshold (Table 2). According to the field research it has been estimated that in case monthly rainfall in a cell is above its suitability threshold, first signals of increased malaria transmission occur after 2 months. In these months the larvae and nymphs obviously have been able to develop into an adult population. This time delay might be of importance in varying seasonal conditions. If the monthly rainfall is below the threshold, no transmission is possible and no infection risk exists.

Table 2. Malaria risk in relation to land cover and precipitation

Land cover	Precipitation threshold (mm/month)	Risk classification
Water	0	0
Forest	120	1
Cash crops	80	1
Grassland	80	2
Small-scale agriculture	60	4
Rice	20	4

The threshold approach has been used before (Martens et al. 1999; Craig, Snow and Le Sueur 1999). What the LEMRA model adds is the dependence of the threshold on the land cover in the cell (Table 2). The abundance of habitats determines the presence and survival probability of the mosquito population. The presence of undisturbed sunlit pools is a precondition for the existence of the vector, in particular *Anopheles gambiae*, in sufficient densities. *An. gambiae* is the dominant species in rainy periods. *An funestus* is less dependent on rainfall, and more dependent on the presence of stagnant waters. *An. funestus* is the dominant vector in dryer periods (Minakawa et al. 2002). In case of an area with standing water, obviously no threshold is implemented, whereas due to, e.g., dense leaf coverage, a forest provides fewer opportunities for sunlit pools and accordingly needs more rain to provide suitable circumstances.

At the end risk classification is related to the mutual dependence of land cover and precipitation. Water has a low risk classification because of the preferences of the *An. gambiae* and the small chance of human mosquito contact. In contrast, the presence of water (in case of irrigation) in rice fields and the great chance of human vector contact make rice fields rather high-risk areas.

One could argue that the relation between precipitation and vector abundance is not that rigid, and one should rather implement more gradual changes. The way it is currently implemented might show rather rigorous changes and should be interpreted carefully. Other studies (Hartman et al. 2002) have implemented the precipitation–risk relationship in a more fuzzy rather than Boolean way.

Infrastructure
The presence of infrastructure, and in particular roads, might be linked to increased malaria risk. Roads indirectly affect the presence of both hosts and mosquitoes. The construction of roads and railways has facilitated the gradual spread of malaria. Humans, in general, settle near roads, and both humans and cattle travel along the roads. This leads to the creation of many puddles, footsteps and tracks along the roads, which provide suitable breeding sites for the malaria mosquitoes. For the current assessment the effect of changing infrastructure has been neglected.

When quantifying the land-cover – malaria relation, it is not evident which factors should be considered part of this relation and which should be considered separately. For example, many land covers are associated with certain temperature regimes: rice can only grow in warm and humid areas, while tea and coffee are most profitable in less warm and dryer climates. It can therefore be argued that this association with temperature is an inherent part of the malaria risk associated with land cover. However, in the LEMRA model temperature is separately modelled using the Transmission Potential. If the temperature correlation had been considered inherent to the malaria risk associated with the land cover, the temperature influence would be counted double. Therefore, the LEMRA model tries to ignore the association with specific temperature regimes when estimating the amount of influence each land-cover category has on malaria risk. Besides temperature this also applies to precipitation, the presence of humans and the interactions between neighbouring cells, which all are explicitly modelled.

Intra- and intercellular risk

To define the risk in a cell, i.e. the intracellular risk, the index of TP is combined with the discrete risk classification of land cover and precipitation to form a new discrete classification for each cell (Table 3).

Table 3. Intracellular risk based on temperature and land-cover-related risk

Temperature-related risk (TP)	*Land-cover-related risk*					
		Non	Low	Medium	High	Very high
	Non	0	0	0	0	0
	Low	0	1	2	3	4
	Medium	0	2	4	6	8
	High	0	3	6	9	12
	Very high	0	4	8	12	16

Taking into consideration that the grid cells enclose an area of 1x1 km^2, the malaria risk of a separate cell cannot be considered without regard to the conditions outside this area. The interaction with the surroundings is not simulated for each separate factor; instead interaction is modelled at the level of malaria risk.

It is assumed that the influences of the various factors on neighbouring cells can be generalized to one influence at the abstract level of the risk class. In the preceding steps the intracellular risk class is determined for each cell solely on the basis of the internal conditions of the cell. The intercellular risk class is determined by adjusting the intracellular risk class to the intracellular risk classes of the surrounding cells (Figure 4, see Colour pages elsewhere in this book).

Since the strength of the intercellular influences is not exactly known, neither for the composite of the factors nor for each individual factor, a distance decay function is assumed. The algorithm defines the risk of a cell using a weighted mean of the previously determined intracellular risks of the cell and its neighbouring cells. Currently the extended Moore neighbourhood is used, which exists of the two rings of cells surrounding the cell of interest. The weighted mean is such that the cell and each ring of cells surrounding it have an equal weight in the final result.

The used numbers of rings represent a distance of three kilometres around the centre of the cell. This distance roughly corresponds to the flight range of the *Anopheles* mosquito. Note that this implies that the factors included in the intercellular influences are only concerned with mosquito behaviour and not with human displacement. Human displacement has been 'modelled' separately by means of qualitative scenario analysis. Human migration might be quite significant with respect to the (gradual) spread of malaria. In literature examples are discussed related to the hypothesis that the spread of malaria into low-risk areas may be caused by displacement of infected humans, e.g. in case of tea-plantation workers (Malakooti, Biomndo and Shanks 1998).

The main implemented mathematical relations have been derived in a laboratory setting, in other regions or at other scale levels, and have neither been calibrated nor validated adequately by lack of sufficient appropriate data. In case of the development of regional projections, there is a definite need to validate these relationships by means of field research. Where available and possible, data of the field research have been incorporated in this part of the CAMERA project.

The current results depend on the many assumptions underlying the model. Two examples of these assumptions are the implemented land-use – precipitation threshold relation, and the weighting mechanism used for the intercellular correction e.g. with regard to the validity of the used weights and the acceptance of the three-kilometre range. These and many other assumptions will need further investigation. Notwithstanding the many questions remaining the LEMRA model already provides a framework to underpin the assessment of future change.

It is has proved difficult to identify adequate indicators that could be used to model future adaptation to changes in disease risk associated with climate change and socioeconomic development within an integrated-assessment model (Martens and McMichael 2001). First, malaria incidence is hugely influenced by geography and prevailing climate. The poorest countries tend to be in high-risk tropical and subtropical regions. Apportioning malaria causality between environment, income and social practices is, therefore, problematic. Applying a quantitative relationship between socioeconomic development and malaria incidence has not been seriously attempted. The socioeconomic aspects have, however, been taken into consideration qualitatively in providing the images on the future.

Malaria in Kisumu: A complex web of factors

Malaria prevalence

Malaria is holo-endemic in Miwani (White 1972) with a 70-90% malaria prevalence (Githeko et al. 1996) in much of the population. In the nearby Kericho highlands, however, malaria is unstable with prevalence varying annually between 10% and 60% (unstable non-endemic). Due to this instability, epidemics are common with a high morbidity and mortality as a result. The unstable endemic situation in Fort Ternan is somewhere in between these two extremes. Figure 5 (see Colour pages elsewhere in this book) illustrates current malaria risk as modelled by the LEMRA model.

Due to the poor socioeconomic situation, health infrastructure has poorly developed and people are not able to afford precautionary means to prevent infection, like bednets or drugs to treat the disease. Lack of means increases chances of getting ill, and thus limits labour productivity, consequently affecting the economic growth. The interaction between illness and scarcity of financial means can be characterized as a negative feedback cycle (Gallup and Sachs 2000).

To account for the variability of the available climatic time series of the area (MARA/ARMA 1998) the impact of a relatively wet (1995) and a relatively dry year (1987) has been modelled (Figure 6). Figures below provide an illustration of the potentials of modelling by showing grid-based outcomes for both years. Besides inter-annual differences, seasonal differences could also be identified. The darker the cell, the higher the risk of malaria is.

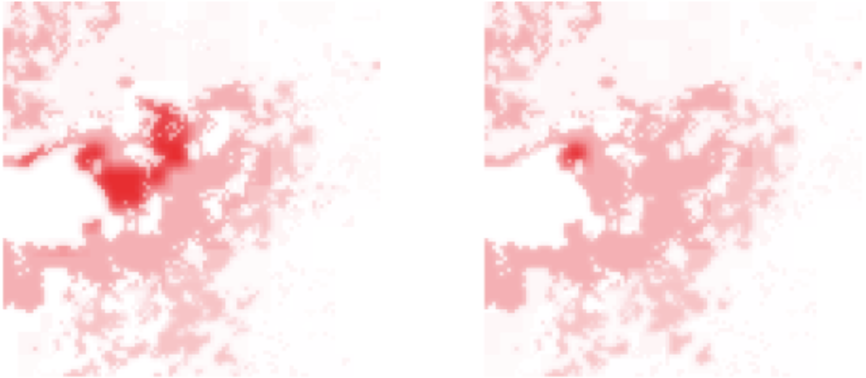


Figure 6. Modelling the impact of precipitation variability (left: relatively wet; right: relatively dry)

Since in general precipitation in Fort Ternan is higher than in Miwani, the vector abundance is not limited by this factor; both areas are more or less equally suitable. However, based on the number of mosquitoes caught, although it is rather limited, it appears that the mosquito density in Fort Ternan is ‘much’ lower than in Miwani (Koenraadt 2003). One of the main obvious reasons why the model does not illustrate this, stems from the fact that the model does not yet incorporate a relation for the derived minimum temperature. Minimum temperature in Fort Ternan is lower than in Miwani, possibly hampering the development of a stable vector population.

Obviously the process of spread of malaria depends on the properties of the mosquito population and its interaction with the human population. Apart from the factors mentioned in the next paragraphs, which to a certain extent directly influence exposure and the incidence rates, these factors are also intertwined and may have an indirect effect. For example, an increased population density in general puts further pressure on the biological and physical system, manifested as land-use change, downturns in food-producing systems, the depletion of freshwater supplies and the loss of biodiversity. Before we shall elaborate on the future of malaria risk, the main characteristics of the risk-related environmental and socioeconomic conditions of the study area will be described in the next paragraphs.

Malaria and Kisumu's environment

The distribution of malaria is in theory limited by the climatic tolerance of the mosquito vectors and by biological restrictions that limit the survival and incubation of the infective agent in the vector population. The climate in terms of relatively high temperatures and seasonal rain provides rather ideal circumstances for adequate breeding places and for rapid development of both mosquito and parasite.

The main vectors in Kisumu region are the *An. gambiae* and *An. funestus*. The two vectors show a different behaviour and different densities in relation to climatic circumstances. Whether or not a stable population can develop depends on both minimum and maximum temperatures. According to the MARA/ARMA study, below a daily minimum temperature threshold of 4°C the survival probability of the mosquito population is zero, preventing the persistence of a stable year-round mosquito population. Field experiments during the course of the project showed however that the larvae did not survive temperatures below 11°C in Kisumu region (Koenraadt 2003). These results provided a first indication that a stable population cannot develop in spite of ambient temperatures above the minimum threshold for mosquitoes to survive. *Plasmodium falciparum* is the prevalent pathogen. The development rate of the parasite is highly dependent on temperature. At an ambient mean temperature of 23°C the parasite requires 16 days to mature. At a temperature of 27°C the parasite only requires 10 days to become infectious. It is argued that the spread of malaria at higher altitudes, being a proxy for temperature, is limited by the survival probability of the pathogen rather than the vector (Malakooti, Biomndo and Shanks 1998).

Besides precipitation many other factors, such as land use and the development of irrigation systems, largely influence the presence of suitable breeding grounds. Large-scale vector control programmes could only to a certain extent eliminate breeding sites, whether or not done by governmental bodies. Kisumu region's land cover is dominated by rice fields in the valleys and cash crops and to a lesser extent small-scale agriculture in the higher regions (Figure 7, see Colour pages elsewhere in this book). As mentioned, particularly rice fields and small-scale agricultural areas are considered high-risk areas. It should be noted, however, that at the time of the visit, March 2002, the fields were not irrigated and hence provided less suitable habitat conditions. Urban areas are lacking in the distinguished types of land use. In general, urban areas show lower risk profiles than surrounding rural areas. In the case of Kisumu town this is similar, but not simulated.

Figure 8 and Figure 9 illustrate 'current' malaria risk for two representative years, 1987 and 1995. The results are based on the climate series 1951-1995 commissioned and disseminated by the MARA/ARMA initiative. The yearly and seasonal influence can be clearly observed. These differences are caused by the combined effect of a variation in precipitation and monthly mean temperature. The year 1995 will be used as reference year.

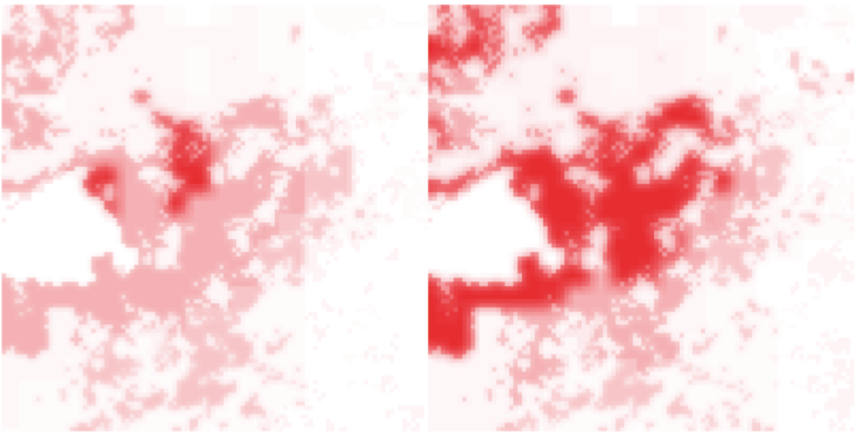


Figure 8. Modelled malaria risk: June (left) and April (right) 1987

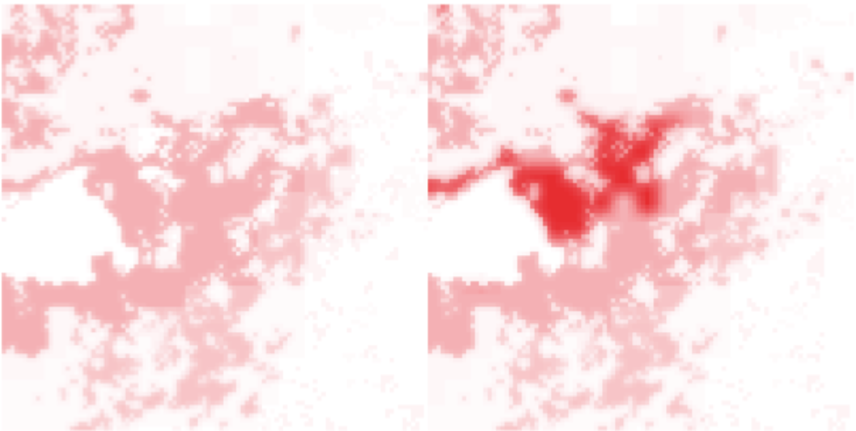


Figure 9. Modelled malaria risk: June (left) and April (right) 1995

Malaria and Kisumu's social-cultural environment

The demographic structure gives an indication of the degree of susceptibility and vulnerability within the affected population. Population density and age structure are main demographic factors that are related to malaria risk. Like in the whole of Kenya the demographic structure of the area can be characterized by a pyramid-like shape, having a broad basis and a small top. Because of its fertile grounds the population density in Kisumu region is amongst the highest of the country.

Within the demographic distribution, the number of persons in the lower fringe indicates the extent to which this factor is significant. Like in the rest of Kenya, the population has a high proportion of young people, i.e. 40-45 % of the population is younger than 14, and solely less than 3% is older than 64. Due to low immunity, malaria morbidity and especially mortality occur to a dominant extent among children. However, in recent years the aids epidemic has also become a major factor of influence. Latest figures show a prevalence of 14% of the sexually active. The decrease in the immunity system makes HIV-infected people more vulnerable to other infectious diseases like malaria, so-called co-infection. An increase in the fraction of these vulnerable subgroups has an aggravating effect on the impact of malaria risk.

Mainly in the rural areas homesteads, which are often built in a traditional way with openings for doors and windows, provide sufficient opportunities for mosquitoes looking for a blood meal to enter during the night. Once people are infected and get ill, it is of utmost importance that these people are treated adequately.

Availability of drugs and access to the public-health infrastructure are of vital interest. These factors depend to a large extent on the economic situation of both households and the nation, but also on political priorities and political willingness, and the availability of (donor) funds. The Ministry of Health administers over 50% of the health-care institutions, and the Ministry of Local Government just over 3%. The private, mission and NGO sectors operate the remainder. In Kenya private hospitals are well equipped with sophisticated diagnostic facilities, but because of their high cost, only a few people can afford these facilities. Mobile outreach services have been established by both the government and NGOs for communities that have no static health facilities.

Malaria and Kisumu's economic environment

The extent to which an exposed population, or in more general terms a region or nation, is able to adapt to a given ecological risk is primarily considered to depend crucially on the economic resources at its disposal. While national income (growth) can be used to approximate the financial resources available for state-led adaptation measures, like e.g. public-health infrastructure, income per capita or income per household provides a rough indicator for the auto-adaptive capacity of the population. Auto-adaptive measures are those which the individual can take without a change in public policy or state intervention. They range from the use of bednets to prophylactic medical treatment.

The direct costs of treating and preventing malaria morbidity and lost productivity are considerable, in relation to available funds. Malaria has been shown to slow economic growth in low-income African countries, creating an ever-widening gap in prosperity between malaria-endemic and malaria-free countries. The reduced growth in countries with endemic malaria was estimated to be over 1% of GDP per year. The cumulative effect of this 'growth penalty' is severe and restrains the economic growth of the entire region (Gallup and Sachs 2001). Although no specific figures are known for Kenya, it is expected that the high malaria prevalence in Kisumu region also has considerably affected economic growth in the past years.

Over the past 50 years the simplicity of paternalism and village-based production has been lost as populations have migrated to new areas and taken on new kinds of jobs. Increasing welfare for the rural population stagnated and declined after the 1990s. The GDP/capita p.p.p. yielded 1000 US$, and 62% of the Kenyan population lived below a 2 US$ expenditure per day in 1999. A higher percentage of the rural families have become food-insecure, have fewer job opportunities and less income per family. This combination of factors has increased the risk of getting ill and has negatively affected the ability to be treated accurately.

Long-term risk assessment implies understanding the processes underlying malaria risk. Although a broad range of literature is available, the assumed relations and relevance of certain factors are often disputed (e.g., Epstein, Haines and Reiter 1998).

Malaria in Kisumu: What if……images of the future

Introduction

Within the scope of the project scenarios have been developed by blending quantitative and qualitative information. The qualitative information consists of different plausible integrated descriptions of images on the development of the previously described factors and actors that affect the future of malaria risk. These images have been translated to changing the input parameters of the LEMRA model. The simulation results have eventually provided spatial illustration of possible shifts in malaria risk in the future. Other than predictions these scenarios provide 'what if' images and are developed to identify knowledge gaps, future important issues (envisioning, early warning), and to anticipate possible futures.

Ideally, the point of departure for the CAMERA project would have been a widely vetted, comprehensive, narratively rich and fully quantified set of scenarios for Kisumu. However, this ideal source does not exist. Available, in particular globally and continentally developed, scenarios provide a wide variety of information on sectoral and regional efforts, which are important sources of insight but could not on their own provide a comprehensive platform for the project.

The scenarios developed for Kisumu region have been inspired by the four storylines as described in Kenya at the crossroads: Flying Geese, Katiba, Maendelo and El Niño (IEA 2000). These scenarios, presented as storylines, assume that Kenya has reached its limits from an economic, political and social point of view, differing in their prediction whether and how political and/or economic reformation will be implemented. The storylines primarily address questions of how Kenya's growing population will be fed, and how the governing institutions can be modernized, given the skills and resources it has.

The 'Crossroads' scenarios have been enriched by the outcomes of the African Environmental Outlook (UNEP 2002), some of our own ideas, the model results, and the results of a workshop attended by about twenty scientists in 1999. Important quantitative information on how the environment might evolve, and in particular the local climatic conditions irrespective of local changes, is not included in these sources. Information of climate-change scenarios has been adopted from the SRES scenarios (Nakicenovic and Swart 2000), and has been regionally disaggregated. Developments on the spatial level of Kisumu region depend on the interaction between local highly dynamic processes and slower processes on a higher, both national and supranational level. Ideally integration across scales takes place both bottom-up and top-down. In the current study only one-way integrating, i.e. top-down has taken place (Figure 10).

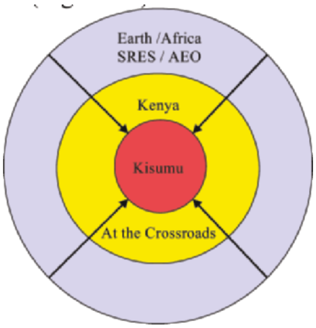


Figure 10. Scenarios for Kisumu imbedded in a wider context

Kenya at the Crossroads
Stories about possible futures

The Kenyan scenario team foresaw four possible outcomes depending on the answers to four crucial questions:

Will confusion and inertia thwart efforts at both economic and political reform? If so, the status quo is maintained, tension heightens and Kenya fractures into ethnic districts with new systems of government within them. This is the El Niño scenario.

Will the transformation concentrate on reordering the economy while resisting agreements on needed changes in the political structures and environment? If so, economic gains will not last long as political tensions will emerge that will require sorting out in order to preserve economic headway. This is a scenario of initial rapid gains, but full of inequalities and instability, labelled Maendeleo.

Will the transformation focus on institutional reorganization and the creation of democratic and locally accountable institutions while ignoring fundamental economic reform? If so, though responsive institutions will emerge, Kenya will not achieve substantial economic transformation. This is the scenario of institutional reorganization labelled Katiba.

Will there be a definite departure from destructive politics? Will the incumbency realize its position is untenable and will it reach a political settlement with the key adversaries? Will a reorganization of the institutions improve representation and participation that reflects the diversity of Kenya's people? Will this be accompanied by radical transformation of the economy to spur growth and improve distribution? If all the major actors engage in this transformation, Kenya can achieve inclusive democracy and growth. This is the scenario of Flying Geese.

The main drawback of using the Crossroads scenarios lies in the policy-oriented assumptions. Rather than focussing on possible societal developments and policy, policy is now regarded as the main steering mechanism. In this way the description of action–reaction mechanisms within society and societal developments as a whole are rather limited and sometimes stereotype.

The time-horizon considered corresponds to the time span of the scenarios described in "Kenya at the crossroads" – until 2020. One generation is considered to be short enough to connect current trends to new futures, and long enough for rather drastic changes.

Although a wider range of scenarios is interesting from a policy point of view, in this paper two of the four scenarios in terms of malaria risk are further elaborated. The developments described within the context of Flying Geese and El Niño are expected to provide the widest range of change in malaria risk in the future.

Flying geese – Simultaneous economic and political reforms

Kenya 2020: In this scenario Kenya has regained respect of the regional and international community. Institutions work (albeit not without some problems). Social tensions have been largely tamed and the country was covered by optimism and hope.

Although initially the dominated agricultural society of Kisumu region had difficulties coping with the transition towards the service economy, at the end society as a whole profited. A well-thought retraining programme and help for small-scale agriculture farmers helped them to integrate and increase their living standard. Small-scale agriculture has to a large extent been replaced by large-scale high-technology agriculture. Consequently, the percentage of land used for cash crops has increased. Prosperity and large-scale irrigation schemes have led to increased production of rice fields. Overall agriculture has become less vulnerable for inter- and intra-annual variation in rainfall.

In the Flying-Geese scenario, small-scale agriculture (light yellow) has been transformed into cash-crop areas (dark yellow) (Figure 11, see Colour pages elsewhere in this book). These areas are less suitable for malaria vectors, and thus in general show a lower malaria risk. In addition, cash crops are related to a higher monthly-precipitation threshold value, than in case of small-scale agriculture, decreasing overall malaria risk.

Climate change has become more profound than expected. Reduced rainfall and increased evapotranspiration have had a strong positive effect in terms of a decrease of months with suitable conditions. On the other hand, both average and minimum temperature have increased. In particular the highland areas, previously less vulnerable, have become (more) suitable from temperature point of view.

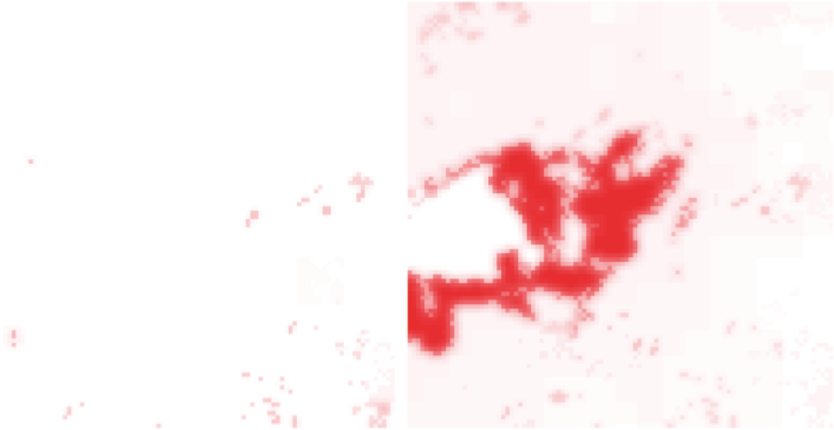


Figure 12. Malaria risk Flying Geese: June (left) and April (right) 2020

Due to the combined effects of a monthly mean-temperature increase between 1.5 °C and 3.4 °C (adopted Hadley SRES results), a reduced rainfall between –0.8 and –4 mm per day, and the projected land-use change, the vast majority of the area has become less suitable for malaria. For the months of April and June a projected temperature increase of 1.7 and 3.4 °C, respectively, and a precipitation decrease of 20 and 120 mm per month, respectively, have had a considerable effect on the distribution of malaria risk. Due to the large decrease, the amount of precipitation has dropped below the threshold value for the month of June. Under these extreme conditions malaria risk no longer poses a serious threat. In the month of April the risk decreases in particular in the northwestern and southern part, due to the combined effects of land-use change and precipitation decrease.

However, due to the temperature increase, the risk has increased considerably along the southern borders of Lake Victoria and halfway between Kisumu and Kericho in April (Figure 13). The rice fields have become the main type of land use being negatively affected.

Obviously future malaria risk is, in our model, strongly affected by land-use changes. To illustrate the sensitivity of land-use change, malaria risk in case of land transformation from cash crops into small-scale agriculture has been analysed (Figure 13). Compared to the previous results the increase in malaria risk is obvious. Moreover, in particular the high-population-density areas, north to northwest of Kisumu town, have become increasingly vulnerable. Whereas these areas did not show malaria risk in Figure 12, now it has become apparent. Obviously the precipitation threshold in relation to the projected change plays a major role. In this case the projected temperature increase has become the dominant factor determining malaria risk, apart from the region east of Kisumu town in June. Beside the northern region, also the highland areas have become more vulnerable. In contrast to Figure 13 the lengthening of the high-risk season can be noticed.

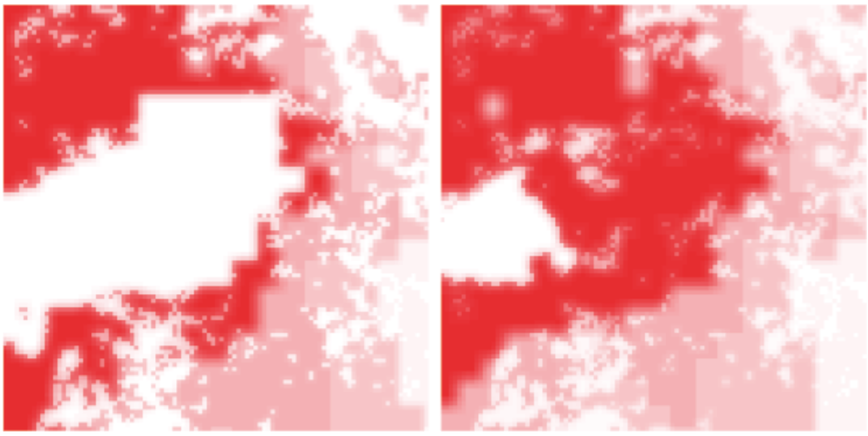


Figure 13. Malaria risk: June (left) and April (right) 2020; land-use change from cash crops to small-scale agriculture

In the transition towards a service economy, the need for educated people increased. Government primarily invested in educational programmes. The higher educational level and abound opportunities in urban areas made many of the young people migrate to urban centres, amongst which Kisumu town. High population densities, and land and previously food shortage have pushed the rural population towards urban areas. Increased urban population density and consequently deteriorating environmental conditions have made urban areas more vulnerable for vector-borne diseases other than malaria, such as dengue. The poor segment of society is pushed off to marginal land into marginal areas.

In Kenya income per head has grown considerably, reducing the number of people below poverty level. In contrast to the increased income per capita, the gap between a rich urban population and the poor though smaller rural population that stayed behind grew. Nevertheless, the increased income per head offers more possibilities to buy precautionary means, and adequate treatment in case one is infected. In addition, like in the rest of Kenya, the increased national income and public interest in human health have provided means to invest in both private and public health care. Due to economic and political reformation the average living standard and public institutions, and social care in general improved significantly. In the past decades a lot of progress was made related to the development of a vaccine. The first results of a prophylactic vaccine seem promising but are not yet available to the public.

In spite of the increased number of irrigated fields, which in theory provide rather ideal circumstances for breeding sites, the number of vectors has decreased. Land-use change, growing awareness, and additionally the implemented biological vector-control programmes have led to a sharp decrease in possible breeding sites. Climate change and human migration towards marginal grounds have however altered the spatial distribution to a certain extent. However, in particular those areas where small-scale agriculture is still, or has become prevailing due to population migration provide suitable conditions. *An. funestus* has become the dominant species due to changed characteristics of habitats.

At the beginning of the century the consequences of climate change were feared. Increased welfare, however, has led to higher adaptive capacity, and has made society less vulnerable. Overall the number of malaria cases has decreased. A combination of less suitable environmental conditions, increased awareness, increased means to buy precautionary measures and increased health in general have made Kisumu region less vulnerable to malaria. A risk of epidemics still exists. Troublesome is the shift of suitable conditions towards higher regions, and in particular the population migration towards marginal grounds. In particular the poor segment of society with fewer means to take precautionary measures and less access to health infrastructure occupies these areas.

El Niño – No political reforms, no economic reforms

In this scenario, Kenya has increasingly been caught up in a system of conflict as a consequence of the absence of political and economic reforms. The existence of Kenya as one nation is not given. As the country degenerated Kisumu region has turned into an enclave. Due to years of militarization and complete chaos, the economy is characterized by low productivity, which has made it impossible for the population to realize upward economic mobility. To survive the majority of people of Kisumu, who did not flee the country, depend on small-scale agriculture and informal and illicit trade. Former land-reform programmes have been abandoned. Due to the wars people have spread over the country looking for new opportunities. To supply their needs for fuel, shelter and food, the local population falls back on their traditional uses of the forest. [1]

In the El Niño scenario small-scale agriculture (light yellow) has replaced previous rice fields (light green) and forest (dark green) to supply basic needs (Figure 14, see Colour pages elsewhere in this book). From a habitat point of view small-scale agriculture is equally suitable as rice fields, and more suitable than forest. Independent of rainfall, due to the land reformation the malaria risk has increased in general.

The combination of vast disappearance of trees and increased heavy rains has considerably increased the risk of landslides. Soil erosion accounts for the majority of

---

[1] The El Niño scenario sketches a rather pessimistic view of the future of Kenya. It is a scenario in which no political reforms and no economic reforms will be put in place. The current pathway the Kenyan government turned into differs from that assumption. Therefore the scenario might sketch a less likely scenario from current point of view. At the time the Kenyan scenarios were written by the Kenyans, both the political and economic situation was different

environmental degradation in the region. In addition, due to deforestation the local temperature has increased. On top of the microclimate change, the impact of global climate change is clearly visible. Temperature increase due to global warming is less than in the case of Flying Geese, but due to deforestation the average monthly temperature increase also varies between 1.5°C and 3.4°C. Average monthly precipitation has not changed significantly compared to the reference year 1995. However, in particular the climate variability in terms of extremes, both in terms of temperature and precipitation has turned out to be devastating, especially for the poor, who have no means to adapt.

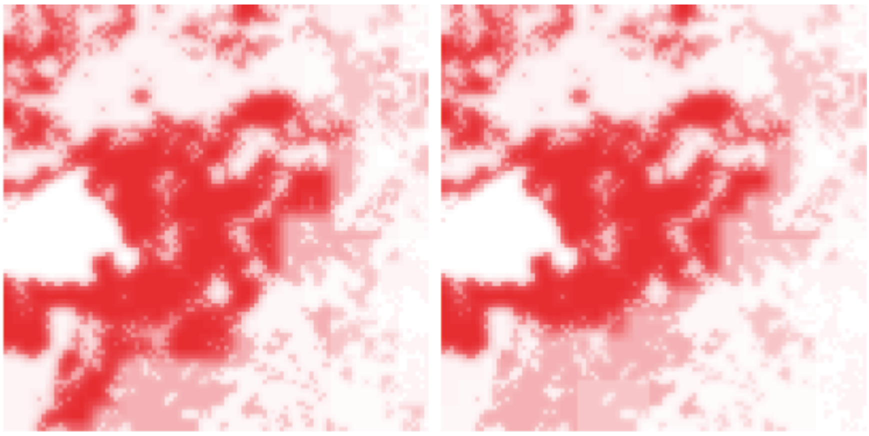


Figure 15. Malaria risk, El Niño scenario: June (left) and April (right) 2020

Due to climate change, in terms of an increase in monthly mean ambient temperature, malaria risk has increased considerably over the whole region (Figure 15). In particular northeast of Kisumu town, the southern borders of Lake Victoria and the highland regions have become more vulnerable. The effect of the deforestation can be clearly observed in the southern part of the study area. The combined effect of an increase in monthly mean ambient temperature and the transformation towards, from a habitat point of view more suitable, small-scale agriculture has likely increased the risk of malaria. Due to the higher temperature increase in June, this month has become even more vulnerable than April. The current difference in malaria risk between April and June has blurred. Hence, in the case of the El Niño scenario the high-risk transmission season most obviously has been prolonged.

Because of the poor economic situation the average household income has declined sharply. Over 80% of the people are currently living below poverty limits. The years of ethnic wars have destroyed much of the public-health infrastructure. What is left is only available and accessible for those very few who gained from the war or from the market mechanism in general. Access to health infrastructure or means to afford precautionary measures is lacking for the majority of society. Human health has declined, which is putting an additional pressure on society as a whole.

The deteriorated environmental conditions and the declined socioeconomic and institutional conditions in combination with a poor health condition have resulted in a sharp increase in the number of people infected and dying of malaria. In addition to the negative societal changes, climate change has led to a visible increase in malaria at higher altitudes. Besides at higher altitudes, newly reclaimed areas, which were not inhabited before, have shown an increasing trend of malaria risk. Since international help is lacking, Kisumu has been caught in a downward spiral with no expectations of improvement on the short and mid term.

Conclusions

Although both scenarios show two extremely different projections of the future of Kisumu region, they also show some striking resemblances. In both scenarios local circumstances for the rural population do not seem to improve significantly, or even seem to decline in the case of the El Niño scenario. A combination of lack of access to health infrastructure, lack of economic means, and climate change have made populations living at high altitudes and particularly those at newly reclaimed areas exposed to higher malaria risk.

Figure 16. Malaria risk: April 1995 (left), Flying Geese 2020 (centre) and El Niño 2020 (right)

Due to environmental changes in terms of land use, ambient temperature and eventually precipitation, the preconditions for malaria risk are changing. In both scenarios an increase along the southern borders of Lake Victoria and halfway Kisumu town and Kericho, reaching to the higher regions, can be observed (Figure 16).

Depending on the type of land transformation malaria risk may differ considerably according to the implemented land use – precipitation relations in the case of the Flying-Geese scenario. Under projected climate-change conditions, the region might provide a range of more or less suitable environmental conditions for malaria risk, according to the projected land use. In case of a shift towards precipitation-dependent land use, like in the case of cash crops, malaria risk has decreased considerably. Whereas in case of a shift towards less precipitation-dependent land use, like small-scale agriculture, both malaria risk in absolute number as in number of months has increased. The relatively small difference in threshold values between small-scale agriculture and cash crops makes that these results should be treated with care.

In addition, in the case of the El Niño scenario, in particular the northeastern and southern parts of the area are likely to show an increase in the risk of malaria due to deforestation in combination with higher mean ambient temperatures. Unfortunately these are, and might remain, amongst the most densely populated areas. Moreover, also the higher altitudes have become more vulnerable due to temperature increase.

In general the high population growth in relation to the already high densities is considered to be an additional threat for the region. Due to high pressures people are forced to move to more marginal grounds, herewith extending the areas vulnerable for malaria transmission, or to the urban areas. Obviously depending on the socioeconomic developments the high rate of incidence may remain, increase or may decline in case of a combined economic growth, improved health infrastructure and growing public awareness.

Climate change, in particular a temperature increase, does not seem to be a blessing for Kisumu. Besides on the impact on future land use, and hence possibly negative impact on the rural economy, the increasing temperature might shift the limits of malaria transmission to higher altitudes.

Highlands have always been regarded as areas of little or no malaria transmission, mainly because of low temperatures. However, this appears to be changing. There is a lot of recent evidence that shows an increase in the number of epidemics in highland areas, as well as a spread of endemic malaria into the highland fringes. Various reasons for this apparent change in epidemiology have been put forward. Most prominent are those arguments that implicate climatic and ecological change. Unfortunately the lack of reliable malaria data for most highland areas has made analysis of these issues difficult (MARA/ARMA).

Epidemic malaria in highland areas represents a significant public-health problem. Historically, low risk of infection in highland areas has created little functional immunity in local populations, resulting in relatively high mortality in adults and children during epidemics. At the same time, national malaria control programmes have not been well equipped to identify and respond to epidemics. There is, therefore, a need for increased scientific understanding of the epidemiology of highland malaria, as well as greater capacity in epidemic surveillance and response. Multiple factors act simultaneously. Correlations are not well understood, in particular with respect to whether or not specific factors are dominant.

Acknowledgments

The Netherlands Foundation for the Advancement of Tropical Research (WOTRO), through its project Integrating Geographical Information Systems and Cellular Automata for the Assessment of Malaria Risk and Control (project no. W –1-65 (WAA)), has funded this research The work has largely benefited from the work previously done by Piebe de Vries, the programming done by Matthieu Bolt, and the fruitful discussions with Sander Koenraadt and Willem Takken. Many thanks also go to the KEMRI team, in particular Andrew Githeko, Judith Awino Otete and Richard Kibet Maritim for their warm welcoming and help during my site visit to Kisumu, March 2002.

References

Alene, G.D. and Bennett, S., 1996. Chloroquine resistance of *Plasmodium falciparum* malaria in Ethiopia and Eritrea. *Tropical Medicine and International Health,* 1 (6), 810-815.

Casman, E. and Dowlatabadi, H. (eds.), 2002. *The contextual determinants of malaria*. Resources for the Future, Washington.

Craig, M.H., Snow, R.W. and Le Sueur, D., 1999. A climate-based distribution model of malaria transmission in sub-Saharan Africa. *Parasitology Today,* 15 (3), 105-111.

De Vries, P., 2000. The Local Eco-epidemiological malaria Risk Assessment (LEMRA) Model. *In: Proceedings of the section Experimental and Applied Entomology of the Netherlands Entomological Society (NEV)*. Nederlandse Entomologische Vereniging, Amsterdam.

Epstein, P.R., Haines, A. and Reiter, P., 1998. Correspondence: global warming and vector-borne disease. *The Lancet,* 351 (9117), 1737-1738.

Gallup, J.L. and Sachs, J.D., 2000. *The economic burden of malaria*. Center for International Development, Harvard University. CID Working Paper no. 52. [http://www.cid.harvard.edu/cidwp/052.htm]

Gallup, J.L. and Sachs, L.D., 2001. *The economic burden of malaria*. Center for International Development, Harvard University, Cambridge. CMH Working Paper Series no. WG1:10. [http://www.cmhealth.org/docs/wg1_paper10.pdf]

Githeko, A.K., Adungo, N.I., Karanja, D.M., et al., 1996. Some observations on the biting behavior of *Anopheles gambiae s.s.*, *Anopheles arabiensis*, and *Anopheles funestus* and their implications for malaria control. *Experimental Parasitology,* 82 (3), 306-315.

Hartman, J., Ebi, K., McConnell, K.J., et al., 2002. Climate suitability: for stable malaria transmission in Zimbabwe under different climate change scenarios. *Global Change and Human Health,* 3 (1), 42-54.

IEA, 2000. *Kenya at the crossroads: scenarios for our future*. Institute of Economic Affairs, Society for International Development, Nairobi. [http://www.kenyascenarios.org/]

Koenraadt, C.J.M., 2003. *Mosquitoes, men and malaria in Kenya: a study on ecological factors affecting malaria risk*. PhD Thesis Wageningen University, Wageningen.

Malakooti, M.A., Biomndo, K. and Shanks, G.D., 1998. Reemergence of epidemic malaria in the highlands of western Kenya. *Emerging Infectious Diseases,* 4 (4), 671-676.

MARA/ARMA, 1998. *Towards an atlas of malaria risk in Africa*. MARA/ARMA, Durban. [http://www.mara.org.za/tech_report_eng.htm]

Martens, P., Kovats, R.S., Nijhof, S., et al., 1999. Climate change and future populations at risk of malaria. *Global Environmental Change. Part A. Human and Policy Dimensions,* 9 (1), S89-S107.

Martens, P. and Rotmans, J. (eds.), 2002. *Transitions in a globalising world.* Swets & Zeitlinger, Lisse. Integrated Assessment Studies no. 1.

Minakawa, N., Sonye, G., Mogi, M., et al., 2002. The effects of climatic factors on the distribution and abundance of malaria vectors in Kenya. *Journal of Medical Entomology,* 39 (6), 833-841.

Nakicenovic, N. and Swart, R. (eds.), 2000. *IPCC special report on emissions scenarios*. Secretariat Intergovernmental Panel on Climate Change IPCC, Geneva. IPCC Special Reports on Climate Change. [http://www.grida.no/climate/ipcc/emission/]

Rogers, D.J. and Randolph, S.E., 2000. The global spread of malaria in a future, warmer world. *Science,* 289 (5485), 1763-1766.

UNEP, 2002. *Africa environment outlook: past, present and future perspectives.* United Nations Environment Programme. [http://www.grida.no/aeo/]

White, G.B., 1972. The *Anopheles gambiae* complex and malaria transmission around Kisumu, Kenya. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 66 (4), 572-581.

9

INDEPTH Network: a viable platform for the assessment of malaria risk in developing countries

Osman Sankoh [#] *and Fred Binka* [#]

Abstract

The INDEPTH Network is an international network currently consisting of 33 demographic surveillance system (DSS) field sites in 19 countries in Africa, Asia and Oceania that collectively monitor over 2,000,000 people at a household level. Each INDEPTH site has a geographically defined population under continuous demographic evaluation, with timely production of data on all births, deaths and migrations. This monitoring system provides a platform for a wide range of health-system innovations, as well as social, economic, behavioural and health interventions, all closely associated with research activities. INDEPTH launched the Malaria Transmission Intensity and Mortality Burden Across Africa (MTIMBA) initiative to generate reliable information that will guide malaria control policies in Africa, as well as to generate new understanding of the relationship between malaria transmission intensity, mortality and the effect of malaria control. The MTIMBA project produces estimates of all-cause and malaria-attributable mortality by age across Africa and documents trends in malaria in INDEPTH sites. INDEPTH now plans to link DSS data to geographical and meteorological data, using remote sensing (RS) and a Geographical Information System (GIS). This will enable much deeper and/or novel insights into parameters that influence the spread of diseases, especially malaria. The meteorological data will complement the DSS data with the introduction of the spatio-temporal fluctuations of temperature, humidity, precipitation, evapo-transpiration and wind. Hence, the different data sets can be used for geo-statistical modelling, mapping and geographical and epidemiological analyses. An INDEPTH environment and health platform has been established with the first initiative to study the relationship between climate variability and the transmission of infectious diseases, focussing on malaria. This paper presents a brief overview of the INDEPTH Network, its MTIMBA project and the proposed research work on climate variability and the spread of infectious diseases.

Keywords: demographic surveillance systems; climate variability; environmental change; malaria transmission

Introduction

INDEPTH is an international network currently consisting of 33 demographic surveillance system (DSS) field sites in 19 developing countries that collectively monitor over 2,000,000 people at a household level. (See Table 1 for list of current

---

[#] INDEPTH Network, P.O. Box KD 213 Kanda, Accra, Ghana. E-mail: osman.sankoh@indepth-network.org

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 99-105.

INDEPTH member sites and Figure 1 for a map showing the distribution of countries with INDEPTH sites.) The INDEPTH Network exists as an independent entity with a Secretariat in Accra, Ghana. The Network utilizes the resources from its development partners (funders/donors) to foster, fund and coordinate cross-site studies, multi-site research and other network-level activities.

Figure 1. Countries with INDEPTH DSS Sites by March 2005

INDEPTH's vision is that it will be an international platform of sentinel demographic sites that provides health and demographic data and research to enable developing countries to set health priorities and policies based on longitudinal evidence. INDEPTH's data and research will guide the cost-effective use of tools, interventions and systems to ensure and monitor progress towards national goals. Its mission is to harness the collective potential of these DSS sites to provide a better, empirical understanding of health and social issues and to apply this understanding to alleviate the most severe health and social changes. INDEPTH's objectives are: to initiate and facilitate cross-site health and social studies and impact assessments in resource-constrained populations; to disseminate study findings to maximize impact on policy and practice; to foster and support capacity building and cross-site collaborations among member sites; and to facilitate the process for donors to fund multi-site health and social research projects in the developing world and especially in Africa and Asia.

Briefly, the key activities of INDEPTH are to:

- cultivate cross-site activity through comparative studies and exchange of experiences on critical common problems;
- generate longitudinal data and analysis that can be used to impact ongoing health and social reforms, inform health and social policy and practice and contribute to governmental, NGO, private and community health efforts;
- broaden the scope of health research by addressing the emerging agenda of non-communicable diseases and aging, accidents, violence and injury, and the problems associated with vulnerable populations;
- continually improve the methods and technologies used by member sites to ensure that all participating groups have access to the most valid and appropriate methodologies available; and
- generate visibility and recognition for INDEPTH and member sites among critical constituencies, including academic, government and international agencies and donors.

Table 1. List of current Network membership

Status	Country	Name	Approximate start date	Age (years)	Population
Africa					
Full member	Burkina Faso	Centre National de Recherche et de Formation sur le Paludisme (OUBRITENGA).	15/02/93	10	150,000
Full member	Burkina Faso	Centre National de Recherche en Santé de NOUNA (NOUNA)	07/01/92	11	70,000
Full member	Burkina Faso	Host Institution**:** Observatoire de Population de Quagadougou (Quagadougou Urban Health and Equity Initiative, Burkina Faso)	01/02/2002	1	5,000
Full member	Ethiopia	Butajira Rural Health Project	07/01/87	16	40,000
Full member	Gambia	Farafenni Field Station.	07/01/81	22	17,000
Full member	Ghana	Navrongo Health Research Centre	07/01/93	10	140,000
Full member	Ghana	Kintampo Health Research Centre	10/2003	1	145,000
Full member	Guinea Bissau	Bandim Project.	07/01/78	25	101,000
Full member	Kenya	Kisumu Project	07/01/92	11	135,000
Full member	Kenya	African Population Health Research Centre (Nairobi)	09/2000	3	60,000
Full member	Moçambique	Manhica	07/01/96	7	68,000
Full member	Malawi	Karonga Prevention Study	01/10/2002	1	40,000
Full member	South Africa	Agincourt Health and Population Programme	07/01/92	11	70,000
Full member	South Africa	Dikgale Demographic and Health Study	07/01/95	8	8,000
Full member	South Africa	Africa Centre Demographic Information System	01/01/99	4	90,000
Full member	Senegal	Mlomp	01/01/85	18	7,500
Full member	Senegal	Bandafassi	15/01/70	33	11,000
	Senegal	Niakhar	1962	41	29,000
Full member	Tanzania	Ifakara Health Research and Development Centre	07/01/96	7	67,000
Full member	Tanzania	Tanzanian Essential Health Intervention Project (TEHIP) Rufiji Project.	07/15/98	5	90,000
Full member	Uganda	Rakai project.	07/01/89	14	12,000
Asia					
Full member	Bangladesh	Matlab	07/01/1966	37	212,000
Full member	Bangladesh	Health System and Infectious Disease Surveillance (HSID)	15/01/1982	21	127,000
Full member	Bangladesh	Watch Project			90,000
Full member	India	Ballabgarh DSS (All India Institute of Medical Sciences (AIIMS)	1972	31	41,000
Full member	India	Host Institution: Vadu Rural Health Project, KEM Hospital, Pune District, India (Vadu)	01/10/2002	1	64,000
Full member	Indonesia	Community Health Nutrition and Research Laboratories (Purworejo)	07/01/1994	9	18,000
Full member	Thailand	Institute for Population and Social Research, Mahidol University (Kanchanaburi)	2000	3	42,600
Full member	Vietnam	Chilinh Demographic Surveillance System, Hanoi School of Public Health (Chilillab)	1990	13	64,000
Full member	Vietnam	Epidemiological Field Laboratory for Health System Research (Filabavi).	10/15/1998	5	52,000
Full member	Papua new Guinea	Wosera DSS, PNG Institute of Medical Research	2003	1	140,000
Central America					
Full member	Nicaragua	Center for Demographic and Health Research (CIDS) , Leon University	2003	1	55,000

The INDEPTH Secretariat supports its member sites in a number of ways. First, it facilitates knowledge sharing among sites. By disseminating data, convening analysis workshops, coordinating multi-site research collaborations, funding cross-site scientific visits and promoting on-site training courses and internships, INDEPTH builds capacity and standardizes research methods across the network. Second, it provides practical tools for sites. These include assistance with website development and dissemination of models for survey design, data processing and analysis, and quality control. Third, it raises the profile of DSS sites among the international policy community by synthesizing and presenting results to governments, international agencies, donors and academics.

A full member of the Network is any demographic surveillance system (DSS)-based site with existing or committed funding, and the DSS site fulfils the following characteristics:

- A geographically defined population is under continuous demographic monitoring, with timely production of data on all births, deaths and migrations –sometimes called a demographic surveillance system (DSS); and
- This monitoring system provides a platform for a wide range of health-system innovations, as well as social, economic, behavioural and health interventions, all closely associated with research activities.

INDEPTH/Malaria transmission intensity and mortality burden across Africa

For many of the INDEPTH member sites, malaria has long been an area of focus. These sites possess significant experience in malaria research and interventions and are collecting a tremendous amount of population-based data in support of various anti-malaria initiatives. The existing foundation of malaria data and expertise combined with the high-level external interest in funding anti-malaria initiatives of proven effectiveness create strong ongoing potential for multi-country malaria studies conducted by INDEPTH.

INDEPTH launched the Malaria Transmission Intensity and Mortality Burden Across Africa (MTIMBA) initiative in 2002 to generate reliable information that will guide malaria control policies in Africa. The objectives of the continental platform are to: 1) generate new understanding of the relationship between malaria transmission intensity, mortality and the effect of malaria control; 2) collaborate with the Roll Back Malaria Initiative at the regional, national and global levels for monitoring and evaluation; and 3) further develop and strengthen Africa’s expertise in the field of malaria control, planning and evaluation.

The MTIMBA project has been able to produce estimates of all-cause and malaria-attributable mortality by age across Africa, documented trends in malaria in INDEPTH sites, and is establishing malaria expertise and strengthened methodology in a continental demographic surveillance platform. The work of MTIMBA and that of INDEPTH’s broad-based work on causes of death are leading to a publication in the INDEPTH monograph series –Population and Health in Developing Countries (see www.indepth-network.org). INDEPTH support to the MTIMBA project involves extending the causes of death beyond malaria and including sites where malaria is not a public-health problem.

Current achievements of the project include the following: Estimates of cause-specific mortality in Africa are being generated using harmonized Verbal Autopsy tools; overall, 1,600 mosquito collection nights per month are carried out throughout Africa and will generate for the first time reliable comparisons of malaria transmission intensity across the continent; data on malaria control activities are currently being systematically collected using RBM tools; and an African network of scientists with expertise in the use of harmonized methods in malaria research is emerging.

The Network will extend the use of the existing platform to address other research / policy issues. These include intervention trials against malaria; impact of antimalarial drug resistance / drug policy change on mortality; the mutual impact of Malaria and HIV/AIDS; and the impact of malaria at the household level.Table 2 shows the sites currently participating in the MTIMBA work and the populations under evaluation.

Table 2. Current INDEPTH sites participating in MTIMBA work

SITE	COUNTRY	POPULATION
Manhiça	Mozambique	36,000
Ifakara	Tanzania	55,000
Rufiji	Tanzania	85,000
Navrongo	Ghana	139,000
Obitrenga	Burkina Faso	170,000
Nouna	Burkina Faso	55,000
Bandafassi	Senegal	9,000
Bandim	Guinea-Bissau	101,000
Farafeni	The Gambia	16,400
Butajira	Ethiopia	36,000
Kisumu	Kenya	130,000

Extending site capabilities to monitor environmental change

The INDEPTH Network has seen a great potential for its member sites to couple environmental and population surveillance and extend their capabilities to monitor environmental change. To understand the nexus between global environmental change (GEC) and health, surveillance systems that focus on social and spatio-temporal patterns of health effects are needed. Health effects of GEC must be detected early enough so that countermeasures can be developed and tested. DSS data can be linked to geographic and meteorological data, using remote sensing (RS) and a Geographical Information System (GIS). This will enable much deeper and/or novel insights into parameters that influence the spread of diseases. The meteorological data complement the DSS data with the introduction of the spatio-temporal fluctuations of temperature, humidity, precipitation, evapo-transpiration and wind. Hence, the different data sets can be used for geo-statistical modelling, mapping and geographical and epidemiological analyses. There is also the important issue of how local communities adapt to global changes.

The Network has established a platform for environment and health research and its first initiative involves a multi-site study on climate variability and the spread of malaria at INDEPTH sites where malaria transmission occurs. Data on geographic differences in mortality or incidence of malaria as they can be provided by DSS tend to be related to other variables which show a similar distribution pattern, for example climate data. But due to the multifactorial nature of the causation of most human health disorders there is little published evidence that changes in population health status actually have occurred as yet in response to observed trends in climate over recent decades. As a result of this situation, the occurrence of malaria and its changes are currently investigated in context with the impacts of climate change and variability on ecological and social systems. This investigation requires population-based data of malaria cases and climate data at the regional or local level which can be provided by the INDEPTH Network sites in Africa and Asia that will participate in this research.

The main research focus will be the extent to which climate variability can be a predictor for malaria transmission at INDEPTH sites. The research will aim to generate an early-warning system based on climate variability for prediction of malaria in INDEPTH sites in Africa and Asia in order to facilitate well-targeted and cost-effective preventive response measures to decision-makers.

Specifically, the research objectives of the proposed study are to:

1. Examine associations between climate variability and changes in malaria transmission in the study areas.
   We will utilize land-based measurements of temperature, rainfall and humidity over a three-year period from digital weather stations to be established at the study sites. In addition, historical data collected over the last 30 years from national meteorological systems and remote-sensing data will be used.
2. Monitor malaria incidence in children under five in the study areas over a three-year period.
   Malaria incidence will be assessed through active case detection.
3. Monitor the effects of land use and land cover on mosquito population dynamics and assess the entomological inoculation rate (EIR) in the study areas over a three-year period.
   Mosquito characteristics (e.g. species, age, sex, breeding sites, feeding and resting behaviours and infectivity) will be measured using standard entomological survey methods. Remote sensing will be used to identify land use.
4. Develop and validate models for predicting malaria transmission using the generated data and establish an early-warning system. Both site-specific and generalized models using data from all the sites will be developed.

Conclusion

INDEPTH is committed to harnessing the potential of the world's demographic surveillance initiatives through its trans-continental network of sites. This network generates significant value for both the member sites and external stakeholders who both stand to benefit from the knowledge and resources of the network. By coordinating the activities of individual demographic surveillance initiatives and facilitating ongoing collaboration within the network, INDEPTH can generate new knowledge and insights for critical health and social challenges. It can greatly enhance the efficiency and effectiveness of multi-site research initiatives. The combined influence and credibility of INDEPTH and member sites enable the network to have significant influence on key decision- and policy-makers. INDEPTH will use this influence to ensure knowledge is disseminated and is translated into improved policy and practice.

INDEPTH studies have the unique advantage of incorporating longitudinal data from multiple sites that are located across different countries, regions and continents. INDEPTH has the unique ability to undertake studies across a broad geography while maintaining the rich longitudinal data that exist at an individual-site level. This capability enables new insights to be drawn from studies that have traditionally been limited to a targeted geographic region. It also enables a new category of multi-site studies to be designed and executed that can generate new knowledge and insights that have previously been unavailable or infeasible. INDEPTH improves the efficiency of the studies by coordinating site activities through the relationships and infrastructure that exist within the network. By creating an integrated network of sites, INDEPTH offers project sponsors with a single, integrated solution for studies that require the identification, selection and coordination of multiple sites.

By utilizing its broad membership base, geographic reach and credibility with the scientific community and governmental bodies, INDEPTH can effectively translate research findings into improved policy and practice.

10

Challenges for dengue control in Brazil: overview of socioeconomic and environmental factors associated with virus circulation

Paulo de Tarso R. Vilarinhos [#]

Abstract

Successive epidemics of dengue have been occurring in Brazil since 1986 and more than three million cases of dengue fever (DF) had already been recorded by November 2003. The introduction of the three serotypes in circulation (DEN-1, DEN-2 and DEN-3) has always started in Rio de Janeiro. During the nineteen nineties, the incidence of dengue increased greatly as a consequence of the dissemination of *Aedes aegypti* in the country, beginning mainly in 1994. Between 1990 and 2000, several epidemics occurred, principally in the major urban centres of the southeast and the northeast of Brazil, where the majority of reported cases were concentrated. The first great incidence of the disease was observed in 1998, with 528,000 DF cases. Circulation of serotype 3 of the virus was detected for the first time in December 2000, in the state of Rio de Janeiro. In the period of 2001-2002, epidemics occurred in several states of the country, with more than 1.2 million of notified DF cases. Two years after the introduction of Den-3, the number of DHF cases notified achieved more than 3000, representing almost 0.3% of the total DF cases. By 1997 more than 50% of the 5543 counties were infested by *Ae. aegypti*. Unplanned urban growth, with deficiencies in water supply and urban cleaning, has increased the opportunities for the mosquito reproduction.

Keywords: dengue; *Aedes aegypti*; vector control

Background

Dengue is a global disease of the tropics, and one of the most important emerging tropical diseases, affecting nearly half of the world population. According to the World Health Organization (WHO 2002) the disease is now endemic in more than 100 countries in Africa, the Americas, the Eastern Mediterranean, Southeast Asia and the Western Pacific. Southeast Asia and the Western Pacific are most seriously affected. WHO currently estimates there may be 50 million cases of dengue infection worldwide, 550 million hospitalizations and at least twelve thousand deaths per year.

In 2001 alone, there were more than 609,000 reported cases of dengue in the Americas, of which 15,000 cases were DHF. This is greater than double the number of dengue cases that were recorded in the same region in 1995 (WHO 2002).

Successive epidemics of dengue have been occurring in Brazil since 1986 and more than three million cases of dengue fever (DF) had already been recorded by

---

[#] Diretoria de Vigilância Ambiental, SAIN Estrada Contorno do Bosque Lote 04, 70620-000 Brasília - DF, Brazil. E-mail: paulo.vilarinhos@terra.com.br

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 107-111.

November 2003 (Figure 1, see Colour pages elsewhere in this book). The introduction of the three serotypes in circulation (DEN-1, DEN-2 and DEN-3) has always started in Rio de Janeiro (Da Silva Jr et al. 2002).

Epidemiology

The occurrence of dengue in Brazil is well-defined by the seasons, the greater incidence occurring in the first months of the year, particularly between March and May (Figure 2, see Colour pages elsewhere in this book), when the prevailing temperature and humidity conditions around the country favour the proliferation of the vector *Aedes aegypti* (Teixeira et al. 2002).

During the nineteen nineties, the incidence of dengue increased greatly as a consequence of the dissemination of *Ae. aegypti* in the country, beginning mainly in 1994 (Figure 3). Dispersion of the vector was followed by the dissemination of serotypes 1 and 2 in 20 of the 27 states of the country. Between 1990 and 2000, several epidemics occurred, principally in the major urban centres of the southeast and the northeast of Brazil, where the majority of reported cases were concentrated (Figure 1, see Colour pages elsewhere in this book). The midwestern and northern regions were subsequently affected by dengue epidemics starting in the second half of the 1990s. The first great incidence of the disease was observed in 1998, with 528,000 DF cases (Figure 1, see Colour pages elsewhere in this book).

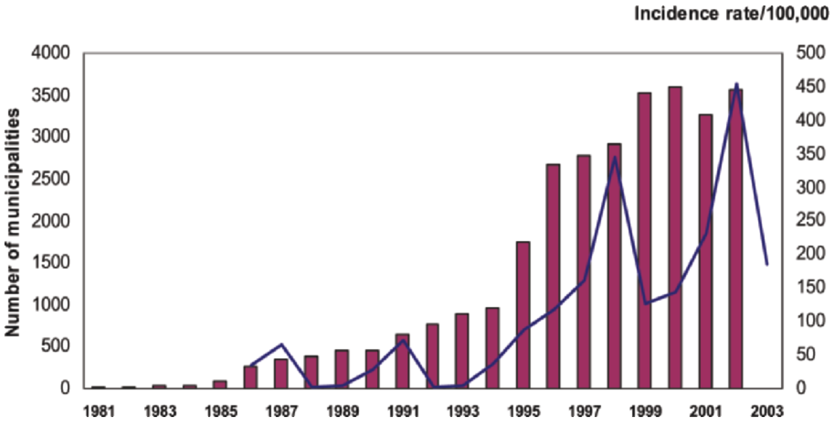
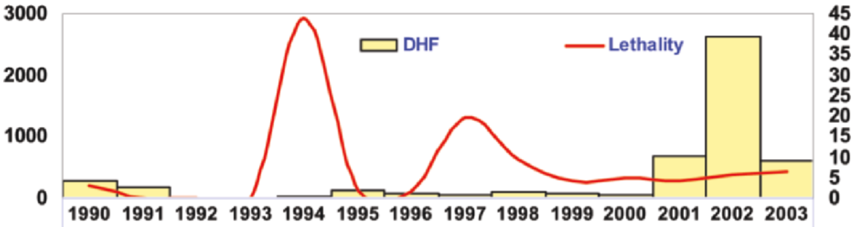


Figure 3. Incidence rate of notified cases of dengue fever and number of municipalities with Aedes aegypti in Brazil, 1986-2003 (Source: SVS)

Current status

Circulation of serotype 3 of the virus was detected for the first time in December 2000, in the state of Rio de Janeiro. In 2002, it has been observed that the diffusion of serotype 3 from the state where it was originally detected presents a different profile from the diffusion observed with serotypes 1 and 2. Previously, diffusion of a new serotype occurred slowly and some years elapsed before indigenous cases occurred in other states. In the first three months of the year 2002, the presence of the new serotype of the virus had been detected in ten more states (Bahia, Ceará, Goiás, Mato Grosso, Mato Grosso do Sul, Minas Gerais, Pará, Paraíba, Pernambuco and São

Paulo) (Figure 4, see Colour pages elsewhere in this book). At the same time, the suspected and confirmed cases of dengue increased considerably in some states, strengthening the trend toward the increase in cases observed in 2000 and 2001. In the period of 2001-2002, epidemics occurred in several states of the country, with more than 1.2 million of notified DF cases. During the same period, a switch on DHF profile was observed (Figure 5). Up to the year 2000, when only Den-1 and Den-2 virus were circulating, DHF records represented 0.05% of the more than 1.7 million DF cases. Two years after the introduction of Den-3, the number of DHF cases notified achieved more than 3000, representing almost 0.3% of the total DF cases. Previous exposure to the two other serotypes in the population hit by Den-3 may explain this raise in DHF cases (Teixeira et al. 2002). Also of concern is the high fatality rate (over 5% observed), when compared with levels below 1% reported for Southeast Asia (Rojanapithayakorn 1998).



	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003
DHF	274	188	0	0	25	114	69	46	105	72	59	682	2617	607
Deaths	8	0	0	0	11	2	1	9	10	3	3	29	145	39
Lethality	2,92	0	0	0	44	1,75	1,45	19,57	9,52	4,17	5,08	4,25	5,56	6,32

Figure 5. Dengue haemorragic fever reported cases and deaths in Brazil, 1990-2003 (Source: SVS)

Fight against the vector

In 1973 it was declared that *Ae. aegypti* had been eradicated from Brazil. However, three years later, the vector reappeared and since then has gradually spread throughout the country. Figure 5 shows that during the 1990s the number of municipalities infested increased steadily, followed by a rise in dengue incidence. By 1997 more than 50% of the 5543 counties were infested by *Ae. aegypti*. Data from the 2000 demographic census comparing the population growth in some metropolitan regions show growth rates varying from 3 to 29% in counties around large cities such as São Paulo, Rio de Janeiro, Belo Horizonte and Recife (IBGE 2004). It is recognized that unplanned urban growth, with deficiencies in water supply and urban cleaning has increased the opportunities for the mosquito reproduction. The intensive disposure of non-biodegradable materials such as plastic containers and tyres in the environment plays an important role in the dispersion and maintenance of foci for the mosquito (Gubler 1997). Entomological surveillance presented in Figure 6 shows the main foci of *Ae. aegypti* in 2001, per county. In the Northeast region, where less than 70% of premises are equipped with piped water (IBGE 2004) and water supply is often unreliable, the main breeding site is related with water reservoirs (tanks, metal drums etc.). In the Southwest region, where most of the large urban centres and high-population-density areas are, the main foci of the vector are associated with waste collection and tyres.

Methods traditionally used in the fight against vector-borne diseases in Brazil and on the continent have not been successful in controlling the vector. Previous programmes centred on chemicals, with limited or no community participation, without intersectorial integration and with little utilization of epidemiological instruments. These programmes were unable to contain the vector because of its great capacity for adaptation to an environment rapidly changing by urbanization and new customs.

In 1996, the Ministry of Health decided to revise the strategy against *Ae. aegypti* and proposed a Programme of Eradication of the vector (PEAa). The new programme took into account the difficulties of the previous control strategy and, paradoxically, it proposed an even more complex objective, stemming from the assumption that the vector could be eradicated. Though the PEAa stemmed from this mistaken assumption and presented omissions or deficiencies in important areas such as community participation and epidemiological surveillance, it had undeniable merits. For example, the programme proposed multisectorial action and foresaw the participation of the three levels of government –federal, state and municipal –in the endeavour.

In practice, the PEAa contributed to strengthening the fight against the vector, considerably increasing resources for the project. Prevention activities however were centred mainly on utilization of insecticides.

Results obtained in Brazil and at the international level brought into question the viability of a short-term policy of eradication of the vector. This led the Ministry of Health to re-evaluate the progress and limitations of the programme, with the objective of establishing a new programme to control dengue.

Prevention and control strategy

The increase in observed incidence of dengue in the last two years and the introduction of a new serotype (DEN 3) led to a prediction of increased risk of dengue epidemics and an increase of the cases of DHF. To face the expected risks for 2002, the Ministry of Health, in collaboration with the Pan-American Health Organization, carried out an international seminar in June 2000 to evaluate the situation and prepare a National Dengue Control Plan (PNCD). The plan targeted the 657 municipalities of greatest risk in the country, with the objective of more effectively utilizing the positive results of previously adopted initiatives. These include: 1) a large infrastructure for vector control in the states and municipalities (vehicles, spraying equipment, microscopes and computers); 2) nearly 40,000 agents trained in vector control, in more than 3,500 municipalities; and 3) a set of nationally standardized activities and technical standards for vector control.

The PNCD was conceived with three goals: i) to bring *Ae. aegypti* infestation levels (house index) bellow 1%; ii) to reduce DF cases by 50% in 2003, in comparison with 2002, and by 25% every year after; and iii) to reduce DHF fatalities to less than 1%. To accomplish these goals the Plan was focused in the 657 counties that historically have held more than 70% of the notified dengue cases, in the 25 states where transmission occurs. The guidelines developed to implement the Plan are:

- **Strengthening epidemiologic surveillance** – to seek early detection of virus circulation;
- **Integrating vector control with epidemiological surveillance** – aiming to block transmission at initial focus;

- **Basic health-care integration (health family programme)** – to support detection of suspected cases and orient at prevention of breeding sites;
- **Reduction of DHF burden** – to improve clinical management of cases to reduce fatality rates;
- **Environmental-management support** – to develop sanitation solutions for low-income communities;
- **Proposing new laws** – to support and enforce behavioural change, to sustain infestation levels below 1%;
- **Social mobilization for behaviour changes** – integrate actions of health education with social communication to induce preventive behaviour;
- **Setting up a political agenda** – sensitize and mobilize political sectors to bring more funds and facilitate intersectorial actions of the programme.

The Plan is very comprehensive and covers all activities necessary for its implementation, including the application of recent regulations on the attributions of Federal, State and Municipal levels regarding epidemiology and disease control. In this regard a National Fund has been created establishing rules for a monthly flow of money to all country states and municipalities, based on an annually agreed set of activities and goals for the main diseases.

References

Da Silva Jr, J.B., Siqueira, J. B., Coelho, G.E., et al., 2002. Dengue in Brazil: current situation and prevention and control activities. *Epidemiological Bulletin / Pan American Health Organization,* 23 (1), 3-6. [http://www.paho.org/english/dd/ais/EB_v23n1.pdf]

Gubler, D.J., 1997. Dengue and dengue haemorragic fever: its history and resurgence as a global public health problem. *In:* Gubler, D.J. and Kuno, G. eds. *Dengue and dengue hemorrhagic fever*. CAB International, New York, 1-22.

IBGE, 2004. *Atlas do Censo Demográfico de 2000.* Instituto Brasileiro de Geografia e Estatística.

Rojanapithayakorn, W., 1998. Dengue haemorrhagic fever in Thailand. *Dengue Bulletin,* 22, 60-68. [http://w3.whosea.org/en/Section10/Section332/Section520_2417.htm]

SVS, *Programa nacional de controle da dengue (website)*. Ministério da Saúde, Secretaria de Vigilância em Saúde. [http://dtr2001.saude.gov.br/svs/epi/dengue/dengue0.htm]

Teixeira, M.G., Costa, M.C.N., Guerra, Z., et al., 2002. Dengue in Brazil: situation-2001 and trends. *Dengue Bulletin,* 26, 70-76. [http://w3.whosea.org/LinkFiles/Dengue_Bulletin_Volume_26_Chap08.pdf]

WHO, 2002. *Dengue and dengue haemorrhagic fever*. World Health Organization, Geneva. Fact sheet no. 117. [http://www.who.int/mediacentre/factsheets/fs117/en/]

11

Effects of environmental change on malaria in the Amazon region of Brazil

Willem Takken[1], *Paulo de Tarso R. Vilarinhos*[2], *Petra Schneider*[1,3] *and Fatima dos Santos*[4]

Abstract

Malaria is endemic in Brazil, affecting mostly the Amazon states. Whereas 50 years ago good progress was made towards its control, since the opening up of the Amazon region for forestry, agriculture and livestock activities, the disease has rapidly increased in incidence, peaking to >500,000 cases annually in the 1990s. Rondônia state was particularly hard hit, with thousands of new immigrants suffering malaria attacks. It is argued that the environmental change caused by deforestation has favoured the main malaria vector *Anopheles darlingi*, creating numerous sunlit larval habitats and bringing potential blood hosts in the vicinity of the mosquitoes. The creation of malaria clinics and strengthened control programmes has reduced the malaria situation, but risk is still high, particularly in rural and peri-urban areas where humans and mosquitoes are in close contact. The continuing environmental change, caused mainly by deforestation, is likely to favour the malaria situation in Brazil as it creates new malarial habitats and affects large numbers of non-immune settlers who are attracted to the Amazon region.

Keywords: malaria; *Anopheles darlingi*; Amazon; risk; deforestation; environmental change

Introduction

Recent publications about climate change as a result of anthropogenic activities predict a warming of the earth from 2.5 to 4 °C in the next century and dramatic variations in the intensities of precipitation with large differences between geographic areas (Watson, Zinyowera and Moss 1998). Apart from creating numerous effects on the environment, these changes are likely to affect human health as well. It has been suggested that vector-borne diseases may be one of the major health impact factors that will be affected (Patz and Balbus 1996; McMichael and Beaglehole 2000; Haines and Patz 2004). Among these, malaria has been singled out as a particularly vulnerable target, as both vectors (mosquitoes of the genus *Anopheles*) and parasites may be affected, and also because thousands of people are currently living in areas where the malaria vectors are present but the parasites are absent or circumstances are

---

[1] Laboratory of Entomology, Wageningen University, The Netherlands. E-mail: willem.takken@wur.nl

[2] Diretoria de Vigilância Ambiental, SAIN Estrada Contorno do Bosque Lote 04, 70620-000 Brasília - DF, Brazil. E-mail: paulo.vilarinhos@terra.com.br

[3] Current address: Laboratory of Medical Microbiology, UMC St Radboud, Nijmegen, The Netherlands

[4] Fundação Nacional de Saúde, Porto Velho, Rondônia, Brazil

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 113-123.

unsuitable for parasite development (Martens et al. 1999). Current epidemiological models predict malaria risk based on generalized climate data, using average annual temperatures and rainfall, with little regard for local variation. As the climate changes will affect regions differently, it is of critical importance to be able to study the effects of the changes on local malaria risk, taking into consideration the topography, land use, habitat structure and demography of each area. Other changes may also affect malaria risk, such as rapid changes in land use, deforestation, urbanization and human migration. As the predicted climate change may affect these entities differently, the study of environmental change and malaria becomes complex and challenging.

Malaria in Brazil is currently confined mostly to the tropical regions of the country, with the Amazon basin as the endemic region. Major threats to the Amazonian environment have taken place in the last 35 years, chiefly because of the large-scale deforestation of primary rainforest in connection with road construction and agricultural development (Cruz Marques 1987; Skole and Tucker 1993; Camargo et al. 1994; Cardille and Foley 2003; Souza et al. 2003). Indeed, the destruction of the rainforest has grown into a global debate as this is considered one of the contributions to climate change (Laurance 2000). These developments are still continuing at a rate of 2.4 million hectares of forest per year, in spite of scientific consensus that urgent measures are required to stop or reverse these developments for the principle reason that rainforests are critical sources of biodiversity and climate stability, and essential as carbon sinks (Laurance et al. 2001; 2004).

It has often been assumed that the disappearance of the rainforest would be accompanied at least by beneficial effects on vector-borne diseases, as the habitat of the vectors would be destroyed, and with this the transmission of infectious diseases would be reduced or even eliminated. However, recent studies have shown that this scenario is untrue, and surprising increases in the incidence of vector-borne diseases such as leishmaniasis, Chagas and malaria have been recorded following the disappearance of the rainforest. Notorious is the rise of malaria in Rondônia State, Brazil, where between 1970 and 1990 the annual incidence of malaria increased from 10,000 to >250,000 per year (Kingman 1989). Indeed, this situation has become a classic example of vector-borne disease risk and environmental change. However, it should be noted that this increase was accompanied by a huge influx of immigrants from elsewhere, which may have exacerbated the situation.

The present study was undertaken to examine whether climate change would similarly contribute to malaria risk in the Brazilian Amazon basin, and which other human activities might indirectly cause increased risk for malaria infections. To this, we assessed the current situation of malaria in Brazil and the effects of climate change on malaria with emphasis on the Amazon rainforest as baseline information for the elucidation of factors that now and in the future might determine malaria risk in this area. Potential mitigating factors to reverse the emergence of risk factors are discussed.

Malaria in Brazil

Historically, malaria was endemic in much of Brazil, from the tropical Amazon region to the southern coastal regions as far south as São Paulo. Both *Plasmodium vivax* and *P. falciparum* occurred, with the former more prevalent than the latter. Numerous mosquito vector species are present in the country, with *Anopheles darlingi* and *An. nunetzovari* being the most important species in the rainforest, and *An. aquasalis* the vector in coastal regions. Locally, other species can also be involved in malaria transmission (Deane 1986; Rosa-Freitas et al. 1998). As malaria control has been highly effective in the southern and eastern regions of Brazil, today the disease is restricted mostly to the Amazon region, with *An. darlingi* as the main vector.

In the 1940s, all Brazilian regions were affected by malaria with the occurrence of millions of cases per year. Social changes and development, coupled with the intense work of the Malaria Eradication Campaign, led to a relative control of the disease, lowering the annual records to less than 100,000 cases, spatially restricted to the states of the Amazon Region.

The Amazon Legal Region is made up of the states Acre, Amapa, Amazonas, Maranhao, Mato Grosso, Para, Rondônia, Roraima and Tocantins. The risk of acquiring malaria is not uniform in the region. The Annual Parasite Index (API) is used to measure the malaria risk, which is given by the number of positive blood smears per 1000 persons at risk. According to this index, endemic areas are classified as high, medium and low transmission risk (Figure 1, see Colour pages elsewhere in this book).

After 1970, Amazon development projects with highways opening, hydroelectric dams, expansion of mining activities, logging and rural settlements, stimulated intense population migration and anthropogenic environmental changes. This process resulted in the dispersion of malaria throughout the region, with a significant increase in the number of cases to an average of 520,000 cases per year during the 1990s (Figure 2). A steep rise in the malaria trend was observed in 1999/2000 when the number of cases was above 600,000 and the average API achieved 30 (Figure 3). This rise led the Brazilian Ministry of Health in July 2000 to conceive and implement, with Amazon states and 254 counties, the Plan of Intensification of Malaria Control Actions (PIACM). The main goal was to achieve a 50% reduction of malaria cases by December 2001. The strategy was focused on political mobilization, capacity building in local health systems, early diagnosis and treatment, health education, social mobilization and intersectorial actions. With a budget of US$ 50.2 millions the PIACM was able to decentralize diagnosis and treatment to states and counties, integrating community health agents and health family teams. This initiative provided easiest and quick access of Amazon populations to prompt health care. Vector control activities were expanded with more field personnel, new vehicles and spray equipment. This made it possible to increase coverage of indoor residual insecticide spraying and spatial treatments to interrupt outbreaks. Draining and other environmental measures were applied in urban areas, such as Manaus and Porto Velho, to eliminate breeding sites. Another important initiative in March 2001 was the development of a protocol with the National Institute of Land Reform and Colonization (INCRA) to submit new settlements to extensive evaluation by the Ministry of Health to prevent malaria outbreaks. The National Environmental Council (CONAMA) issued a resolution in August 2001 establishing that the environmental license for developments in endemic regions requires evaluation of the health authorities regarding malaria prevention.

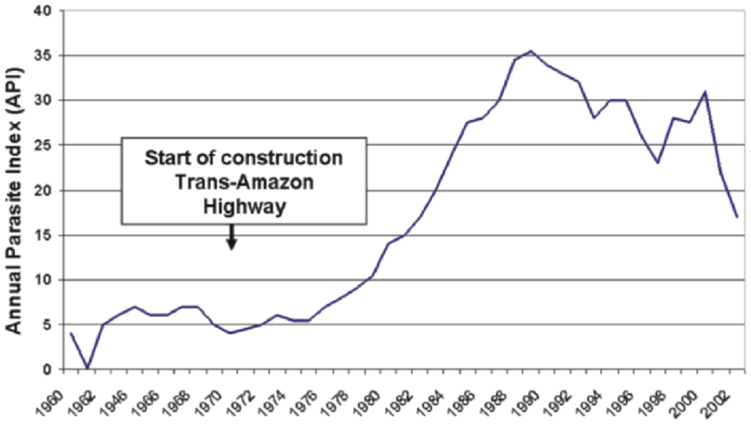


Figure 2. Annual Parasite Index, Amazonia, Brazil between 1960 and 2002 (source: PNCM 2003)

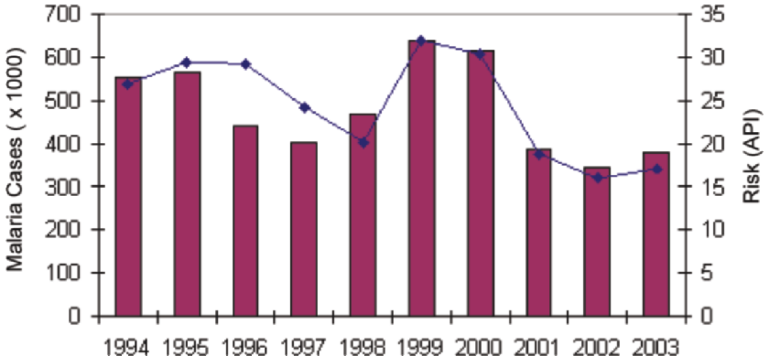


Figure 3. Malaria incidence and risk (expressed as Annual Parasite Index) in Brazilian Amazonia between 1994 and 2003
Bars: the number of malaria cases; Line: the Annual Parasite Index per 1000 inhabitants

The impact of the actions developed by the PIACM was observed by the end of the year 2001, with a reduction of 38.9% in the overall number of cases and 41.1% in the API (Figure 2). The number of hospitalizations and deaths was reduced significantly by 69.2% and 36.5%, respectively (PNCM 2003). In spite of the increased control of malaria, transmission levels still remained high after 2001. The results differ significantly among states (data not shown). While Amazon and Acre achieved more than 60% reduction, Rondônia and Amapa obtained reductions of 9% and 15%, respectively. In 98 counties (38% of 254 in total) the malaria risk is considered high (API>50), with half of them showing an API >100. The proportion of malaria caused by *Plasmodium falciparum*, which causes the most serious clinical complications and high death rates, remains above 20% of the total, and is increasing in eight of the nine states (Table 1).

Table 1. Relative changes in all-cause malaria incidence (expressed as API) and *P. falciparum* rate in the Amazon region, Brazil, between the first quarters of 2003 and 2004

	2003			2004			Relative changes 2003/2004	
State Name	No. of cases	*P.falc + (Pf+Pv)*	*%P.f*	No. of cases	*P.falc + (Pf+Pv)*	*% Pf*	Relative change in API	Relative change in *Pf* ratio
AC	1,449	449	31.0	786	267	34.0	-47.0	9.6
AM	17,714	1,524	8.6	20,824	3,295	15.8	14.9	83.9
AP	1,789	735	41.1	3,202	1,605	50.1	73.1	22.0
MA	1,188	215	18.1	713	198	27.8	-40.7	53.5
MT	946	119	12.6	573	69	12.0	-40.5	-4.3
PA	19,396	5,184	26.7	9,976	2,845	28.5	-49.5	6.7
RO	10,102	3,306	32.7	16,546	5,635	34.1	61.1	4.1
RR	1,015	187	18.4	2,700	284	10.5	158.5	42.9
TO	230	42	18.3	106	29	27.4	-54.8	49.8
AMAZôNIA	53,829	11,761	21.8	55,426	14,227	25.7	1.2	17.5

AC = Acre; AM = Amazonas; AP = Amapa; MA = Maranhao; MT = Mato Grosso; PA = Para; RO = Rondônia; RR = Roraima; TO = Tocantins

API = Annual Parasite Index = number of positive blood smears per 1000 inhabitants

P.falc + (Pf+Pv) = all cases of *P. falciparum* and mixed infections

The malaria control activities, guidelines and financial support are now organized in the National Malaria Control Programme (PNCM 2003) from the Ministry of Health. The programme was formulated to sustain the advances obtained with the PIACM, and to improve the results in some areas and activities. The major objectives are (i) to achieve a reduction in incidence, mortality and severe-and-complicated malaria; (ii) to eliminate transmission in the urban areas from capital cities; (iii) to keep areas where transmission has been interrupted free from malaria.

Environmental changes in Brazil affecting malaria

The epidemiology of malaria is much determined by climate, vector habitat, susceptibility of the human population and vector and parasite behaviour, amongst other things. The major vector in Brazil, *Anopheles darlingi*, is widely distributed in Central and South America (Manguin et al. 1999), determined by a suitable habitat and the availability of blood hosts. In much of the Amazon region the habitat for *An. darlingi* is optimal, with the mosquito profiting from the destruction of rainforests (Cruz Marques 1987). Thus, as an apparent paradox, the environmental change witnessed in the Amazon region does not lead to the disappearance of malaria vectors; on the contrary. Recent figures demonstrate the high incidence of the disease in Brazil (Figure 3), and nearly all of these cases originate in (former) rainforest zones. It should be mentioned here that some indigenous populations of the Amazon region experience a high parasite rate, but it is not well known to what extent they suffer from malaria morbidity and mortality (De Arruda et al. 1996; 1998; Perez Mato 1998; Camargo, Alves and Pereira da Silva 1999). It is assumed that here, too, *An. darlingi* is the principal vector. This anopheline species benefits much from the reported deforestation by rapidly expanding its population in sunlit areas, where numerous newly created water bodies provide adequate larval habitats. As the biting habits of

An. darlingi include humans, the presence of new settlements, anopheline vectors and malaria parasites combined is sufficient to maintain the parasite transmission cycle and a high malaria incidence.

Case study: malaria in Rondônia

Rondônia state is located in the southwestern Amazon region, bordering with Bolivia. The state is bisected by the Madeira river, which runs from the eastern slopes of the Andes and merges with the Amazon river near Manaus. The general topography is flat country, with an average elevation of 300 m above sea level. The climate is characterized as tropical, with a long rainy season from January till May. However, some rainfall is recorded during other months of the year as well. Up to the 1960s, Rondônia was covered with near-complete lowland rainforest and sparsely populated. This situation changed when construction began of the Amazon highway (road BR364), which runs from the southern state border north to the capital city of Porto Velho, and then continues west to Acre state and beyond into Peru (Figure 4). Road BR364 is an all-weather road covered with tarmac, and serves mainly as a transport line for goods entering or leaving Rondônia. From Porto Velho road BR319 runs north to Manaus, but this road it not surfaced and rarely used. Most goods arriving in Porto Velho with destination Manaus are transported by ship across the Madeira river. In the 1960s Porto Velho had the character of a frontier town, serving transport companies and settlers from the north of the state. Gold was found in the Madeira river, and gold mining became a major economic activity in the 1980s, attracting thousands of settlers. From 1970 onwards, the Federal Government of Brazil initiated a development plan for Rondônia, encouraging landless people from the southern states to settle in Rondônia to become farmers. Settlers were given a piece of land that had been cleared of forest. Thus began one of the largest deforestation programmes witnessed. Originally, the activities began in the southern parts of the state. By the 1980s, the town of Ariquemes became the centre of this development, with large-scale logging and deforestation. This can be seen from a series of Landsat images taken in 1976, 1986 and 1992 (Figure 5, see Colour pages elsewhere in this book). Most activities occurred on both sides of BR364, with roads being built perpendicular to the highway, providing a fishbone structure when viewed from the air. New immigrants settled along these new roads to grow commercial crops such as fruit, maize, cotton and rice. The land they occupied had been clear-cut, with the timber being processed in Ariquemes and other commercial centres. As the land became rapidly exhausted by the crop farming, settlers switched to beef production or sold their land. Today many of these original farms are no longer used for crop production, most having turned over into rangeland (Browder, Pedlowski and Summers 2004; Guild, Cohen and Kauffman 2004).

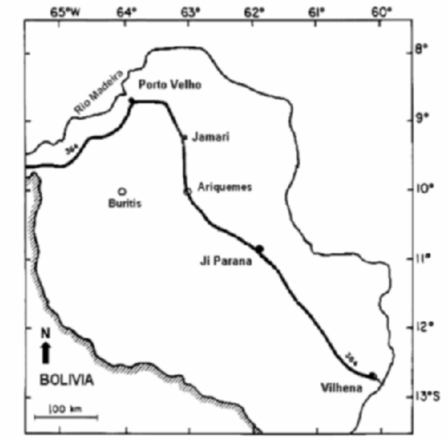


Figure 4. Map of Rondônia, Brazil, showing the position of highway BR364, along which much of the deforestation occurred (for details see Figure 5, see Colour pages elsewhere in this book). Source: Guild, Cohen and Kauffman (2004)

By the year 2000, these developments had reached Porto Velho in the north, and extending westwards along the BR364 all the way to Acre state. Within a 50-km radius from the highways, deforestation was dominant, while further away primary rainforest could still be found. However, even there land-use changes are occurring rapidly. In 2001 the authors witnessed the development of Buritis, a new town situated 100 km northwest of Ariquemes and accessible only by newly constructed roads. On either side of these roads, clear-cut deforestation was ongoing, with new farms being established (W. Takken and F. dos Santos, personal observation).

What are the consequences of these developments for malaria? The main malaria vector in Rondônia is *An. darlingi*, with other anopheline species present, but these are of little epidemiological significance (De Oliveira-Ferreira et al. 1990). As mentioned above, *An. darlingi* is the natural malaria vector in lowland rainforests of South America. The species breeds in large pools of stagnant water, mainly along the edges, as well as in slow-moving streams. As the species is heliophilic, larvae thrive in sunlit pools. The methods of deforestation in Rondônia, aided by road construction, have caused the creation of thousands of small dams, increasing the larval habitats of *An. darlingi*. Because this was followed by human settlement and often also by the introduction of livestock such as cattle and horses, new blood sources for the mosquitoes were introduced as well. *An. darlingi* benefited from these developments by expanding its population size. Several studies have demonstrated an increased risk in malaria associated with the forest industry in Rondônia, and the inhabitants of towns are frequently affected by the diseases (Camargo et al. 1994; 1996; 1999; Lima et al. 1996) (Figure 6). Even at the suburban areas of the capital city Porto Velho, malaria is frequently contracted, presumably because of vector mosquitoes breeding in man-made pools and forest islands. It has been observed that after an initial surge in malaria incidence following forest clearance and the arrival of new settlers, the malaria incidence is reduced and becomes stable. In addition, malaria diagnosis and treatment are freely available from government clinics, and patients can be rapidly identified and treated. In spite of these excellent public-health measures, in Rondônia malaria remains present and continues to pose a major public-health threat. It is important to realize that the low level of infection risk does not allow for the development of immunity, and this is one of the main reasons for the continuous malaria incidence at all ages. Forest workers are most affected, but also others who venture into the forests.

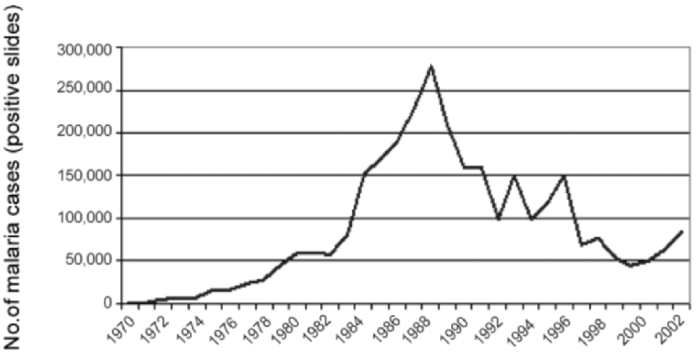


Figure 6. Malaria incidence as measured by number of positive blood slides in Rondônia between 1970 and 2004

Malaria risk under climate change in the Brazilian Amazon forest

As malaria incidence and prevalence is likely to change under climate change (see above) and current indications are that malaria remains one of the main diseases affecting public health in the Brazilian Amazon region (PNCM 2003), we may consider the implications of the predicted changes for malaria in the region. Past and current deforestation has caused considerable environmental changes, but the effects of these on malaria are that the disease has become firmly associated with peri-urban settlements and rural development. The predicted increase in mean temperature, resulting from greenhouse-gas emissions, is unlikely to `affect the biology of the mosquito vectors, although higher maximum temperatures may be detrimental to larval and adult-mosquito survival (Clements 1992). Increased precipitation will result in filling up of water reservoirs, but since the annual rainfall is already high in the entire region, it remains to be seen to what extent extra rainfall enhances mosquito breeding. Human behaviour may lead to seeking more escape from the heat, by retiring indoors with air-conditioning. However, this is unlikely to be the case among the relatively poor sections of the Amazon population. The central question will be how current measures to restrict deforestation and protect natural ecosystems will be affected by climate change (Laurance 1998). Successful environmental protection is likely to favour the natural mosquito habitats and, hence, an important determinant of malaria. Unlike other regions, where malaria is seasonal or epidemic in some years, the Amazon region exhibits a continuous transmission. For these reasons the predicted changes are unlikely to affect malaria risk, and the latter is much more affected by environmental change associated with deforestation and urbanization.

Discussion

The data presented show that malaria is present throughout the Amazon region of Brazil, and that anthropogenic activities of the past 40 years have caused large increases in disease incidence both in rural and peri-urban areas. In spite of a high level of public-health care through clinics and free treatment programmes, malaria maintains a presence of significance. For these reasons, the National Malaria Control Programme received fresh inputs in 2001 and has been successful in reducing the incidence of malaria in many areas. Without this programme, the disease is likely to increase again. The environmental conditions appear highly suitable for the continuing transmission of the disease, even in areas with a relatively low human population density. Ongoing deforestation will favour malaria in other areas, affecting the health of new settlers. We predict that the main vector, *An. darlingi*, will be little affected by climate change, as this mosquito can adapt to varying environmental conditions. Higher temperatures may cause a reduction in parasite incubation time, but this is unlikely to affect the transmission rate of the parasite. Therefore, the main determinants of malaria in the Amazon region will be little affected by the predicted change. By contrast, further east and south, in areas of Brazil where malaria has previously been eradicated, climate change may favour an environmental change suitable for renewed malaria transmission. The consequences of these changes should be studied with renewed malaria risk strategies (Van Lieshout elsewhere in this volume).

References

Browder, J.O., Pedlowski, M.A. and Summers, P.M., 2004. Land use patterns in the Brazilian Amazon: comparative farm-level evidence from Rondonia. *Human Ecology,* 32 (2), 197-224.

Camargo, E.P., Alves, F. and Pereira da Silva, L.H., 1999. Symptomless *Plasmodium vivax* infections in native Amazonians. *Lancet,* 353 (9162), 1415-1416.

Camargo, L.M., Duccini dal Colletto, G.M., Ferreira, M.U., et al., 1996. Hypoendemic malaria in Rondonia (Brazil, western Amazon region): seasonal variation and risk groups in an urban locality. *American Journal of Tropical and Medical Hygiene,* 55 (1), 32-38.

Camargo, L.M., Ferreira, M.U., Krieger, H., et al., 1994. Unstable hypoendemic malaria in Rondonia (Western Amazon region, Brazil): epidemic outbreaks and work-associated incidence in an agro-industrial rural settlement. *American Journal of Tropical Medicine and Hygiene,* 51 (1), 16-25.

Camargo, L.M., Noronha, E., Salcedo, J.M., et al., 1999. The epidemiology of malaria in Rondonia (Western Amazon region, Brazil): study of a riverine population. *Acta Tropicana,* 72 (1), 1-11.

Cardille, J.A. and Foley, J.A., 2003. Agricultural land-use change in Brazilian Amazonia between 1980 and 1995: evidence from integrated satellite and census data. *Remote Sensing of Environment,* 87 (4), 551-562.

Clements, A.N., 1992. *The biology of mosquitoes. Vol. 1. Development, nutrition and reproduction*. Chapman & Hall, London.

Cruz Marques, A., 1987. Human migration and the spread of malaria in Brazil. *Parasitology Today,* 3 (6), 166-170.

de Arruda, M., Souza, R.C., Veiga, M.E., et al., 1998. Prevalence of *Plasmodium vivax* variants VK247 and *P. vivax*-like human malaria: a retrospective study in indigenous Indian populations of the Amazon region of Brazil. *Transactions of the Royal Society of Tropical Medicine and Hygiene,* 92 (6), 268.

de Arruda, M.E., Aragaki, C., Gagliardi, F., et al., 1996. A seroprevalence and descriptive epidemiological study of malaria among indian tribes of the Amazon Basin of Brazil. *Annals of Tropical Medicine and Parasitology,* 90 (2), 135-143.

de Oliveira-Ferreira, J., Lourenco-de-Oliveira, R., Teva, A., et al., 1990. Natural malaria infections in Anophelines in Rondania State, Brazilian Amazon. *American Journal of Tropical and Medical Hygiene,* 43 (1), 6-10.

Deane, L.M., 1986. Malaria vectors in Brazil. *Memorias do Instituto Oswaldo Cruz,* 81 (Suppl. 2), 5-14.

Guild, L.S., Cohen, W.B. and Kauffman, J.B., 2004. Detection of deforestation and land conversion in Rondonia, Brazil using change detection techniques. *International Journal of Remote Sensing,* 25 (4), 731-750.

Haines, A. and Patz, J.A., 2004. Health effects of climate change. *Jama : Journal of the American Medical Association,* 291 (1), 99-103.

Kingman, S., 1989. Malaria runs riot on Brazil's wild frontier. *New Scientist* (1677), 24-25.

Laurance, W.F., 1998. A crisis in the making: responses of Amazonian forests to land use and climate change. *Trends in Ecology and Evolution,* 13 (10), 411-415.

Laurance, W.F., 2000. Mega-development trends in the Amazon: implications for global change. *Environmental Monitoring and Assessment,* 61 (1), 113-122.

Laurance, W.F., Albernaz, A.K.M., Fearnside, P.M., et al., 2004. Deforestation in Amazonia. *Science,* 304 (5674), 1109-1109.

Laurance, W.F., Cochrane, M.A., Bergen, S., et al., 2001. Environment: the future of the Brazilian Amazon. *Science,* 291 (5503), 438-439.

Lima, D.C., Lourenco-de-Oliviera, R., Honorio, N.A., et al., 1996. Sobre a transmissão da malária em duas areas endémicas no estado de Rondonia. *In: Reunião Nacional de Pesquisadores em Malária*. 136.

Manguin, S., Wilkerson, R.C., Conn, J.E., et al., 1999. Population structure of the primary malaria vector in South America, *Anopheles darlingi*, using isozyme, random amplified polymorphic DNA, internal transcribed spacer 2, and morphologic markers. *American Journal of Tropical and Medical Hygiene,* 60 (3), 364-376.

Martens, P., Kovats, R.S., Nijhof, S., et al., 1999. Climate change and future populations at risk of malaria. *Global Environmental Change. Part A. Human and Policy Dimensions,* 9 (1), S89-S107.

McMichael, A.J. and Beaglehole, R., 2000. The changing global context of public health. *Lancet,* 356 (9228), 495-499.

Patz, J.A. and Balbus, J.M., 1996. Methods for assessing public health vulnerability to global climate change. *Climate Research,* 6 (2), 113-125.

Perez Mato, S., 1998. Anemia and malaria in a Yanomami Amerindian population from the southern Venezuelan Amazon. *American Journal of Tropical Medicine and Hygiene,* 59 (6), 998-1001.

PNCM, 2003. *Programa Nacional de Prevenção e Controle da Malária PNCM.* Ministério da Saúde, Secretaria de Vigilância em Saúde, Brasilia. [http://dtr2001.saude.gov.br/svs/epi/malaria/pdfs/pncm.pdf]

Rosa-Freitas, M.G., Lourenco-de-Oliveira, R., De Carvalho-Pinto, C.J., et al., 1998. Anopheline species complexes in Brazil: current knowledge of those related to malaria transmission. *Memorias do Instituto Oswaldo Cruz,* 93 (5), 651-655. [http://www.scielo.br/pdf/mioc/v93n5/10m.pdf]

Skole, D. and Tucker, C., 1993. Tropical deforestation and habitat fragmentation in the Amazon: satellite data from 1978 to 1988. *Science,* 260 (5116), 1905-1910.

Souza, C., Firestone, L., Silva, L.M., et al., 2003. Mapping forest degradation in the eastern Amazon from SPOT 4 through spectral mixture models. *Remote Sensing of Environment,* 87 (4), 494-506.

Watson, R.T., Zinyowera, M.C. and Moss, R.H. (eds.), 1998. *The regional impacts of climate change: an assessment of vulnerability*. Cambridge University Press, Cambridge. Special Report of IPCC Working Group II.

12

Bluetongue in the Mediterranean: prediction of risk in space and time

B.V. Purse [#]*, P.S. Mellor and M. Baylis*

Abstract

Bluetongue virus (BTV) causes an infectious, non-contagious disease of ruminants and is transmitted by *Culicoides* biting midges. Currently an unprecedented epidemic of bluetongue (BT) is sweeping the Mediterranean Basin and a large number of countries are now involved in managing the disease. Therefore the development of new methods for accurate prediction of BT risk in space and time is essential. The life-history parameters of *Culicoides* and other parameters of the BTV transmission cycle are highly sensitive to climatic conditions. Thus the potential exists to define the limiting conditions and likelihood of spread of BTV, using geographical information systems (GIS) to combine vector, virus and environmental information. This paper reviews the progress and current status of GIS and remote sensing (RS) as applied to BTV in the Mediterranean Basin. These analytical tools have aided the determination of the relative roles of different *Culicoides* vectors in BTV transmission across the region and have facilitated prediction of the wide-scale distribution of the major field vector *C. imicola* from RS climate variables. On the basis of findings and lessons from statistical models of vector distribution, a strategy for development of dynamic biological or process-based models of BT risk is suggested.

Keywords: Bluetongue virus; Mediterranean; *Culicoides obsoletus*; *Culicoides pulicaris*; *Culicoides imicola*; distribution; climate; remote sensing; risk map

Bluetongue virus, its vectors and the changing face of bluetongue epidemiology in the Mediterranean

Bluetongue virus (BTV) causes an infectious, non-contagious disease of ruminants (bluetongue, BT) and is transmitted between its vertebrate hosts by *Culicoides* biting midges (*Diptera*: *Ceratopogonidae*). Although severe disease is restricted to certain breeds of sheep and some species of deer (Taylor 1986), it has been estimated that BTV causes losses of US $3 billion a year to trade in animals and animal products. Thus BT is classified as a List-A disease by the Office International des Epizooties (OIE). *Culicoides* are significant as arbovirus vectors since they inhabit a wide range of moist habitats, rapidly reach high abundances under suitable climatic conditions, and are passively dispersed on the wind, producing rapid spread of *Culicoides*-borne diseases (Mellor, Boorman and Baylis 2000). *Culicoides* broadly require the presence of host for blood meals and moist breeding sites for egg and larval development. Their life-history parameters and other parameters of the BTV transmission cycle (rates of

---

[#] Institute for Animal Health, Ash Road, Pirbright, Surrey, UK, GU24 0NF. Tel: +44 1483 232441. Fax: +44 01483 23248. E-mail: beth.purse@bbsrc.ac.uk

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 125-136.

BTV infection and virogenesis, efficiency of gut barriers to infection in the midge) are highly influenced by climatic factors, especially temperature and moisture (Mellor, Boorman and Baylis 2000). *Culicoides* development and survival rates are temperature-dependent as adults and larvae, and fecundity is inversely related to temperature once the lower temperature threshold has been exceeded (Wittmann and Baylis 2000, and refs. therein). Larvae may be desiccated by low soil moisture but equally may drown if breeding sites are flooded. Adults, being small, are susceptible to desiccation at low humidity (Murray 1991) and thus require moist microhabitats for shelter as well as oviposition. Only a handful of *Culicoides* species are of transmission importance and different vectors operate in different continental episystems within the global distribution of BTV (Mellor, Boorman and Baylis 2000).

Considering the Mediterranean Basin, only brief periodic incursions of BTV and the closely related *African horse-sickness virus* (AHSV) occurred before 1998, with only one or two countries affected at a time and one viral serotype being involved in each epidemic (Figure 1a, see Colour pages elsewhere in this book). Also, prior to the current series of outbreaks only one main vector species was known to be involved in BTV transmission - *Culicoides imicola sensu stricto* (Linto et al. 2002), a member of the *C. imicola* Kieffer species group. All outbreaks before 1998 caused by BTV and AHSV occurred within the region delineated by the known northern distribution limit of this species (Figure 1a, see Colour pages elsewhere in this book). However, between 1998 and 2003, an unprecedented BT epidemic has occurred (Baylis 2002; Mellor and Wittmann 2002), affecting many countries in both the east and west Mediterranean areas, including many that were unaffected in previous outbreaks. BTV has expanded northwards (over 700 km) and beyond even the updated northern distribution limit of *C. imicola* (Figure 1b, see Colour pages elsewhere in this book), in northwest Greece, Bulgaria, west European Turkey and parts of Italy (Mellor and Wittmann 2002; Baylis and Mellor 2001). Therefore, novel *Culicoides* vectors must now be involved in transmission, possibly the widespread *C. obsoletus* Meigen and *C. pulicaris* Linnaeus complexes (Mellor and Wittmann 2002). Indeed, BTV has previously been detected in wild-caught *C. obsoletus* in Cyprus (Mellor and Pitzolis 1979) and, more recently, in southern mainland Italy (Savini et al. 2003) and in wild-caught *C. pulicaris* in Sicily (Caracappa et al. 2003). The current epidemic has persisted for six years to date (affecting Italy for four consecutive years since 2000) and several viral serotypes are circulating. With over a million sheep dead so far (Mellor and Wittmann 2002; Calistri and Caporale 2003) and many Mediterranean countries now forced to manage BT, it is essential to develop methods for accurate prediction of BT risk in space and time.

Prediction of where and when disease might spread involves three main steps (Rogers and Randolph 2003). First, the pathogen and its routes of transmission must be identified; secondly, the patterns of disease in space and time must be recorded in relation to the environment. Finally, it is imperative to understand the dynamic processes of transmission that ultimately determine the observed patterns.

During previous BT epidemics in the Mediterranean Basin, the identity of the vector, *C. imicola,* was determined by periodic local vector surveillance in the infected areas (Mellor et al. 1983; Jennings, Boorman and Ergun 1983; Boorman and Wilkinson 1983; Boorman 1986) in combination with virus isolations from wild-caught adult *Culicoides* (Mellor et al. 1990; Mellor and Pitzolis 1979). Following the advent of GPS technology, spatio-temporal patterns of *Culicoides*-borne virus transmission and *Culicoides* abundance have been recorded more systematically within Geographical Information Systems (GIS) and compared over extensive areas at a fine resolution. These new analytical tools retrospectively supported the role of *C. imicola* in BTV transmission in Morocco and Iberia (Rawlings et al. 1997; Baylis et al. 1997; Capela et al. 2003). At a local scale, the relative roles of *C. imicola* and novel *Culicoides* vectors in BTV transmission in Sicily have recently been investigated (Torina et al. 2004). Vector and disease information can now be integrated with information about the environment, including both ground-based weather-station and remotely sensed (RS) climate variables, within the same geographical framework. Statistical models have been developed, at different spatial scales, to elucidate the relationship between environmental factors and vector *Culicoides* presence in sampled locations to permit prediction of the distribution of BTV and *Culicoides* in unsampled locations. This paper reviews the relatively short history of GIS and RS for prediction of BT risk in space and time in the Mediterranean. We show that RS climate variables can be used to predict the wide-scale distribution of *C. imicola*, with thermal requirements being particularly important at this species' northern range limit. Lessons learned in the development of statistical models can direct us towards a strategy for dynamic biological or process-based models that are much more versatile for disease prediction (Rogers and Randolph 2003).

Wide-scale determinants of *Culicoides* distribution

Climate models based on weather-station data

A preliminary attempt to relate the distribution of BTV and vector *Culicoides* to environmental factors at a continental scale was made by Sellers and Mellor (1993) and was based on the thermal requirements for BTV transmission over winter. BTV probably has no long-term vertebrate reservoir or trans-ovarial transmission (Mellor, Boorman and Baylis 2000). Thus persistence between years should only be possible where adult *Culicoides* vectors are present year-round and are of sufficient abundance and competence to permit continual host-midge cycling of BTV over winter (Mellor and Boorman 1995). Sellers and Mellor (1993) found an average daily maximum temperature of the coldest month of 12.5ºC across locations where BTV persisted in Turkey over the winters of 1977-1978 and 1978-1979. The 12.5ºC isotherm for the average daily maximum temperature of the coldest month of the year was then superimposed on the distribution of outbreaks and *Culicoides* across the Mediterranean. This isotherm broadly delineated the areas where adult *C. imicola* could survive year round and hence where overwintering of BTV was possible.

Wittmann, Mellor and Baylis (2001) showed that the Mediterranean distribution limits of *C. imicola* could be broadly predicted from a model of this species' thermal requirements. These authors compared historic (1931-1960) monthly weather-station-derived temperature, saturation deficit, rainfall variables and altitude in sites in Iberia where *C. imicola* was known to be present versus those where it was known to be absent. The resultant logistic regression model correctly predicted *C. imicola* distribution at 83% of sites in Iberia and included the average temperature of the coldest and the warmest month and the number of months with mean temperature ≥ 12.5°C but did not include any rainfall variables. The predicted distribution for *C. imicola* (Figure 2, see Colour pages elsewhere in this book) showed broad correspondence to the current distribution limits, indicated by the red line in Figure 1 (see Colour pages elsewhere in this book).

Why are RS climate databases useful for prediction of the distributions of vector *Culicoides*?

In the search for predictors of the distributions of a range of vectors, climatic databases have been superseded by RS databases derived from the Advanced Very High Resolution Radiometer (AVHRR) on the National Oceanic and Atmospheric Administration's (NOAA) meteorological satellites (Hay et al. 2000; Rogers and Randolph 1991; Rogers et al. 1997; Rogers 2000; Randolph 2000; Hendrickx et al. 2001). From RS imagery, continuous layers of environmental information can be derived at high spatial (8 km by 8 km and 1 km by 1 km) and temporal resolutions (10-day cloud-free images are produced). This information, in contrast to ground-based weather-station data, requires no interpolation for extensive prediction across environments not sampled on the ground. Weather-station data may seem easier to interpret biologically, but processing of RS imagery from different spectral channels produces variables that are highly relevant to insect microhabitats, namely: Normalized Difference Vegetation Index (NDVI), Middle Infra-Red Reflectance (MIR), Land Surface Temperature (LST) and Air Temperature (TAIR). For example, NDVI specifically measures chlorophyll abundance and light absorption, but is correlated with soil moisture, rainfall and vegetation biomass, coverage and productivity (Campbell 1996). MIR is correlated with the water content, surface temperature and structure of vegetation canopies (Boyd and Curran 1998). LST is a general index of the apparent environmental surface temperature (whether soil or vegetation) and TAIR is an estimate of the air temperature a few metres above the land surface (Goetz, Prince and Small 2000). The biological relevance of these variables can be further enhanced by Fourier-processing monthly time series of variables (Rogers, Hay and Packer 1996), a technique that extracts information about their seasonal cycles in terms of their annual, biannual and triannual cycles, each described by their phase and amplitude. This can be carried out for each pixel, so that geographical patterns in the seasonal variations of the environment can be related to vector distributions.

RS climate models for explanation and prediction of *C. imicola* distribution

Initially, at a national level, within Morocco, Baylis et al. (1998) found a significant positive relationship between *C. imicola* abundance in 22 sampled sites and annual minimum of NDVI. The best two-variable regression model of these authors also contained average wind speeds (to which abundance was negatively related, probably due to adverse affects of wind on adult activity rates, mortality and trap efficiency) and accurately predicted *C. imicola* abundance at a further 27 sampled sites in Iberia (Baylis and Rawlings 1998). Predictions were less accurate in northerly sites, where *C. imicola* was absent despite high NDVIs. This is again suggestive of thermal limitation of this species at its northern range margin.

Two studies have confirmed the relevance of NOAA RS climate variables at different resolutions (8 km – Baylis et al. 2001; 1 km – Tatem et al. 2003), for prediction of the distribution of *C. imicola* at a continental scale - across the Mediterranean Basin. With both of these models, sites in Iberia were divided into high, medium and low *C. imicola* abundance categories on the basis of surveillance data (a different set of such data being used in each case). Non-linear discriminant analysis was used to identify which of the 40 temporally Fourier-processed RS variables and altitude best divided the Iberian sites into the observed abundance categories. Coefficients from the models were then used to predict *C. imicola* abundance elsewhere across Europe and North Africa in unsampled pixels, with predictions restricted to pixels that were broadly similar in environment and climate to the original training set. These predictions are shown in Figures 3a and 3b. Both models are of high accuracy, correctly predicting *C. imicola* distribution in 93% and 87% of sites respectively, and predicted *C. imicola* presence in areas such as southern Iberia, northern Morocco, northern Algeria, northern Tunisia, Mallorca, Menorca, Sardinia, Sicily, Lazio, Tuscany and Calabria (in mainland Italy), the eastern and western edges of mainland Greece, Lesbos, Rhodes, western Turkey, Syria and Cyprus. In the absence of fine-scale surveillance data from the northern edge of the *C. imicola* range, these models also highlight countries or provinces where BT has recently occurred, but where *C. imicola* is predicted to be rare or absent. Such information supports the involvement of novel vector species of *Culicoides* in BTV transmission in many geographical locations during the current epidemic, e.g. in Croatia, Bosnia-Herzegovina, Kosovo, Serbia, Montenegro, Macedonia, Bulgaria and north-west Greece.

The predicted distribution of *C. imicola* from Tatem et al. (2003) corresponds particularly well with the new observed northern distribution limit of *C. imicola* (Figure 1, see Colour pages elsewhere in this book), including pixels near Barcelona, the southern coast of France in Alpes-Maritimes (J. Delacolle pers. comm., http://blue-tongue.cirad.fr/) and the northwest coast of Italy. Neither model predicts the recently observed presence of *C. imicola* in southern Switzerland (Ariane Cagienard pers. comm.), suggesting that the thermal requirements of this species in some marginal populations may differ from those further south or that the Swiss finding is based upon wind-borne vagrants. In addition, the effect of recent climatic changes on the expansion of *C. imicola* in Europe may not have been captured in these analyses since they were based only upon RS variables derived from NOAA imagery from 1982 to 1994. The training set of sites used by Tatem et al. (2003) were located only in Portugal whilst those used by Baylis et al. (2001) were spread across Iberia and in Morocco. However, the finer resolution of imagery available to Tatem et al. (2003) and the larger number of trap sites meant that this model was based upon a wider range of climatic or environmental conditions across both *C. imicola*-suitable and *C. imicola*-unsuitable areas. In turn, this model could be used to predict the potential distribution of *C. imicola* across a much larger proportion of pixels in the Mediterranean, i.e. in Figure 3b (see Colour pages elsewhere in this book) the grey, unpredictable areas are much less extensive than in Figure 3a (see Colour pages elsewhere in this book). This illustrates the importance of defining the relationship between vector abundance and climate on the basis of large vector surveillance data sets and up-to-date, fine-resolution imagery, extending across a wide range of environmental conditions.

What is the biological basis for the relationship between *C. imicola* abundance and NDVI?

The single most important remotely sensed predictor of *C. imicola* abundance in both models was the timing of the annual peak of vegetation abundance (i.e. NDVI), which is itself related to soil moisture levels. In Portugal, between 2000 and 2002, *C. imicola* occurred in high abundance where the NDVI peaked in mid-March but was rare or absent where the NDVI peaked in late April (Tatem et al. 2003). It is essential to consider the biological basis for these relationships with NDVI, i.e. what NDVI-correlated, environmental factor is determining vector distribution and abundance on the ground? The most robust ecological explanations are those founded on demographic processes (births and deaths), whose rates determine population performance (Randolph 2000). Since *C. imicola* breeds in wet, organically rich soil and mud (Braverman, Galun and Ziv 1974; Braverman 1978), recruitment to the population in spring will depend on early availability of moist breeding habitat and temperature-dependent immature development and survival rates. In some areas, the number of completed generations in summer and thus the annual total of recruitment may be increased by such early availability of breeding sites. Vegetation abundance and NDVI in spring will similarly increase with early availability of moist soil conditions, hence the relationship between the timing of the annual peak of NDVI and *C. imicola* abundance.

RS climatic determinants of distribution differ between *Culicoides* vectors

However, a recent study of the distributions of both *C. imicola* and potential novel vector *Culicoides* across 268 sites in Sicily has revealed that the RS climatic determinants of distribution are species-specific, presumably due to the differing life-history requirements of different species of *Culicoides* (Purse et al. 2004). This is indicated by the different rank and order of climatic variables added to the discriminant, presence–absence model for each potential vector (models were developed from 1km by 1km NOAA data as in Tatem et al. (2003) and are shown in Table 1). The distributions of the *C. obsoletus* group and *C. newsteadi* were predicted by temperature variables (LST, MIR and TAIR). *C. obsoletus*, a northern Paleoarctic species on the southern margin of its range in Sicily, preferred warmer, less variable thermal regimes whilst *C. newsteadi,* a southern Paleoarctic species, was associated with high values of MIR and TAIR. The distributions of *C. pulicaris* and *C. imicola* were determined mainly by NDVI. *C. pulicaris,* a wet soil and bog breeding species, was associated with high, stable, levels of moisture (high, less variable NDVI) for optimal survival and development. These species-specific models produced strikingly different predicted distributions when extrapolated to unsampled environments in mainland Italy (Figure 4, see Colour pages elsewhere in this book), which, should they prove accurate, will have important implications for disease prediction, surveillance and control. For example, the predicted continuous presence of *C. pulicaris* along the Appenine Mountains, from north to south Italy, suggests BTV transmission may be possible in a large proportion of this region. Thus traditional seasonal transhumance between mountainous *C. imicola*-free areas and the coast may not be as safe as had been suggested by Conte et al. (2003) since it could provide a mechanism for hand-over of BTV between the traditonal vector (*C. imicola*) and the novel vector (*C. pulicaris*) (Mellor and Boorman 1995). *C. obsoletus*, another potential vector, is predicted to be widespread across Italy, including areas where *C. pulicaris* is predicted to be absent or rare, i.e. along the Adriatic coast and in Tuscany, and further increases the area of Italy at risk of BTV incursion. Consequently, predictive risk maps for BT derived entirely from the distribution of the main European vector, *C. imicola*, will omit extensive regions at risk of transmission via other vector species.

Table 1. The first four of ten variables, ranked in order of importance, which best allocated Sicilian trap sites to the observed *Culicoides* species presence–absence classes (Purse, unpublished data)

Rank	*C. obsoletus*	K	*C. newsteadi*	K	*C. pulicaris*	K	*C. imicola*	K
1	LST mean	0.24	MIR mean	0.26	NDVI mean	0.42	LST tri-ann. phase	0.04
2	LST variance	0.32	LST ann. amp.	0.30	NDVI tri-ann. amp.	0.47	MIR tri-ann. phase	0.26
3	MIR bi-ann. amp.	0.38	TAIR min.	0.37	NDVI variance	0.50	NDVI ann. phase	0.45
4	TAIR min.	0.41	LST min.	0.39	LST variance	0.48	NDVI mean	0.49

Key: K = Kappa value for the model at the step when the variable was added; LST = land surface temperature; NDVI = Normalized Difference Vegetation Index; MIR = Middle Infrared; TAIR= air temperature xm above ground; DEM = altitude derived from Digital Elevation Model; amp. = amplitude; ann. = annual; bi-ann. = bi=annual; tri-ann = tri-annual.

Local-scale determinants of *Culicoides* distribution

Models of *Culicoides* abundance incorporating RS correlates of temperature and moisture have successfully predicted the countries and regions at risk of BT. However, these models perform only moderately well when validated at a finer scale, for example at a farm level. For example, the model of Baylis et al. (2001) successfully predicted the *C. imicola* abundance category of only 51.4% of those sites in Portugal sampled after the training set, in 2000 and 2001 (Capela et al. 2003). The Sicilian model of *C. imicola* distribution (Purse et al. 2004), previous RS climate models (Baylis et al. 2001; Tatem et al. 2003) and a model based on interpolated weather-station data (Conte et al. 2003) all predict *C. imicola* to be much more widely distributed across Sicily than is observed to be. It is probable that in Sicily the restricted distribution of *C. imicola* is caused by environmental factors other than climatic ones – factors that may influence its breeding requirements. For example, a negative relationship has been found between *C. imicola* abundance and soil sandiness in South Africa (Baylis, Meiswinkel and Venter 1999). Similarly, Calistri and Caporale (2003) suggest that the porous, freely draining volcanic soils with a poor moisture content that predominate in Sicily are unsuitable as *C. imicola* breeding sites.

Being dependent on the rate of recruitment from breeding sites, *Culicoides* population sizes are highly heterogeneous at a local scale, and will vary in response to host and breeding-site factors in addition to climatic ones. This is likely to be reflected in significant variation in the risk of BTV transmission at a local scale. The size and quality of breeding sites may depend on soil type, slope of terrain, rate of dung removal from animal holdings and availability of water sources – irrigation pipes and channels, leaky taps etc. Host variables that may affect vector biting rates include the number and type of livestock and ease of access to them (e.g. Meiswinkel, Baylis and Labuschagne 2000). Thus, some factors that affect important parameters of the BTV transmission cycle (e.g. recruitment rate and biting rate) will not be measurable by RS, even using fine-resolution imagery (e.g. SPOT or MODIS). Although data collection can be expensive and time-consuming, it is imperative to determine the relative role of climate and farm-level factors at a local scale. Such local processes may contribute to the distribution of BTV and *Culicoides* at broad scales, and, if unaccounted for, produce inaccuracies in broad-scale predictive models.

Future directions

Improvements to statistical models

Errors in BT risk maps based on statistical models of vector abundance may arise for several reasons, one of which is that the input data may be wrong or inaccurate. Given that adult vector *Culicoides* activity and trap efficiency can depend on daily climatic conditions, the estimate of vector abundance per site should be based on several catches made during the peak of *Culicoides* abundance (Baylis and Rawlings 1998). Also, given the species-specific climatic requirements of different *Culicoides* vectors, the distribution of each potential vector species should be modelled individually. In addition, for extrapolation across wide geographic areas and accurate determination of the relationship between vector abundance and climate, the model training set should include observations across a wide range of environmental and climatic conditions, preferably across the entire geographic range of the vector. The use of finer-scale RS data such as that derived from MODIS imagery (0.5 km) will provide a more accurate assessment of climatic factors. The statistical models reviewed here and the wide range in vector seasonal incidence between countries (Mellor, Boorman and Baylis 2000) indicate that the climatic requirements of *C. imicola* and other vectors may vary across their ranges. When constructing continental-scale models, regional heterogeneity in eco-climatic conditions and the response of *Culicoides* vectors to them can be accounted for using ecozonation (Hendrickx et al. 1999). This involves the division of pixels into clusters of environmental similarity prior to analysis and the development of a separate model for each eco-zone.

Why are biological process-based models of BT risk required and how can they be developed?

Rogers and Randolph (2003) pointed out that risk maps based on statistical models often indicate larger areas ‘at risk’ than are known to be affected by the disease at present, because a vector or disease will not occupy all ‘suitable’ habitats. Similarly, BTV does not occur across the entire distribution of *C. imicola, C. obsoletus* and *C. pulicaris* in the Mediterranean Basin and may not depend solely on the abundance of these vectors but also on spatio-temporal variations in other factors. Firstly, BTV transmission is seasonal being related to the timing of peak abundance of *Culicoides* vectors in different areas (Mellor, Boorman and Baylis 2000). There is compelling evidence that vector competence for BTV varies widely between different vector species of *Culicoides* and even between populations of the same species, for example, for *C. obsoletus* in Europe (Simon Carpenter, unpublished data). This may be due either to genetic differences in susceptibility to infection between populations (Tabachnick 1991) or to differences in the climatic regimes to which populations are subjected (affecting infection rates, rates of virogenesis or the efficacy of infection barriers) or to both (Mellor, Boorman and Baylis 2000). Additionally, whether BTV titres develop to transmissible levels in the vertebrate host and the vector depends also on the strain or type of BTV circulating. Indeed, most ruminant hosts of BTV do not develop clinical signs of infection, and so, generally speaking, evidence of BT in a vertebrate population is a very poor indicator of the level of BTV transmission. Where a species of *Culicoides* is in the process of expanding its range, its populations may not permanently occupy all suitable habitats, due to isolation from source populations. For example, in New South Wales, Australia, near the southern range limit of the BTV vector *C. brevitarsis*, colonization of marginal sites occurs seasonally by passive wind dispersal when climatic conditions are suitable for population multiplication, but population establishment only occurs if conditions also facilitate survival over winter. Bishop, Barchia and Spohr (2000) found that between-population movements of *C. brevitarsis* over 8 years depended on wind direction, wind speeds (allowing adult activity) and temperature during vector movements.

Given these considerations, only biological-process-based models of *Culicoides* population dynamics and BTV transmission dynamics will permit integration of predictions between spatial scales (local and continental) and time scales (ecological and evolutionary). Given the high-temporal resolution of RS data, the same data that are used to describe the patterns of *Culicoides* or BTV abundance can be correlated with key transmission-cycle parameters in intensive studies, and used to generate predictions extensively (Rogers and Randolph 2003). Considering the vector and virus surveillance data available from the current BT epidemic, there is potential to model seasonal rates of *Culicoides* population change in relation to RS climate variables, as has already been done successfully for ticks and tsetse flies (Rogers 2000; Randolph 2000). This would enable prediction of the geographical and annual variation in the timing of spring appearance and winter disappearance of adult vectors and BTV, and the location of any seasonal dispersal from overwintering foci. The distribution and timing of new outbreaks could be examined in affected countries in the first year of the current epidemic, i.e. when clinical signs are severe and most BTV transmission is likely to be manifested as outbreaks. Rates of movement of BTV in space and time could then be correlated with wind speed and direction data and RS climate data to determine the factors affecting the probability of dispersal of infected midges during an epidemic. Collection of appropriate data on other parameters of the transmission cycle, especially biting rates, via the design of intensive field experiments should be considered a priority.

References

Baylis, M., 2002. The re-emergence of bluetongue. *The Veterinary Journal,* 164 (1), 5-6.

Baylis, M., Bouayoune, H., Touti, J., et al., 1998. Use of climatic data and satellite imagery to model the abundance of *Culicoides imicola*, the vector of African horse sickness virus, in Morocco. *Medical and Veterinary Entomology,* 12 (3), 255-266.

Baylis, M., El Hasnaoui, H., Bouayoune, H., et al., 1997. The spatial and seasonal distribution of African horse sickness and its potential *Culicoides* vectors in Morocco. *Medical and Veterinary Entomology,* 11 (3), 203-212.

Baylis, M., Meiswinkel, R. and Venter, G.J., 1999. A preliminary attempt to use climate data and satellite imagery to model the abundance and distribution of *Culicoides imicola* (Diptera: Ceratopogonidae) in southern Africa. *Journal of the South African Veterinary Association,* 70 (2), 80-89.

Baylis, M. and Mellor, P.S., 2001. Bluetongue around the Mediterranean in 2001. *Veterinary Record,* 149 (21), 659.

Baylis, M., Mellor, P.S., Wittmann, E.J., et al., 2001. Prediction of areas around the Mediterranean at risk of bluetongue by modelling the distribution of its vector using satellite imaging. *Veterinary Record,* 149 (21), 639-643.

Baylis, M. and Rawlings, P., 1998. Modelling the distribution and abundance of *Culicoides imicola* in Morocco and Iberia using climatic data and satellite imagery. *Archives of Virology,* 14 (Suppl.), 137-53.

Bishop, A.L., Barchia, I.M. and Spohr, L.J., 2000. Models for the dispersal in Australia of the arbovirus vector, *Culicoides brevitarsis* Kieffer (Diptera: Ceratopogonidae). *Preventive Veterinary Medicine,* 47 (4), 243-254.

Boorman, J., 1986. Presence of bluetongue virus vectors on Rhodes. *Veterinary Record,* 118 (1), 21.

Boorman, J.P. and Wilkinson, P.J., 1983. Potential vectors of bluetongue in Lesbos, Greece. *Veterinary Record,* 113 (17), 395-396.

Boyd, D.S. and Curran, P.J., 1998. Using remote sensing to reduce uncertainties in the global carbon budget: the potential radiation acquired in the middle infrared wavelenghts. *Remore Sensing Reviews,* 16, 293-327.

Braverman, Y., 1978. Characteristics of *Culicoides* (Diptera, Ceratopogonidae) breeding places near Salisbury, Rhodesia. *Ecological Entomology,* 3 (3), 163-170.

Braverman, Y., Galun, R. and Ziv, M., 1974. Breeding sites of some *Culicoides* species (Diptera, Ceratopogonidae) in Israel. *Mosquito News,* 34 (3), 303-308.

Calistri, P. and Caporale, V., 2003. Bluetongue in Italy: a brief description of the epidemiological situation and the control measures applied. *Bulletin de l'Office International des Epizooties* (2), 15-17.

Campbell, J.B., 1996. *Introduction to remote sensing*. 2nd edn. Taylor & Francis, London.

Capela, R., Purse, B.V., Pena, I., et al., 2003. Spatial distribution of *Culicoides* species in Portugal in relation to the transmission of African horse sickness and bluetongue viruses. *Medical and Veterinary Entomology,* 17 (2), 165-177.

Caracappa, S., Torina, A., Guercio, A., et al., 2003. Identification of a novel bluetongue virus vector species of *Culicoides* in Sicily. *Veterinary Record,* 153 (3), 71-74.

Conte, A., Giovannini, A., Savini, L., et al., 2003. The effect of climate on the presence of *Culicoides imicola* in Italy. *Journal of Veterinary Medicine. B. Infectious Diseases and Veterinary Public Health,* 50 (3), 139-147.

Goetz, S.J., Prince, S.D. and Small, J., 2000. Advances in satellite remote sensing of environmental variables for epidemiological applications. *In:* Hay, S.I., Randolph, S.E., Rogers, D.J., et al. eds. *Remote sensing and geographical information systems in epidemiology*. Academic Press, San Diego, 217-243. Advances in Parasitology no. 47.

Hay, S.I., Omumbo, J.A., Craig, M.H., et al., 2000. Earth observation, geographic information systems and *Plasmodium falciparum* malaria in sub-Saharan Africa. *In:* Hay, S.I., Randolph, S.E., Rogers, D.J., et al. eds. *Remote sensing and geographical information systems in epidemiology*. Academic Press, San Diego, 173-215. Advances in Parasitology no. 47.

Hendrickx, G., De La Rocque, S., Reid, R., et al., 2001. Spatial trypanosomosis management: from data-layers to decision making. *Trends in Parasitology,* 17 (1), 35-41.

Hendrickx, G., Napala, A., Dao, B., et al., 1999. A systematic approach to area-wide tsetse distribution and abundance maps. *Bulletin of Entomological Research,* 89 (3), 231-244.

Jennings, M., Boorman, J.P. and Ergun, H., 1983. *Culicoides* from Western Turkey in relation to bluetongue disease of sheep and cattle. *Revue d'Elevage et de Médecine Vétérinaire des Pays Tropicaux,* 36 (1), 67-70.

Linto, Y.M., Mordue Luntz, A.J., Cruickshank, R.H., et al., 2002. Phylogenetic analysis of the mitochondrial cytochrome oxidase subunit I gene of five species of the *Culicoides imicola* species complex. *Medical and Veterinary Entomolgy,* 16 (2), 139-146.

Meiswinkel, R., Baylis, M. and Labuschagne, K., 2000. Stabling and the protection of horses from *Culicoides bolitinos* (Diptera: Ceratopogonidae), a recently identified vector of African horse sickness. *Bulletin of Entomological Research,* 90 (6), 509-515.

Mellor, P.S., Boned, J., Hamblin, C., et al., 1990. Isolations of African horse sickness virus from vector insects made during the 1988 epizootic in Spain. *Epidemiology and Infection,* 105 (2), 447-454.

Mellor, P.S. and Boorman, J., 1995. The transmission and geographical spread of African horse sickness and bluetongue viruses. *Annals of Tropical Medicine and Parasitology,* 89 (1), 1-15.

Mellor, P.S., Boorman, J. and Baylis, M., 2000. *Culicoides* biting midges: their role as arbovirus vectors. *Annual Review of Entomology,* 45, 307-340.

Mellor, P.S., Boorman, J.P.T., Wilkinson, P.J., et al., 1983. Potential vectors of bluetongue and African horse sickness viruses in Spain. *Veterinary Record,* 112 (10), 229-230.

Mellor, P.S. and Pitzolis, G., 1979. Observations on breeding sites and light-trap collections of *Culicoides* during an outbreak of bluetongue in Cyprus. *Bulletin of Entomological Research,* 69 (2), 229-234.

Mellor, P.S. and Wittmann, E.J., 2002. Bluetongue virus in the Mediterranean Basin 1998-2001. *The Veterinary Journal,* 164 (1), 20-37.

Murray, M.D., 1991. The seasonal abundance of female biting-midges, *Culicoides brevitarsis* Kieffer (Diptera: Ceratopogonidae), in coastal south-eastern Australia. *Australian Journal of Zoology,* 39 (3), 333-342.

Purse, B.V., Tatem, A.J., Caracappa, S., et al., 2004. Modelling the distributions of *Culicoides* bluetongue virus vectors in Sicily in relation to satellite-derived climate variables. *Medical and Veterinary Entomology,* 18 (2), 90-101.

Randolph, S.E., 2000. Ticks and tick-borne disease systems in space and from space. *In:* Hay, S.I., Randolph, S.E., Rogers, D.J., et al. eds. *Remote sensing and geographical information systems in epidemiology*. Academic Press, San Diego, 217-243. Advances in Parasitology no. 47.

Rawlings, P., Pro, M.J., Pena, I., et al., 1997. Spatial and seasonal distribution of *Culicoides imicola* in Iberia in relation to the transmission of African horse sickness virus. *Medical and Veterinary Entomolgy,* 11 (1), 49-57.

Rogers, D.J., 2000. Satellites, space, time and the African trypanosomiases. *In:* Hay, S.I., Randolph, S.E., Rogers, D.J., et al. eds. *Remote sensing and geographical information systems in epidemiology*. Academic Press, San Diego, 129-171. Advances in Parasitology no. 47.

Rogers, D.J., Hay, S.I. and Packer, M.J., 1996. Predicting the distribution of tsetse flies in West Africa using temporal Fourier processed meteorological satellite data. *Annals of Tropical Medicine and Parasitology,* 90 (3), 225-241.

Rogers, D.J., Hay, S.I., Packer, M.J., et al., 1997. Mapping landcover over large areas using multispectral data derived from NOAA-AVHRR: a case study of Nigeria. *International Journal of Remote Sensing,* 18 (15), 3297-3303.

Rogers, D.J. and Randolph, S.E., 1991. Mortality rates and population density of tsetse flies correlated with satellite imagery. *Nature,* 351 (6329), 739-741.

Rogers, D.J. and Randolph, S.E., 2003. Studying the global distribution of infectious diseases using GIS and RS. *Nature Reviews: Microbiology,* 1 (3), 231-237.

Savini, G., Goffredo, M., Monaco, F., et al., 2003. Transmission of bluetongue virus in Italy. *Veterinary Record,* 152 (4), 119.

Sellers, R.F. and Mellor, P.S., 1993. Temperature and the persistence of viruses in *Culicoides* spp. during adverse conditions. *Revue Scientifique et Technique de l'Office International des Epizooties,* 12 (3), 733-755.

Tabachnick, W.J., 1991. Genetic control of oral susceptibility to infection of *Culicoides variipennis* with bluetongue virus. *American Journal of Tropical Medicine and Hygiene,* 45 (6), 666-671.

Tatem, A.J., Baylis, M., Mellor, P.S., et al., 2003. Prediction of bluetongue vector distribution in Europe and north Africa using satellite imagery. *Veterinary Microbiology,* 97 (1/2), 13-29.

Taylor, W.P., 1986. The epidemiology of bluetongue. *Revue Scientifique et Technique de l'Office International des Epizooties,* 5 (2), 351-356.

Torina, A., Caracappa, S., Mellor, P.S., et al., 2004. Spatial distribution of bluetongue virus and its *Culicoides* vectors in Sicily. *Medical and Veterinary Entomolgy,* 18 (2), 81-89.

Wittmann, E.J. and Baylis, M., 2000. Climate change: effects on *Culicoides*-transmitted viruses and implications for the UK. *The Veterinary Journal,* 160 (2), 107-117.

Wittmann, E.J., Mellor, P.S. and Baylis, M., 2001. Using climate data to map the potential distribution of *Culicoides imicola* (Diptera: Ceratopogonidae) in Europe. *Revue Scientifique et Technique de l'Office International des Epizooties,* 20 (3), 731-740.

13

Discussion and epilogue

Pim Martens [#] *and Willem Takken* [##]

Global change is likely to affect human and animal health, as shown by the preceding chapters. Malaria was chosen as the principle example to demonstrate the complex interactions that may affect a vector-borne disease: the mosquito vector, the parasite, human host, climate, topography, vegetation, aquatic habitat, demography, health care, socio-economic status, to name several aspects that all affect the epidemiology of the disease and, hence, the incidence of morbidity and mortality. Had we chosen to focus this workshop on dengue, or leishmaniasis or human African trypanosomiasis, the overall conclusions would not have been much different. There is no doubt that environmental change caused by anthropogenic activities will impact vector-borne diseases severely. The uncertainty of these effects is the level of change we shall witness, and over what time scale we might expect these changes to occur.

Until recently it seemed difficult to provide concrete evidence that environmental change had caused a significant positive impact on a vector-borne disease, leading to increased disease. The reverse has been reported many times when because of deliberate changes in the environment, malaria was eradicated from entire regions. For example, malaria has been eradicated from Italy by drainage of the Pontine marshes near Rome (Bruce-Chwatt and De Zulueta 1980). By contrast, in this workshop evidence was provided that deforestation in the Brazilian Amazon region has caused a huge increase in the number of malaria cases (Cruz Marques 1987). This was caused by deliberate deforestation causing mosquito breeding sites and simultaneous human immigration into the area. The Brazilian government brought this epidemic under control only in recent years by a dedicated programme for malaria control in many of the affected areas (Massarani 2001, Takken et al., this volume).

It is widely accepted that on a global scale malaria is increasing rather than decreasing. This is caused not so much by enhanced environmental conditions as by increasing poverty and lack of resources to combat the disease (Barat et al. 2004; Malaney, Spielman and Sachs 2004). From simulation models and field evidence presented in this workshop it is evident that without mitigating measures, the world's malaria situation will further deteriorate. Environmental conditions are seen as the main reason for this estimate. It is unlikely that socio-economic status of malaria-affected countries will improve soon, and thus it is these countries that will experience the burden of global environmental change concerning malaria: environmental degradation, accelerated by increased precipitation, and higher temperatures favour malaria mosquitoes and parasites. (This is one additional reason why protocols designed to limit global change, such as the Kyoto protocol, need to be adhered to and implemented as soon as possible.) Hence it is expected that the rate of transmission will increase in these countries, which are often too poor to provide adequate health care. By contrast, and contrary to many suggestions, malaria is unlikely to return to

---

[#] International Centre for Integrative Studies, Maastricht University, The Netherlands
[##] Laboratory of Entomology, Wageningen University, The Netherlands

W. Takken, P. Martens and R. J. Bogers (eds.),Environmental Change and Malaria Risk, 137-138.

former endemic countries because the high standard of living and environmental measures prevent a return of malaria endemicity, even under climate change (Rogers and Randolph 2000).

The workshop also discussed two other vector-borne diseases, dengue and blue tongue. The former is a human disease, the latter affects sheep and cattle. Both are transmitted by blood-feeding insects, which are dependent on environmental conditions for their distribution and survival. Dengue was endemic in Southeast Asia until 50 years ago, when it began to spread to other parts of the globe. Today, the virus is found in many parts of Asia, Africa and Central and South America, including the Caribbean. Dengue is transmitted by bites of the infectious yellow-fever mosquitoes, *Aedes aegypti*. Blue tongue was previously restricted to Africa, where it may cause high mortality in sheep and cattle. The virus is transmitted by biting midges of the genus *Culicoides*. In the last decade, both dengue and blue tongue have shifted their distribution into 'new' geographic areas. The reasons for this are not very well understood, other than that it is ascribed to increased trade and human and animal traffic. However, this explanation is unsatisfactory, as hundreds of such migrations 0occur annually, and fortunately most do not survive the arrival in a new, hostile, ecosystem. Yet dengue and blue tongue seem to prosper in their newly acquired habitats. It is tempting to relate this to the effects of global change, and although we agree that this is very plausible, detailed studies are required to identify the principle reasons for these shifts in distribution.

To summarize, we can conclude that global environmental changes will cause both increases and decreases in the areas suitable for vector-borne diseases transmission, but many factors will determine the vulnerability of individual countries for these disease. To elaborate more accurately on future vulnerability of populations – especially those that live in high-risk areas – will be necessary, from both an environmental and a socio-economic point of view.

References

Barat, L.M., Palmer, N., Basu, S., et al., 2004. Do malaria control interventions reach the poor? A view through the equity lens. *American Journal of Tropical Medicine and Hygiene,* 71 (2 Suppl.), 174-178.

Bruce-Chwatt, L.J. and De Zulueta, J., 1980. *The rise and fall of malaria in Europe: a historico-epidemiological study*. Oxford University Press, Oxford.

Cruz Marques, A., 1987. Human migration and the spread of malaria in Brazil. *Parasitology Today,* 3 (6), 166-170.

Malaney, P., Spielman, A. and Sachs, J., 2004. The malaria gap. *American Journal of Tropical Medicine and Hygiene,* 71 (2 Suppl.), 141-146.

Massarani, L., 2001. Brazilian Amazon nearly halves malaria cases in a year. *Bulletin of the World Health Organization,* 79 (12), 1171-1171.

Rogers, D.J. and Randolph, S.E., 2000. The global spread of malaria in a future, warmer world. *Science,* 289 (5485), 1763-1766.

List of participants

Billingsley, Peter	School of Biological Sciences, University of Aberdeen, Aberdeen, UK
Boëte, Christophe	Laboratory of Entomology, Wageningen University and Research Centre, Wageningen, The Netherlands
Bradley, David	London School of Hygiene and Tropical Medicine, London, UK
De Tarso R. Vilarinhos, Paulo	Diretoria de Vigilância Ambiental, Brasília DF, Brazil
Dos Santos, Fatima	Fundação Nacional de Saúde, Porto Velho, Rondônia, Brazil
Gimnig, John	Malaria Epidemiology Branch, Division of Parasitic Diseases, Centers for Disease Control and Prevention, Atlanta GA, USA
Hoshen, Moshe	MALSAT, Liverpool School of Tropical Medicine, Liverpool, UK
Knols, Bart	IAEA, Vienna, Austria
Koenraadt, Sander	Laboratory of Entomology, Wageningen University and Research Centre, Wageningen, The Netherlands
Leemans, Rik	Analyses of Environmental Systems Group, Wageningen University and Research Centre, Wageningen, The Netherlands
Lindsay, Steve	School of Biomedical Sciences, University of Durham, Science Laboratories, Durham, UK
Martens, Pim	ICIS, University of Maastricht, Maastricht, The Netherlands
Purse, Beth	Institute for Animal Health, Surrey, UK
Sankoh, Osman A.	INDEPTH Network, Accra, Ghana
Sauerborn, Rainer	University of Heidelberg, Department of Tropical Hygiene and Public Health, Heidelberg, Germany
Schneider, Petra	Laboratory of Medical Microbiology, Nijmegen University, Nijmegen, The Netherlands
Takken, Willem	Laboratory of Entomology, Wageningen University and Research Centre, Wageningen, The Netherlands
Thomas, Chris	Institute of Ecosystem Science, School of Biological and Biomedical Sciences, University of Durham, Science Laboratories, Durham, UK
Van Lieshout, Michael	ICIS, University of Maastricht, Maastricht, The Netherlands

Wageningen UR Frontis Series

1. A.G.J. Velthuis, L.J. Unnevehr, H. Hogeveen and R.B.M. Huirne (eds.): *New Approaches to Food-Safety Economics*. 2003
ISBN 1-4020-1425-2; Pb: 1-4020-1426-0
2. W. Takken and T.W. Scott (eds.): *Ecological Aspects for Application of Genetically Modified Mosquitoes.* 2003
ISBN 1-4020-1584-4; Pb: 1-4020-1585-2
3. M.A.J.S. van Boekel, A. Stein and A.H.C. van Bruggen (eds.): *Proceedings of the Frontis workshop on Bayesian Statistics and quality modelling*. 2003
ISBN 1-4020-1916-5
4. R.H.G. Jongman (ed.): *The New Dimensions of the European Landscape.* 2004
ISBN 1-4020-2909-8; Pb: 1-4020-2910-1
5. M.J.J.A.A. Korthals and R.J.Bogers (eds.): *Ethics for Life Scientists*. 2004
ISBN 1-4020-3178-5; Pb: 1-4020-3179-3
6. R.A. Feddes, G.H.de Rooij and J.C. van Dam (eds.): *Unsaturated-zone Modeling*. Progress, challenges and applications. 2004 ISBN 1-4020-2919-5
7. J.H.H. Wesseler (ed.): *Environmental Costs and Benefits of Transgenic Crops.* 2005 ISBN 1-4020-3247-1; Pb: 1-4020-3248-X
8. R.S. Schrijver and G. Koch (eds.): *Avian Influenza.* Prevention and Control. 2005 ISBN 1-4020-3439-3; Pb: 1-4020-3440-7
9. W. Takken, P. Martens and R.J. Bogers (eds.): *Environmental Change and Malaria Risk.* Global and Local Implications. 2005
ISBN 1-4020-3927-1; Pb: 1-4020-3928-X
10. L.J.W.J. Gilissen, H.J. Wichers, H.F.J. Savelkoul and R.J. Bogers, (eds.): *Allergy Matters.* New Approaches to Allergy Prevention and Management. 2006
ISBN 1-4020-3895-X; Pb: 1-4020-3896-8
11. B.G.J. Knols and C. Louis (eds.): *Bridging Laboratory and Field Research for Genetic Control of Disease Vectors.* 2006
ISBN 1-4020-3800-3; Pb: 1-4020-3799-6
12. B. Tress, G. Tress, G. Fry and P. Opdam (eds.): *From Landscape Research to Landscape Planning*. Aspects of Integration, Education and Application. 2006
ISBN 1-4020-3979-4; Pb: 1-4020-3978-6
13. J. Hassink and M. van Dijk (eds.): *Farming for Health.* Green-Care Farming Across Europe and the United States of America. 2006
ISBN 1-4020-4540-9; Pb: 1-4020-4541-7

springer.com