Host Community Interfaces: The Wildlife-Livestock

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Contents

Barriers Among Hosts as Opportunities for Pathogens

Living host organisms are part of biological communities, and there are boundaries, i.e., epidemiological interfaces, across which pathogens can be transmitted among these communities (Hassell et al. 2017). For instance, some pathogens are shared between wild and domestic animals, many others are maintained by wildlife reservoirs, or in other cases by livestock and other domestic species causing major outbreaks in wildlife, e.g., ungulates and carnivores. The different epidemiological

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interfaces are characterized by the community of species on both sides of boundaries (or compartments; human, domestic animals, and wildlife), and the habitats and resources where these communities live and interact (Huyvaert et al. 2018). Most disease-causing organisms in nature are capable of infecting multiple hosts (Cleaveland et al. 2001; Haydon et al. 2002) and are thus referred to as multi-host pathogens. Some multi-host pathogens are maintained solely in multiple wildlife species. It is, however, remarkable that among domesticated animal species, roughly 77% of pathogens of livestock and 90% of pathogens of domestic carnivores are known to be multi-host pathogens (Cleaveland et al. 2001).

An epidemiological interface is therefore established among wildlife, domestic animals, and human compartments in an abiotic environment (a potential reservoir itself) (Haydon et al. 2002). *These "barriers" between compartments constitute opportunities for horizontal transmission between species and a new space for evolution, emergence, and maintenance of pathogens.* The epidemiological and ecological connections among host species are dynamic, and new edges and paths continuously break host species barriers (Han et al. 2016). Pathogens must evade their potential new host's immune system to successfully infect it and, therefore, they normally infect more readily host species whose internal environment is similar to that of the original carrier (Pepin et al. 2010). Subsequently, shared pathogens have the opportunity to expand in the newfound compartment. Some pathogens benefit from the existing conditions at the interface and become endemic, spilling easily back, and forth between compartments, e.g., bovine tuberculosis at the wildlife livestock interface (Barasona et al. 2017).

A recent event in geological times over the natural history of Earth (see Chapter "Natural and Historical Overview of the Animal Wildlife-Livestock Interface") has determined the various animal interfaces we see today. The livestock compartment only appeared after human domestication gave rise to three new animal interfaces: human–domestic, wildlife–domestic, and their juxtapositions as human–domestic–wildlife. More recently, anthropogenic effects, especially during the last century, and the subsequent changes in urban areas, farming, food systems, and natural ecosystems, have led to increased exposure of human and animal populations to novel pathogens and the establishment of newly shared diseases, which are considered emergent (Lindahl and Grace 2015). Some examples are swine and avian influenza or African swine fever (ASF) (Gavier-Widen et al. 2015), and more recently, Coronavirus (CoVs) disease 2019 (COVID-19), which likely jumped from infected wild animals to humans resulting in millions of infected people worldwide in just a few months (Morens et al. 2020). Humans, animals (both domestic and wild), and ecosystems are tightly linked, more than ever, and this also affects global health. This vision is increasingly evident and widely accepted by the scientific community. However, the implementation of certain practices (e.g., surveillance) and actions (ranging from local to holistic) under this principle across the animal health, human health, and environment sectors remain a challenge (Berezowski et al. 2019; Savory 2016). From the disease perspective, the risk of unexpected spillover events resulting from interactions between wildlife and domestic populations (in all their varieties and conditions) trying to adapt to a changing world has never been so real.

In modern times, epidemiology and preventive medicine, as medical disciplines of human and animal health, have provided information and a better understanding of how diseases have changed the history of humanity and helped to shape the world. However, they are mostly biased toward the human component. Some examples of such diseases include bubonic plague, cholera, tuberculosis, smallpox, and coronaviruses, which have induced humans to develop and implement control measures to mitigate their spread. The focus of researchers and animal and public health policymakers at the interfaces involving animal compartments is relatively recent, particularly for wild species, and is an area of increasing concern (Fig. 1). Medicine, veterinary science, conservation biology, and other disciplines now converge because *these interfaces are hotspots for pathogen transmission, maintenance, and emergence*. We cannot look at any compartment in isolation from others, as they are ineludibly and functionally linked through ecological and evolutionary processes underlying host jumps by pathogens. Broadly, the factors causing emergence can be defined as ecological or adaptive (Pepin et al. 2010). If the main factor causing emergence is ecological, and adaptation is not required for the jump to occur, the cause of the host jump is known as an ecological driver. An adaptive driver requires a genetic change in the pathogen for its emergence in a new host, although an ecological driver is likely to be involved in this situation as well. An adaptive driver occurs when a selective pressure operates in the new host population after cross-species transmission has occurred, and consequently, pathogen genotypes capable of successful spread and maintenance in the new host species are selected over other genotypes that fail. The adaptive genetic changes leading to adaptation after a host jump can originate either in the new host or in the reservoir host. For instance, surveillance, molecular epidemiology, bioinformatics, and microbiology have shown that SARS-CoV host jumps require viral adaptation. During the early spread of SARS-CoV in humans in 2003, although numerous independent cases of SARS-CoV transmission from reservoir hosts occurred, most died out after just a few human cases, indicating that the introduced strain was not fit for human-to-human transmission (Zhao 2007; Li 2008; Sheahan et al. 2008). Unfortunately, a different outcome is obviously occurring with the present COVID-19 pandemic.

Regardless of transmission mode, the process by which a pathogen moves from one host population (or environmental reservoir) to another is referred to as spillover. This phenomenon depends on complex bidirectional interactions among hosts, pathogen communities, and environments (Alexander et al. 2018). Spillback consists of transmitting infection back to a potential host, which may occasionally play a crucial epidemiological role, for example, serving as maintenance hosts (Haydon et al. 2002, Fig. 6). Disease spread and patterns of transmission at the wildlife-livestock interface are largely due to the effect of the increase in global human population and demand for protein and other commodities. This has led to habitat destruction, bringing livestock closer to wild populations, favoring conditions for interaction among compartments and disease transmission (Chua 2003). Today, increasing globalization has brought additional risk factors that add

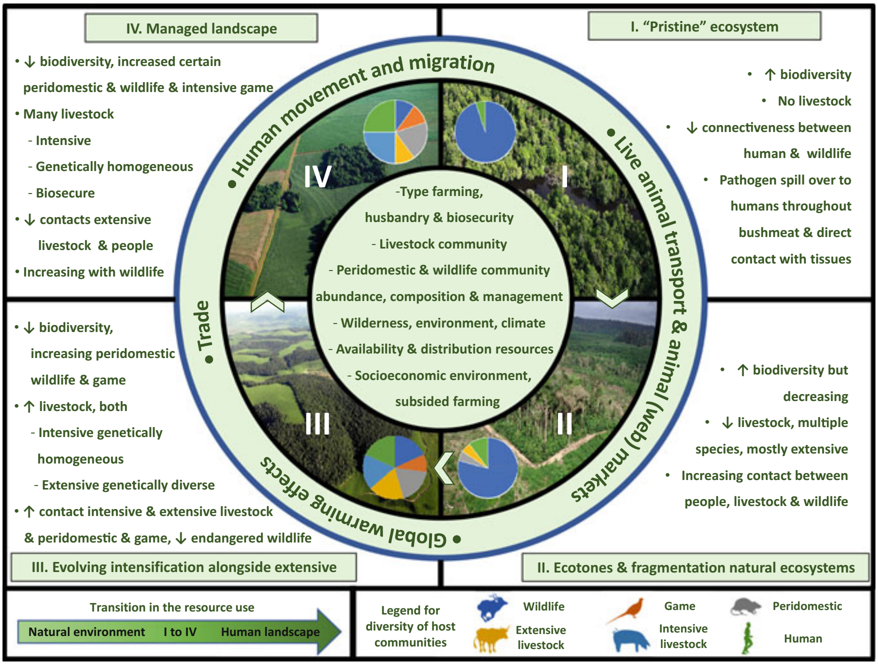


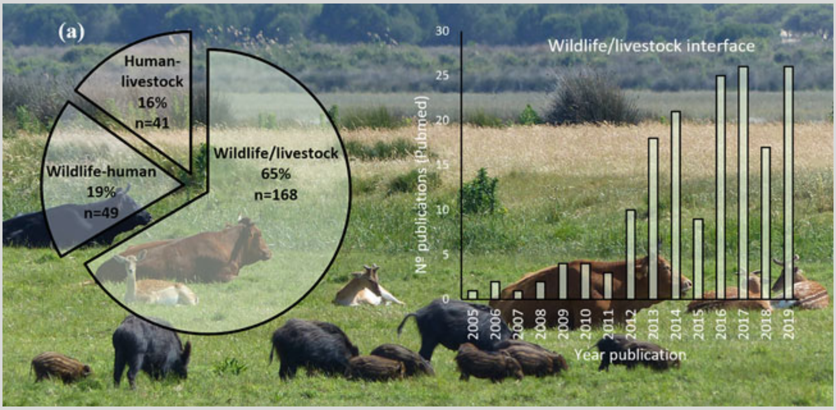
Fig. 1 Increasing human population growth, the subsequent increasing demand for food production (including increased meat and animal product consumption), and the conversion of natural habitats to agricultural land use have all altered interactions between domestic and wild animal populations. This figure depicts the wildlife-livestock-human interface characteristics according to the transition from pristine natural continuous habitats to highly human-modified landscapes (level of biodiversity, livestock farming, connectedness between communities at the interface, based on Jones et al. 2013). The characteristics of the wildlife-livestock interface (inner circle) are fundamentally responsible for local patterns of distribution of hosts, vectors, pathogens, and risks for interaction among these elements and subsequent disease spillover at the interface, with subsequent emergence and/or establishment. The sectorial graphs inside each interface typology indicate the relative abundance of host communities. The outer circle denotes regional and global drivers associated with risk for regional or global expansion, connecting elements from situations characterized by pathogens exclusive to wildlife in the absence of livestock and local pastoral systems with transcontinental-global circulation of pathogens

complexity and allow for very distant spread very quickly, i.e., human movements (such as tourism, refugees, and international workforce), legal and illegal transportation of live animals and animal products, both domestic and wild (e.g., bushmeat), increasing complexity of live animal markets, and the impacts of climate change (Beltran-Alcrudo et al. 2019). This has resulted in an unprecedented emergence and spread of many diseases that in livestock have spilledover to wild populations and have spilledback to livestock. The consequences of pathogen transmission at the interfaces vary from local to global, from affecting livelihoods in a limited region to worldwide pandemics and economic crises (Rhyan and Spraker 2010; Costard et al. 2017). Our planet is changing quickly, with natural habitats transforming into agricultural land, increasing competition of wildlife and livestock for natural resources, and huge biodiversity loss that threatens the contribution of nature to human livelihoods (Jori et al. 2019). The ever-increasing role of these drivers of change suggests future exponential growth in the interactions among wildlife, domestic animals, and humans, which has important implications including additional disease emergence at the interfaces.

"Transboundary," "shared," "emergent," "pandemic," these worrying words are increasingly adjectivizing the term "disease" if we read recent press, scientific literature and reports from international organizations dealing with the control of infectious diseases in humans and animals. This reinforces the increasing concern being given to emergent public health pathogens, followed by those impacting economy and trade, with those thought to only affect ecology or wildlife conservation coming third in importance. By April 2020, the global spread of African Swine Fever had reached well over half of the world's pork markets (China alone is half), causing great economic losses due to pig mortality, control measures, and trade disruptions. Not long ago, this virus was confined to wild suids in Africa. While drafting this introductory chapter, the COVID-19 virus emerged, quickly turning into a pandemic with unprecedented economic and social consequences. The causative agent, named as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is closely related to two major previous zoonotic epidemics: SARS (severe acute respiratory syndrome coronavirus, SARS-CoV or SARS-CoV-1) and MERS (Middle East respiratory syndrome-related coronavirus or MERS-CoV). COVID-19, likely of bat origin, emerged at the animal–human interface found at live animal markets in Wuhan, China. Research has concluded that the lineage from which COVID-19 came has been circulating among bats for decades and is likely to include other viruses with the ability to infect humans (Boni et al. 2020). The magnitude of this pandemic, while certainly huge in proportions, remains to be estimated under its multiple angles, i.e., not just purely from the public health perspective, but in terms of its mounting economic and social impacts. What is clear is that humanity did not learn the lessons from previous disease emergencies. The current pandemic increases our certainty that a systems-wide holistic perspective on pathogen dynamics at the wildlife-livestock-human interface based on interdisciplinary approaches to the examination of biological, ecological, economic, and social drivers of pathogen emergence is required (Jones et al. 2013; Baum et al. 2017; Harrison et al. 2019). It stresses the need to understand, predict, prevent, and control disease emergence at their main origin, the animal interfaces. Unfortunately, historically, One Health international interventions have been the exception. While the world is now directly responding to counteract the effects of COVID-19 on human health and the economy, the international community must apply previous valuable lessons and act in advance to prevent or address future disease emergences. This snapshot of human history will be remembered because, maybe, it could have been prevented.

In summary, *human activities have created new interfaces and opportunities for pathogen emergence and spread, and therefore, the holistic understanding of ecological, epidemiological, social, cultural, and economic mechanisms that operate at animal interfaces must contribute to transdisciplinary integrative approaches* *to prevent and control disease*. Thus, we must step up research cooperation to ensure we can make the best coordinated decisions for similar future challenges in the interest of humanity. Recent disease emergence at animal interfaces, and their spread around the world, also illustrate shortcomings in the monitoring of current wildlife diseases and the surveillance of wildlife populations. We need to detect early warning signs at the origin of pathogen emergence so they can be halted before they lead to dramatic local, regional or global consequences. The increasing risk of pathogen emergence demands we anticipate as far ahead as possible when and where pathogen spillover could occur, which is likely to be more cost effective than adaptation (Pike et al. 2014; Wu et al. 2017) to mitigate consequences at the wildlife-livestock-human interfaces. As we write, most of humanity is trying to reduce contact rates through social distancing and implementing drastic trade and travel restrictions in an effort to contain the spread of COVID-19. This sudden appearance, the third significant coronavirus to emerge in 17 years, together with the high prevalence and virus diversity in bats, suggests that these viruses will likely cross species boundaries again.

Box 1 Bibliographical Analysis of Indexed Publications Referring to Different Animal Interfaces



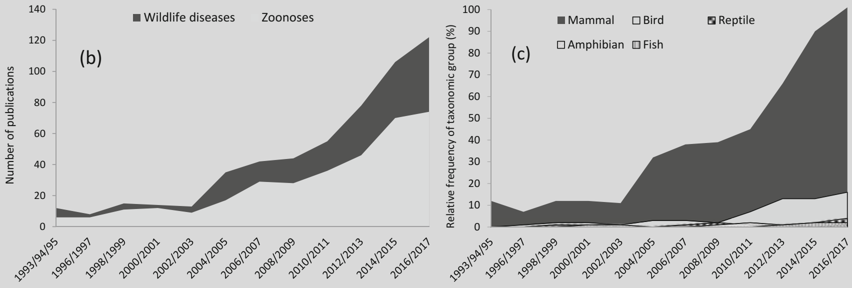
(**a**) Bibliographical analysis of publications indexed in PubMed (*n*° retrieved and proportion of the total) published during the last 15 years. The search terms were "human–wildlife interface"; "human–livestock interface", and "wildlife-livestock interface" (in both orders, PubMed accessed on Mar 25, 2020). The temporal trend (2015–2019) for the wildlife-livestock interface (*n*° publications year) is shown on top right. Image: J.J. Negro ©. Next (**b–d**) we reviewed research works retrieved through a search in Scopus, PubMed, and Web of Science platforms (1**b**, **c** and **d**) using a combination of the search terms "wildlife," "disease," and "long-term" by the Boolean operator "AND" to obtain only the intersection. Selected articles dated from Jan 1993 to Dec

(continued)

Box 1 (continued)

2017 with a study period ≥4 consecutive years and sampling a minimum of 10 individuals per year (studies based on passive surveillance, clinical trials, or which selected for the study experimental animals or captive wildlife populations were excluded). (**b**) Temporal trend of long-term publications (numbers, 1993–2017) on wildlife diseases ($n = 544$), indicating which diseases are zoonoses ($n = 344$) and disease shared only at the wildlife-livestock interface. (**c**) Temporal trend of long-term publications on wildlife diseases ($n = 544$), indicating which host taxa were addressed. (**d**) Representativeness of pathogen agents and host species addressed by long-term studies (period 1993–2017) by continent. The research productivity of each continent ($n°$ of papers) is shown.

Source of graphs and analysis: The authors of the chapter and Patricia Barroso (see Barroso et al. 2020).



The bibliographical analysis of papers published during the last 20 years (**a**) revealed a bias toward more studies assessing or referring to the interface established between wildlife and livestock (Box 1a). The number of long-term publications dated from 1993 to 2017 showed a marked growing temporal trend, which reflects both the overall increased scientific production, but also the increased awareness about wildlife relevant to the epidemiology of shared pathogens, which may have consequences on public health or other aspects. From 2002 to 2003 is when the increase became more obvious, and zoonoses were acquiring importance. Several significant zoonotic events took place around these years. In 2003, a new strain of highly pathogenic avian influenza (HPAI-H5N1) spread throughout Asia, Africa, and Europe (Ellis et al. 2004; Sturm-Ramirez et al. 2004) and at the same time, the first Coronavirus outbreak in humans, SARS, emerged in China (Anderson et al. 2004). In addition, during these years there was a greater economic outlay in veterinary measures for the control of animal disease outbreaks such as foot and mouth disease and influenza viruses (OIE and FAO 2012). The impact of these events on human health and the global economy gave rise to the promotion of

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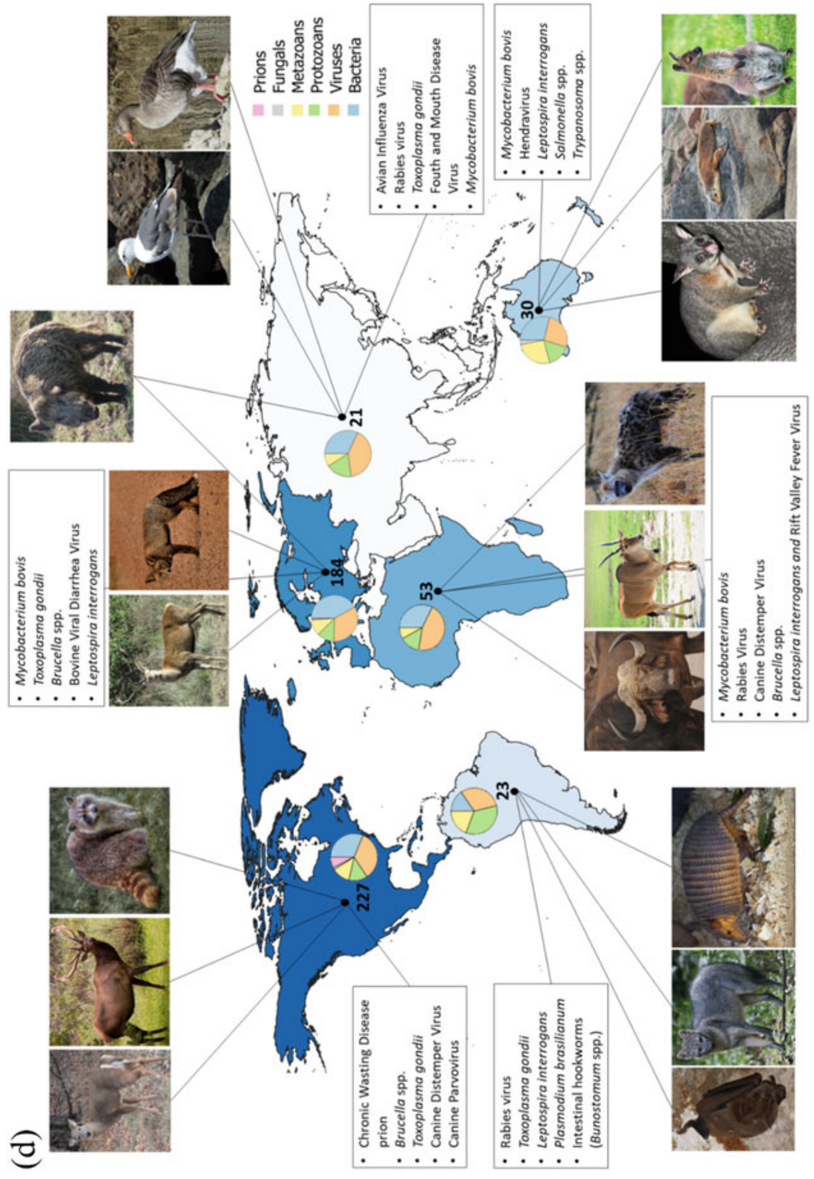
(d)
Prions
Fungals
Metazoans
Protozoans
Viruses
Bacteria
227
23
184
53
21
30
• Chronic Wasting Disease prion
• Brucella spp.
• Toxoplasma gondii
• Canine Distemper Virus
• Canine Parvovirus
• Rabies virus
• Toxoplasma gondii
• Leptospira interrogans
• Plasmodium brasilianum
• Intestinal hookworms (Bunostomum spp.)
• Mycobacterium bovis
• Toxoplasma gondii
• Brucella spp.
• Bovine Viral Diarrhea Virus
• Leptospira interrogans
• Mycobacterium bovis
• Rabies Virus
• Canine Distemper Virus
• Brucella spp.
• Leptospira interrogans and Rift Valley Fever Virus
• Avian Influenza Virus
• Rabies virus
• Toxoplasma gondii
• Fouth and Mouth Disease Virus
• Mycobacterium bovis
• Mycobacterium bovis
• Hendravirus
• Leptospira interrogans
• Salmonella spp.
• Trypanosoma spp.

Box 1 (continued)
research on animal diseases through greater availability of funding for research.

Approximately 25% of total publications referred to more than one pathogen. Figure c indicates that viruses were the most frequently addressed pathogens (40.4%), followed by bacteria (33.3%) and parasites (23%, protozoan and metazoan), whereas prions and fungi were less frequently studied (3% of the articles). Interestingly, most of the pathogens included in the ranking are zoonotic, evidencing that the wildlife reservoir constitutes a major public health problem, leading to increased awareness of governments on the role of wildlife in the epidemiology of shared infections. Mammals (91.4%), followed by birds (6.1%), and reptiles (1.2%), were the most studied hosts. Amphibians (0.8%) and fish (0.5%), though, were scarcely represented in the literature. Ungulates were the most investigated group (40%) due to their role as reservoir hosts of more than 250 species of zoonotic pathogens (Woolhouse and Gowtage-Sequeria 2005), and their increasing expansion and numbers mainly in developed countries. Carnivores were the next most studied group (31%) due to conservation reasons.

Cervids (including red deer, white-tailed deer, roe deer, fallow deer, and elk, all native to the Northern Hemisphere) and wild boar were addressed in more than half of the studies. Research production of long-term studies on wildlife diseases was mainly located in developed countries in the North Hemisphere; North America (41.2%; $n = 229$) and Europe (34.9%; $n = 190$). However, in Africa, Oceania, South America, and Asia long-term studies were far less common (less than 20%, $n = 125$ of the total reviewed publications). The largest proportion of the retrieved articles in North America, Europe, Africa, and Asia addressed viruses, whereas in Oceania and South America it was metazoan and protozoan parasites, respectively. It is worth noting the limited number of long-term studies addressing the epidemiological role of wildlife species, such as bat, as reservoirs of Coronaviruses.

The Wildlife-Livestock Interface

The livestock compartment only appeared after human domestication of wildlife occurred, which gave rise to three new animal interfaces, human–domestic, wildlife–domestic, and human–domestic–wildlife (Chapter “Natural and Historical Overview of the Animal Wildlife-Livestock Interface”). Since then, the wildlife-livestock interfaces are the physical space in which wild and livestock species overlap in range and potentially interact, a continuum of direct and indirect contact between free-ranging wildlife and domestic livestock (Huyvaert et al. 2018). Indirect contact can occur through exposure to infected materials (such as aerosols or any excretion product such as feces, urine, saliva, or ocular or nasal discharge) or through environmental reservoirs (such as soil, water, or forage). Actually, the disease interface between wildlife and livestock is usually through indirect contacts (Kock 2005; Kukielka et al. 2013). However, as we will elaborate below, the delocalization of such interfaces is becoming a common characteristic in modern times. *For shared infections at the wildlife-livestock interface, at least one wild and one livestock host species are infected, and at least one of them maintains the infection.*

The wildlife-livestock interface in all its dimensions is complex and susceptible to changing along with natural landscapes, but especially with increasing human intervention (Jori et al. 2019). The characteristics of the interface are the result of a complex interplay between natural ecosystems within which livestock production takes place (Ostrom 2009). Thus, the wildlife-livestock interface is synonymous with the wildlife-livestock-human interface because the focus is on the interaction between "natural" and "human-influenced" sub-systems (Chapter "Characterization of Wildlife-Livestock Interfaces: The Need for Interdisciplinary Approaches and a Dedicated Thematic Field"). The description of prevalent pathogens in a range of hosts is still a necessary first step in many epidemiological systems (for instance, identifying new viruses in animals and quickly determining their emergent potential is a key way to assess global health threats). However, understanding ecological, epidemiological, and socioeconomic complexity requires an in-depth characterization of underlying processes at this dynamic space of transition and contact between wild and domestic compartments. As an ecological and epidemiological entity, the wildlife-livestock interface has a proper ecosystem with its specific niches, which allows for the emerging, maintaining, and sharing of pathogens (Chapter "The Ecology of Pathogens Transmission at the Wildlife-Livestock Interface: Beyond Disease Ecology, Towards Socio-Ecological System Health"). This interface often defines the suitability for risk distribution of shared pathogens, for instance, the map of anthrax suitability is strongly associated with the elephant–livestock interface (Walsh et al. 2019). The nature and potential for interaction among wildlife, livestock, and human compartments and their characteristics are schematized in Fig. 1 in terms of biodiversity, livestock farming, and connectedness between communities at the interface (based on Jones et al. 2013). It evolves from complex continuous habitats with rich trophic structure and wild host communities throughout a gradient of forest loss. Many human intervened landscapes consist of a mosaic of crops, pasture, and urban areas with natural islands, which has resulted in extremely modified trophic structures, land degradation, and simplified host communities, with increasing presence of peridomestic (e.g., Abrahão et al. 2009) and managed wildlife (Gortazar et al. 2006). Host communities across gradients, though, are difficult to classify (see Fig. 2) relative to the degree of human impact on wildlife. For instance, peridomestic and more anthropic wildlife have adapted to human environments and can promote the transmission of pathogens between other wildlife and livestock or humans, since they circulate both in and around farms. We note (see preface) that we also differentiate between livestock and pets, and this book focuses on the former. There are relevant differences on how the interfaces with wildlife are established, respectively. However, pets are often involved in epidemiological cycles or relevance to livestock and humans, and they are mentioned in different examples throughout this book (e.g., dogs). In the case of livestock, the transition from free ranging, extensive, backyards, outdoor, and intensive is also a gradient. The four main scenarios (consider this as a simplification) indicative of a gradient of the wildlife-livestock-human interfaces where pathogens emerge or are shared include (1) "pristine" ecosystems with human incursion to harvest wildlife and other resources; (2) ecotones and fragmentation of natural ecosystems (farming edges, human incursion to harvest natural resources, i.e., wood); (3) evolving landscapes characterized by rapid intensification of agriculture and livestock, alongside extensive and backyard farming; and (4) managed landscapes that consist of islands of intensive farming, highly regulated, and farmland converted to recreational and conservancy uses (Jones et al. 2013). Urban and periurban areas are increasingly present in these scenarios. Local and regional drivers associated with risk for emergence of pathogens are connected worldwide, ranging from situations characterized by wildlife exclusive pathogens in the absence of livestock and local pastoral systems to transcontinental-global circulation of pathogens to transcontinental-global interconnected food animal production systems and markets. For instance, much of the meat from the wildlife trade is sold through online platforms (Nijman et al. 2019). Illegally imported wildlife products in passengers' luggage, particularly meat, must also be considered. Wildlife, which provides essential services, and pathogens, are both indisputably essential components of ecosystems. However, the importance of wildlife to ecosystems and human communities, while being the natural reservoirs of many relevant economic and zoonotic pathogens, presents a challenge for disease control. Particular attention is needed in developing regions with high biodiversity, where emerging infectious diseases (EIDs) are most likely to arise, and where substantial losses to agricultural production greatly impact national economies. The interplay of ecological and human factors (socioeconomic and anthropogenic) increases opportunities for pathogen spillover, such as with neglected tropical diseases.

During recent decades there has been an increasing amount of research on animal interfaces (Box 1). An extensive literature search looking at infectious diseases shared at the *wildlife-livestock interface* was performed by Wiethoelter et al. (2015). By combining wildlife, livestock, disease, and geographic search terminology they assessed the interest by the scientific community in infectious diseases at the interface, characterizing animal species, regions involved, and trends over time. Results should not be confused with incidence of diseases or absolute occurrence of interfaces. Their analysis of almost 16,000 publications dated from 1912 to 2013 showed an increasing trend over time, a progressive shift from parasitic to viral diseases, and a majority being zoonoses. Most importantly, authors identified and characterized the major wildlife-livestock interfaces, showing that relatively few interfaces have been considered important from a disease ecology perspective. Of those, the bird–poultry interface was the most frequently cited worldwide, followed by the Artiodactyls–cattle and Carnivorans–cattle interfaces. However, the relative importance of interfaces varied among regions, reflecting local circumstances. As expected, the most frequent livestock species worldwide are represented in the top interfaces, i.e., the higher their abundance, the more they will contribute to disease transmission. Results also showed that interfaces between closely phylogenetically related and/or potentially cohabitant species were most frequent. The perceived importance of the order Chiroptera in emerging infectious diseases is not reflected yet in the number of publications on their interface with livestock. Funding plays a key role in shaping these results, with zoonoses and major disease epidemics, e.g., avian influenza, largely driving scientific interest. Wild animal hosts for shared pathogens have been vastly under-recognized because the majority of species have not been sampled at the level needed to detect shared pathogens, and many geographic regions lack adequate data. More basic research is needed at interfaces, to further characterize transmission pathways and specific roles of the involved species.

The *domestic* side of animal interfaces can be found on every continent on Earth. Even sled dogs have been used in Antarctica. Great diversity can be observed within and among livestock, environments, and management systems. Livestock producers living within the wildlife-livestock interface in many regions mostly practice pastoral farming as a sustainable management system. In *rangelands and other extensive production systems*, livestock are integrated into the ecosystem, and they have a variety of positive and negative impacts on soil, vegetation, biodiversity of plants, nutrient recycling, and native wildlife. Livestock have influenced the environment through coevolutionary history with plants and wildlife. Livestock and wildlife ecologically and epidemiologically interact because they share and/or compete for resources (water, food, cover). Often, livestock are relevant and sometimes even the most important source of food for wild carnivores and scavengers, with subsequent ecological and epidemiological connections (Vicente and Vercauteren 2019). On such livestock extensive systems, problems, or what humans sometimes call wildlife conflicts, arise in relation to competition, disease, and depredation. These conflicts stimulate subsequent human intervention at the livestock-wildlife interface. From the producer's perspective, in most cases, preserving wildlife communities (especially large vertebrate species) is incompatible with livestock farming and other agricultural activities because the associated costs are considered nonviable. Livestock husbandry, the provision of supplementary food and water, together with the persecution or prevention of wildlife occurrence, helps livestock to proliferate and/or be economically profitable. However, as they have similar needs, some of these resources are points of attraction for the remaining wildlife. Pathogens can become endemic at the interface ecosystem and especially once endemic free-ranging wildlife they can be difficult to eradicate, and spillover to livestock continues (Gortazar et al. 2007). Managers usually focus on separating livestock from wildlife, which, normally, can only be partially achieved (Barasona et al. 2013). Rangelands are integrated into natural ecosystems (see major particularities for each continent in the subsequent chapters), and the ecological and epidemiological consequences of management are not always direct and easily measurable. The effects of rangeland management on wildlife and ecosystems may vary depending on the composition of ecological communities but may produce cascading effects in terms of community composition, trophic relationships, and pathogen dynamics (Ostfeld et al. 2008; Becker et al. 2015; De Vos et al. 2016).

In recent decades, there has been an enormous expansion of livestock production, driven by increasing demand for animal source foods from a large part of the world's population. This has been linked with a change in livestock production systems. For instance, it is estimated that more than half of current global pork production and three-fourths of poultry meat is produced in *intensive systems* (Steinfeld et al. 2006). Developing countries especially, have accounted for the majority of this increase (Thornton 2010). The driving forces behind this growth have principally been human population growth and changes in dietary preferences associated mostly with increasing income and urbanization. There is increasing evidence (Jones et al. 2013) of the large effect of agricultural intensification and environmental changes on the risk of pathogen emergence, many zoonotic and/or for which there are epidemiological interactions between wildlife and livestock. There are two main paths associated with the increased risk of disease emergence at animal interfaces and subsequent zoonotic events. First, the most intensive production conditions involve crowding tens of thousands of animals in very close contact. Such intensive systems constitute the perfect breeding ground for pathogens to emerge, with high-density populations of generally low genetic diversity, which may favor increased transmission and adaptation in a given species (i.e., avian influenza in poultry). While intensive farms are associated with a lower number of people exposed to zoonoses (per animal unit) compared with extensive systems (e.g., mixed farming systems, which numerically dominate over the world), workers in intensive farms may be more exposed to animal pathogens compared with other people. In contrast to more extensive systems, and in spite of being more isolated from the external ecosystem, intensively produced animals live in closer contact with each other and the humans taking care of them. Intensification is also accompanied by more frequent movement of people and vehicles between farms, which further increases the risk of pathogen transmission. This risk can be reduced by employing effective sanitary management and biosecurity. In addition, it is also common that different production systems for a given livestock species, ranging from extensive to intensive, are connected. For instance, reproduction can be centralized and intensive with young stock then being shipped elsewhere to be reared or fattened in open-door or completely outdoors where wildlife is present (see Fig. 2 for the case of pigs). This provides human-mediated epidemiological links between different animal production systems and wildlife. The risks of pathogen spread from wildlife diseases also occur in chaotic scenarios such as in wet or live animal markets, which become an interface itself among living animals. This risk is exacerbated in such markets by the concentration and interconnectedness of recently trapped wildlife, wildlife that was reared in captivity, semi-domesticated wildlife, domestic animals, and humans. For instance, wet markets in urban areas of Asia are now recognized to be the primary locus of infection for highly pathogenic avian influenza (HPAI) H7N9, H5N1, SARS (Gilbert et al. 2014), and COVID-19.

On the other hand, the agricultural intensification and environmental change driven by expanding human activities stimulate the creation of new wildlife-livestock-human interfaces, sharing emergent pathogens. Anthropogenic environmental change and subsequent encroachment of human settlements and agriculture on

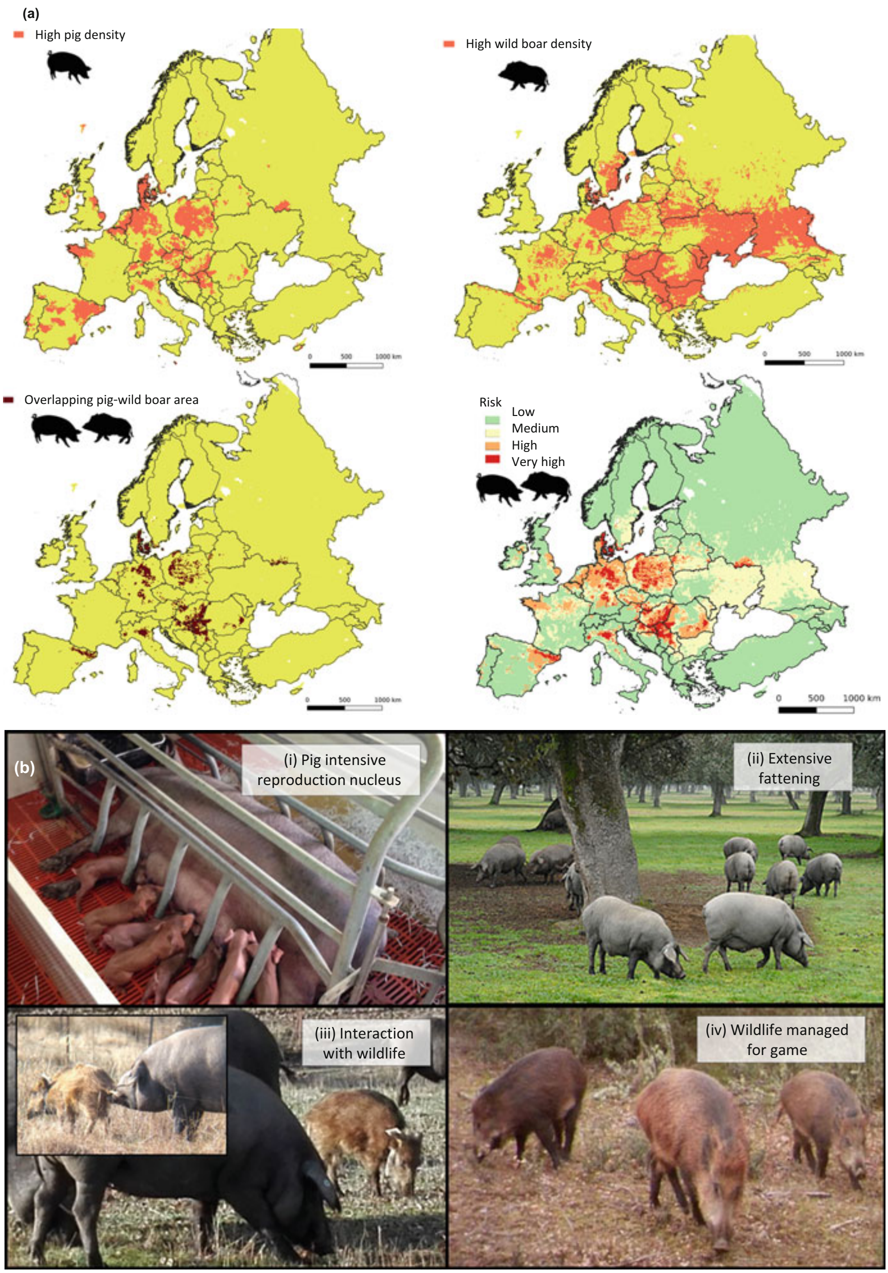

Fig. 2 (**a**) Predicted spatial wild boar–pig interface (irrespective of farming type) at the European scale (Enetwild consortium 2020 for more details). Top: Areas of high wild boar and domestic pig densities (ENETWILD 2020; Robinson et al. 2014). Bottom: Wild boar–domestic pig interface risk maps. Four risk categories that are defined from low to very high risk. (**b**) Example of interconnections between pig farming systems (intensive and extensive are linked) and the interface with wildlife (wild boar)

natural ecosystems have resulted in the expansion of ecotones (transition zones between adjacent ecological systems), where species and communities mix. This provides new opportunities for pathogen spillover, genetic diversification, and adaptation. Most recent emergent zoonoses involve both wildlife and livestock in their epidemiology, such as Nipah virus encephalitis. Growing demand for animal source foods has important implications for agricultural production systems and for producers in poor rural areas, where mostly mixed farming is practiced, i.e., intermediate, semi-intensive production systems, usually mid-sized family farms. As they need to adapt continuously to the changing environmental, social, economic, market and trade circumstances, farmers expand cultivated areas, encroach natural areas, intensify production and close integration of crops and livestock (Jones et al. 2013), often in proximity to wildlife. The two reported paths for pathogen emergence at animal interfaces indicate that assessing the complexity of risk at animal interfaces requires not only addressing different hosts and communities locally or interconnected throughout a given region, but also the more delocalized, scattered, and sparse risk factors that operate at long distances. The animal interfaces are not merely physical spaces where pathogens are passed between communities, but they are built of a number of linked epidemiological scenarios, which are highly determined by human ecology and socio-economy and their intricate complexity is increasing due to globalization. Not only pathogens, but also their associated burdens, such as antimicrobial resistance, are disseminated across interfaces (Ramey and Ahlstrom 2020). This reflection reinforces that the focus is on the interaction between "natural" and "human" sub-systems (Chapter "Characterization of Wildlife-Livestock Interfaces: The Need for Interdisciplinary Approaches and a Dedicated Thematic Field"), and we cannot disregard wildlife-livestock and wildlife-livestock-human interfaces.

The characterization of pathogen transmission events among animals and humans (the *human–animal interface*) remains an important scientific challenge. A recent review of the connections between human, animal, and environmental health revealed that at least 142 viral pathogens of mammalian origin cause disease in humans, i.e., animal to human direction (Johnson et al. 2020, Fig. 3). This list would grow if we considered other pathogens, such as parasites, bacteria, fungi, and prions. Even though livestock represent a small proportion of the total mammal biodiversity and their diseases are more commonly reported relative to wildlife, reports suggest that domesticated species are responsible for half of viral zoonoses. However, no data exist for most wild species. Overall, domesticated species, primates, rodents, and bats were identified as harboring more zoonotic viruses than other species groups. The highest proportion of zoonotic viruses were found among species in the orders Rodentia (61%), Chiroptera (30%), Primates (23%), Artiodactyla (21%), and Carnivora (18%). The only wild animals among the top 10 species in terms of detected zoonotic viruses were the house mouse (*Mus musculus*) and the black rat (*Rattus rattus*), both of which are comparable to domestic species since they most frequently occur in close association with humans.

As a group, domesticated mammals may host 50% of the zoonotic virus richness but represent only 12 species (Johnson et al. 2020). These figures reflect the

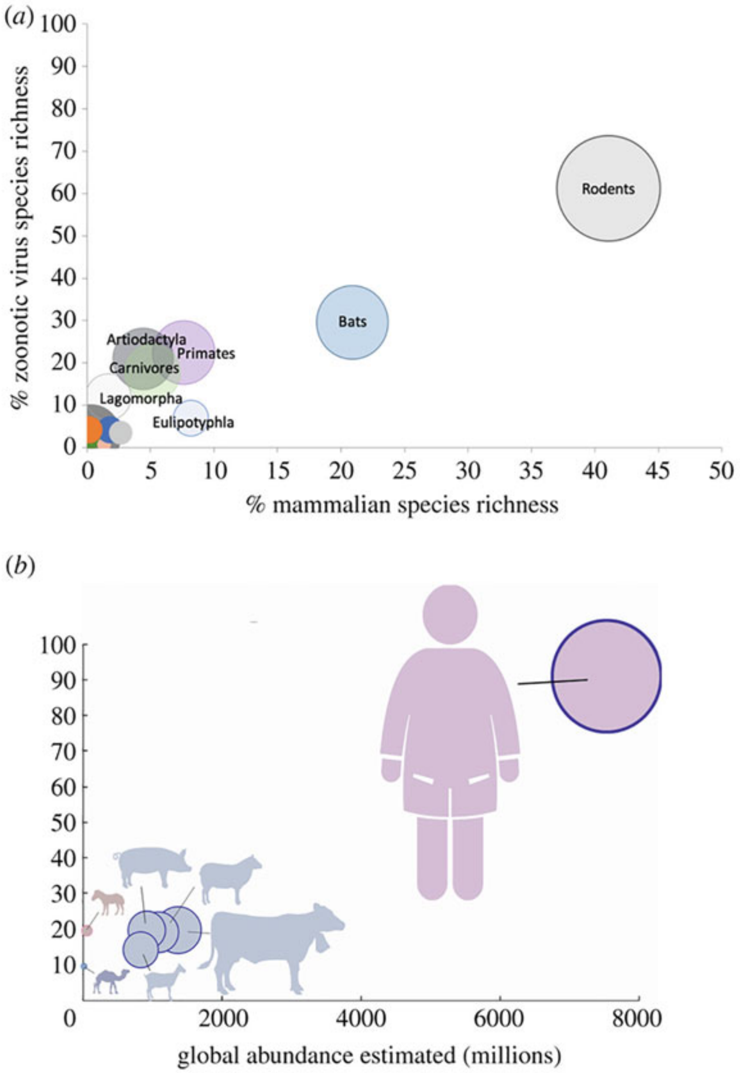

Fig. 3 Richness of zoonotic viruses found in mammalian hosts, by taxonomic order for wildlife and by species for domesticated animals and humans (reproduced from Johnson et al. 2020, under common creation license). (**a**) Zoonotic virus richness corresponding to species richness among wild mammalian orders. Area of the circles represents the proportion of zoonotic viruses found in species in each order out of the total number of zoonotic viruses among all mammalian species. (**b**) Zoonotic virus richness corresponding to estimated global abundance (in millions) for humans and domestic species. Species in (**a**) are colored according to the order in which they belong. Area of the circles reflects the estimated population size for that species relative to the other species shown

relevance of the wildlife-livestock interface (*stricto* sensu) to amplify and mediate as bridge host in the transmission of animal diseases from wildlife to humans, as has unfortunately been confirmed in recent emergences of zoonotic HCoVs. Domestic animals not only can suffer disease caused by wildlife-borne pathogens but may have important roles as intermediate hosts that enable pathogen transmission from natural wild hosts to humans or other animals. For instance, after spilling over from bats, swine acute diarrhea syndrome caused by coronavirus SADS-CoV (Zhou et al. 2018) caused a large-scale outbreak of fatal disease in pigs in China across four farms. Although there is no evidence of infection in humans, this case reveals the continuous threat to animal and human health and food production of wildlife diseases at the interface with livestock. Focusing on terrestrial mammals, the most species-rich orders contain the greatest diversity of zoonoses (Han et al. 2016). Groups with more zoonotic host species than expected for the richness of the clade include the ungulates (Artiodactyla and Perissodactyla), which comprise the majority of domesticated mammal species. Many more wild ungulates are closely related to domesticated livestock species with which humans are in regular close contact, which could facilitate successful transmission. Ungulate reservoirs of zoonotic pathogens have also been of particular interest because of high human contact rates through hunting and consumption over history. Recent work also shows that the time since domestication correlates positively with the number of zoonotic infections shared between ungulates and humans, and that species with the longest history of domestication not only carry more zoonotic pathogens, but may also transmit infection to a greater diversity of alternative host species (Morand et al. 2014). Wild ungulates cover a greater spatial range, for instance, than bats, and other orders of mammals, and a large proportion of species overlap in certain areas, such as Africa and Asia, establishing high levels of mixing with livestock. Some specific features of ungulate species are relevant to the wildlife-livestock interface, since they normally live in spatially discrete small family groups or in larger herds (up to many thousands), with intraspecific fusion-fission herd dynamics (e.g., Pays et al. 2007), which has epidemiological implications, i.e., opportunities for contact and transmission of infection between herds of a given species. Also, mixing or contact between animals or herds of different species and with livestock occurs (illustrated in Fig. 1), but less often. Under certain conditions of food scarceness, such as droughts or hard winters, indirect and direct contact increases at watering points or food locations, leading to increased pathogen transmission. Carnivores have regular contact with domestic species (e.g., dogs), providing an opportunity for human exposure (e.g., Packer et al. 1999). As for birds, particularly migratory, a relevant characteristic is their potential role as bridge hosts at wildlife-livestock-human interfaces, including emerging infections such as avian influenza viruses across wild bird–poultry interfaces (Chapter "The Ecology of Pathogens Transmission at the Wildlife-Livestock Interface: Beyond Disease Ecology, Towards Socio-Ecological System Health").

While addressing the study of diseases in domestic animals is relatively straightforward, it may be hampered in wildlife by pathogen detection limitations. Beyond the methodological limitations, the wildlife-livestock interface has often been neglected. This interface is an essential interplay among host species where disease spillover is largely under-reported, often even for zoonosis, such as in regions where people have limited access to healthcare. Monitoring trends in wildlife populations, large-scale surveillance efforts, and addressing the ecological and epidemiological study of the wildlife-livestock interface to identify epidemiologically relevant animal reservoirs are warranted to understand and prevent diseases of animal relevance, but also those potentially spreading to humans. Also, improved monitoring of livestock and large-scale trends are needed to depict interfaces and evaluate broad-scale risks, for which high-resolution data and discriminating among farming systems would be required. As illustrative of the need for better, harmonized, and standardized data in the livestock compartment, Fig. 2 suggests low reliability when predicting the wild boar–pig interface (irrespective of farming type) at European scale (Enetwild consortium 2020, www.enetwild.com).

Interfaces Among Host Communities: Questions, Theoretical Frameworks, and Approaches

Some questions that also concern the wildlife-livestock interface have, especially arisen in the present times characterized by a global health crisis that is mainly perceived as wildlife–human interface: what will be the next emergent pathogen at the interfaces? a virus? an RNA virus? what will be the role for pathogen emergence, maintenance, and spread within wildlife and livestock? can we predict and prevent pathogen emergence? how will human-induced rapid changes impact the capacity of host communities to adapt to pathogens and vice versa? We are challenged because our understanding of patterns, trends, and drivers associated with disease emergence at interfaces is in its infancy. The same is true about the persistence and transmission of pathogens.

There are essential knowledge gaps, which prevent us from better understanding and managing the dynamics of diseases at the wildlife-livestock interface. Primarily, the first step in many interfaces is to describe the hosts and their pathogens, their distributions and behavioral characteristics, and ultimately their epidemiological consequences. We must then work to comprehend the pathways and transmission rates among these compartments, and which effects pathogens exert at both population and community levels. Subsequently, we must recognize the effect of disease management efforts at the interface, and understand the prevalent socioeconomic and cultural environment, which is crucial to determine the success of disease mitigation strategies.

Some of the abovementioned questions are unfortunately in vogue as we are drafting this book because of the current COVID-19 global pandemic. However, general theoretical frameworks have been developed to understand the ecology, epidemiology, and response to the main drivers for multi-host multi-pathogen systems. Below we approach multi-host pathogen systems simply, though they are intrinsically complex, shaped by pathogen and host dynamics as well as evolutionary and environmental interactions. This basic approach can contribute to the necessary background for understanding ecological and epidemiological networks. For in-depth reading on the subject, several seminar books are available (e.g., Hudson et al. 2002; Ostfeld et al. 2010; Wilson et al. 2019). We also aim to project our current understanding to past scenarios (see Chapter "Natural and Historical Overview of the Animal Wildlife-Livestock Interface"), since the main drivers and mechanisms of wildlife disease ecology also apply. Retrospectively learning from the past will also provide a necessary perspective to address current questions, better understand contemporary circumstances, and inform how we approach the future.

Wildlife Disease Meets Ecology

One of the characteristics of the wildlife-livestock interface is the integration of ecological, agricultural, and human systems, which requires considering multiple and diverse disciplines and solutions. The study of the wildlife-livestock interface is principally and primarily addressed by *disease ecology*, a primary field of interest to us (see Chapter "The Ecology of Pathogens Transmission at the Wildlife-Livestock Interface: Beyond Disease Ecology, Towards Socio-Ecological System Health"). From a "health" perspective, *epidemiology,* applied to the study of the wildlife-livestock-human interfaces has provided a basic understanding on how most infectious agents circulate in communities composed of hosts that are infected by multiple pathogens, and pathogens that can infect a variable diversity of hosts. In turn, ecology has addressed how changes in host and pathogen communities (e.g., within-host competition, host population and community dynamics; this is closely linked to the discipline of disease ecology) result in consequences for the epidemiology of single- or multi-host pathogens. There has been, to date, a tremendous bias toward studies in zoonotic disease systems (e.g., cowpox, Lyme disease, and Nipah and Hendra virus infections). The empirical characterization of disease reservoirs also involves a conceptual ecological approach. The functions of different disease reservoirs and connectivity between source and target populations are challenging to comprehend for current multi-host systems (Haydon et al. 2002), even more so for past scenarios. The current ranges of hosts of many pathogens of wildlife shared at the interface still remain poorly defined, partially because of a relatively low number of isolates and wild species studied to date. Subsequently, there is an incomplete understanding of their roles as disease reservoirs in many systems. The conceptualization of disease reservoirs by Haydon et al. (2002) identifies the elements that determine disease maintenance (i.e., reservoir capacity), and how they are connected: "*A 'reservoir of infection' is defined with respect to a target population as 'one or more epidemiologically connected populations or environments in which a pathogen can be permanently maintained and from which infection is transmitted to the target population. Some reservoirs can be simple and comprise a single nontarget host population. However, they can comprise a more structured set of connected host subpopulations termed 'maintenance community'. Individually,* *some of these populations can maintain the pathogen ('maintenance populations'), whereas others cannot ('non-maintenance populations')."* An interface, including all its elements, can be a reservoir itself. Pathogens evolve and adapt to one or various hosts; wildlife, domestic animals, or humans. The capacity of a pathogen to successfully infect, cause, and transmit disease within the primary (or maintenance) host species by itself makes it a true or maintenance reservoir. This is in contrast to occasional spillover events into their host species in which the full life cycle, in particular the transmission to secondary hosts, is not maintained. When pathogens never spillback, we have a dead-end host. From the point of view of the wildlife-livestock interface, the dynamics of a pathogen in the host community involve the transmission between maintenance and/or non-maintenance host species. Studying the role of wildlife in multi-host disease systems is more complicated, apart from their ecological and behavioral specificities defaulting the application of conceptual models of disease transmission, they are more difficult to observe, monitor, sample, and diagnose. The most basic parameter, prevalence of infection, is often unknown in potential animal reservoirs. In a multi-host pathogen system, wildlife may contribute within the maintenance community (as a maintenance host or non-maintenance host) but also from outside the maintenance community as a bridge host (Table 1, Viana et al. 2014; Caron et al. 2015; see Chapter "The Ecology

Table 1 Definitions of hosts and relevant epidemiological parameters (based on Caron et al. 2015; Hartfield and Alizon 2013; and Faust et al. 2017)

Maintenance host population: Hosts in which the pathogen persists even in complete absence of transmission from other hosts. Population larger than the critical community size (i.e., size under which the pathogen cannot be maintained in the community) in which the pathogen persists.

Maintenance host community/maintenance host complex: One or more epidemiologically connected populations or environments in which the pathogen can be permanently maintained. Any host complex in which disease persists indefinitely is a reservoir. Host for which cross-species transmission and interspecies transmission are high.

Bridge host: Non-maintenance host population able to transmit a pathogen from a maintenance host/complex to the target population, otherwise not or loosely connected to the maintenance complex.

The basic reproductive ratio (R_0): Number of secondary infections caused by a single infected individual, in a susceptible population. It is classically used to measure the rate of pathogen spread. In infinite-population models, a pathogen can emerge if $R_0 > 1$. In a finite population, the pathogen can emerge from a single infection with probability $1–1/R_0$ if $R_0 > 1$, otherwise, extinction is certain.

The critical community size (CCS): Total population size (of susceptible and infected individuals, or others) needed to sustain an outbreak once it has appeared. This idea was classically applied to determining what towns were most likely to maintain measles epidemics, so that there would always be some infected individuals present, unless intervention measures were taken.

Force of infection FOI: Number of infections acquired over time.

Dilution effect: Occurs when the addition of one or more host species to a community makes a pathogen less abundant and less likely to persist than in the presence of one or less highly competent reservoir host species. Increased biodiversity should lead to reduced pathogen abundance. When increased host diversity leads to increased infection prevalence the opposite occurs: *Amplification effect*.

of Pathogens Transmission at the Wildlife-Livestock Interface: Beyond Disease Ecology, Towards Socio-Ecological System Health"). The study of bridge hosts, often birds, is obviously complicated, especially for migratory species. In basic epidemiological models, the persistence required for hosts to maintain a pathogen and thus act as a maintenance community is determined by the basic reproductive number (R_0: the transmission potential of a pathogen for a totally susceptible population) and critical community size, and subsequent risk for spillover transmission out of the maintenance community is defined by the force of infection. R_0 is therefore closely linked to the rate of contact between susceptible and infectious individuals, as are the recovery or mortality rates of infected individuals.

The force of infection is a function of the number of contacts, the transmission rate per contact and the frequency of infectious individuals. Contact is therefore a key feature of both reservoir and disease emergence dynamics. Disease spillover is determined by the prevalence of infection in the maintenance population and/or bridge hosts, the rate of contact between infected individuals, and the probability that infection occurs upon contact. Host ecological traits, such as life-history characteristics (seasonality, aggregation, sociability, sympatry with other species), local population dynamics, and land use are key parameters to determine pathogen transmission and persistence at the wildlife livestock interface. These factors, whose study is mainly addressed by *ecology,* determine the contact between wildlife, livestock, and humans. Further, ecology has provided understanding into many other fundamental aspects relevant to reservoir dynamics and disease emergence in changing landscapes. *Wildlife disease ecology* brings together evolutionary and population biology with epidemiology, and is essential to understand the causes, consequences, and management of wildlife diseases. It aims to answer questions like; How do hosts and parasites co-evolve? What determines how a pathogen spreads through a population and community? How do co-infecting pathogens interact? Why do hosts vary in parasite burden, or risk of exposure and susceptibility against infectious diseases? Which factors determine parasite virulence and host resistance? How do pathogens influence the spread of invasive species? How do we control infectious diseases in wildlife and at the interfaces? (Wilson et al. 2019).

Ecological Hierarchies of Host–Pathogen Interactions

The range of scales of host–pathogen interactions includes within-host ("pathogen infracommunity," i.e., pathogen–pathogen and pathogen–immune system interactions); between-host ("pathogen component community," population biology); among species ("pathogen supracommunity," community ecology); and across regions (macroecology and disease biogeography) (Johnson et al. 2015a). With the emergence of high-profile pathogens that exhibit wide host plasticity (such as Ebola), some of relevance at the wildlife-livestock interface (e.g., avian influenza viruses), a community approach is being increasingly embraced for studying the multi-host ecology of pathogens. A common factor underlying emerging diseases is the involvement of multiple hosts, vectors, or parasite species in complex ecological communities. However, it is difficult to forecast the outcome of the host community. In recent decades, epidemiological theory and empirical research have contributed to a better understanding of inter- and intra-specific interactions among hosts, and between hosts and pathogens. This research can account for the impact of a wide range of complexities on host ecology and transmission dynamics (Roche et al. 2012). Most of what we know relative to multi-host communities is normally based on simplified scenarios and specially focused on infectious diseases of humans and livestock. *Community ecology* aims to identify the factors that determine the structure, assembly, and dynamics of ecological communities (Johnson et al. 2015a, Becker et al. 2019). This discipline integrates processes at the fine-scale of individuals and populations, and the ecological and evolutionary drivers of species distributions at coarser scales. It therefore can be adopted to address the ecological complexity of multihost–multipathogen assemblages to understand multilevel infection processes, identifying the drivers of heterogeneities among individuals, species, and regions, and quantifying how processes link across multiple scales of biological organization to drive disease dynamics. The disciplines of epidemiology and community ecology have developed largely independently of one another. Recently though these disciplines are being integrated into a new discipline known as *disease community ecology.* A theoretical framework for disease community ecology considers the complete set of species that influence infection dynamics (e.g., Roche et al. 2012 for directly transmitted pathogens). Relevant concepts, such as the dilution effect or the amplification effect, occurring when biodiversity increases disease risk, are hot topics of discussion among researchers, in many cases with controversy due to differing observations (Table 1, Norman et al. 1999; Ostfeld and Keesing 2012; Faust et al. 2017). Theoretical frameworks under the umbrella of these disciplines provide support to answer, for instance, if variations in community composition affected the diversity and intensity of pathogen transmission in past assemblages of hosts (see Chapter “Natural and Historical Overview of the Animal Wildlife-Livestock Interface”).

The research focused on one scale of the above-mentioned scales may not consider what is going on at other scales, which are interconnected. Today, our understanding about the global distribution of most infectious diseases is still very limited, even for humans. Global-scale analysis of multi-host pathogens reveals structured variation among host species implicated as a potential source of pathogen spillover (Johnson et al. 2020). Particularly, a review found that there is disproportionate representation in research of mammal-borne zoonoses among emerging human diseases (Han et al. 2016). As an illustration (Johnson et al. 2020, Fig. 3 left), it has been reported that zoonotic virus species richness highly correlates with mammalian species richness, evidencing that the more diverse mammalian taxa are the source of more zoonotic viruses (e.g., of total mammal species on earth, bats account for about 25% and rodents for almost 50%). Interestingly, from the point of view of wildlife-livestock-human interface, zoonotic virus richness in domesticated mammalian species correlates with global abundance estimates for humans and domesticated species. This has been evidenced by recent research on the connection between human, animal, and environmental health (Fig. 3 right).

Analytical Approaches

Quantifying transmission between wild and domestic populations at the interface requires knowledge of epidemiology, ecology (community, see below), and mathematics. *Mathematical models are being applied with increasing frequency to improve our understanding of complex multi-host disease systems. Mathematical models of infectious diseases* use a body of developing theory to construct simplified and dynamic representations of epidemiological systems (e.g. Keeling and Rohani 2008; Lloyd-Smith et al. 2009; Huyvaert et al. 2018, Chapter "Quantifying Transmission Between Wild and Domestic Populations"). Many modern quantitative techniques are currently applied to correlation analysis and risk biogeography, longitudinal sentinel surveillance data, or network analysis. The application of mathematical models to infectious diseases can be used to address both scientific hypotheses and develop disease-control policy, for example, identifying when to intervene to achieve effective disease control (Grassly and Fraser 2008). For such purposes, mathematical models represent the key individuals, groups, populations and communities, and the essential mechanisms determining pathogen transmission (Chapter "Quantifying Transmission Between Wild and Domestic Populations"). Although simplifications, a certain level of complexity is ineludibly required since interactions among individual groups and among populations are complex. Therefore, in order to link the biology of infectious diseases and appropriate mathematic tools, a multidisciplinary approach and solid background information from the field are required. Basically, the fundamental susceptible-infected-recovered (SIR) model (see Chapter "Quantifying Transmission Between Wild and Domestic Populations") classifies groups of individuals within the host population as "susceptible" to infection, "infected" and able to transmit the pathogen, or "recovered" and immune to re-infection. Transmission of infection to new cases is driven by contacts between susceptible and infectious individuals. These models reproduce the classic epidemic curve, and have been remarkably successful in elucidating fundamental principles, such as the threshold for epidemics to take off if the basic reproduction number R_0 is greater than 1, and the potential to achieve natural or artificial "herd immunity."

One of the most useful applications of dynamic network theory and modelling in epidemiology is the possibility to simulate and explore the transmission of pathogens on the basis of the different parameters that characterize them (e.g., Farine 2018). Dynamic network models can simulate the transmission of pathogens transmitted through both direct and indirect pathways, according to spatiotemporal definitions of direct and indirect interaction, and to explore the potential role of wild species in transmission, for example, at the wildlife-livestock interface. The probability of infection given interactions in field conditions is a difficult parameter to estimate (Chapter "Quantifying Transmission Between Wild and Domestic Populations"). Network analysis can simulate different probabilities of infection, according to the species that initiated the transmission, conditions such as seasonal variations in contact rates and probability of transmissions, or include the environmental reservoir. Simplifying, networks are a connected matrix consisting of nodes representing individuals within a population (or population within a community of metapopulation), and edges (links) that represent interactions between individuals (or whatever nodes they represent). In an epidemiological context, this provides a framework for visualizing potential pathways of transmission within populations, metapopulation, or communities. Network analyses are useful to capture the complexities of multi-host pathogens, which allow us to estimate and compare the potential effectiveness of management actions for mitigating or suppressing disease in wildlife and/or livestock host populations.

Huyvaert et al. (2018) (see also Chapter "Quantifying Transmission Between Wild and Domestic Populations") recently reviewed the gaps and challenges in modelling pathogen transmission at the wildlife-livestock interface, and the available quantitative methods and approaches to complete gaps, concluding that modelling diseases across the wildlife-livestock interface involves many challenges and only transdisciplinary approaches are able to integrate modern quantitative techniques to produce robust, powerful and, most importantly, useful multi-host dynamic transmission models. They identified four key components necessary for effectively modelling disease at the wildlife-livestock interface: (1) host and pathogen distributions and movement patterns, (2) transmission rates and pathways, and (3) estimates of disease effects. Interestingly, they noted (4) the need for effective communication among wildlife biologists, mathematical modelers, veterinary medicine professionals, producers, and other stakeholders concerned with the consequences of pathogen transmission.

The Evolutionary Perspective

What were the specific barriers to the flow of pathogens among hosts operating along natural history of host communities–species? (Chapter "Natural and Historical Overview of the Animal Wildlife-Livestock Interface"). What have the relative contribution of ecological scales been to host–parasite interactions, parasite emergence, maintenance, and spread (i.e., before and after anthropogenic impacts appeared)? In which scenarios? Can we identify the paths that permitted pathogens to breach host barriers and spillover to other species? Summarizing, a general flow proposed for present communities (Becker et al. 2019; Plowright et al. 2017) can look like this: (1) *pathogen pressure* is determined by interactions among reservoir host distribution, pathogen prevalence, pathogen excretion by the reservoir host, subsequent pathogen survival, development, and dissemination outside of the reservoir hosts; (2) vector behavior and human factors modulate *pathogen exposure* (likelihood, route, and dose) and (3) *genetic, physiological, and immunological attributes of the recipient host* determine host invasion for a given pathogen.

Host–pathogen coevolution has shaped both their relationships and the diversity and population structure of hosts and their pathogens (Morgan and Koskella 2011). Coevolution has been demonstrated in a diverse set of host–pathogen systems; it is ubiquitous across ecosystems. In particular, it has probably had a key role in animal and human diseases after domestication, once the wildlife-livestock-human interface appeared (Chapter “Natural and Historical Overview of the Animal Wildlife-Livestock Interface”). Pathogens and hosts exhibit remarkable abilities to adapt to each other (convergent evolution), which is driven by evolution, either as a direct relatively short response or through long-term coevolution generating host or parasite traits that interact. *Evolutionary biology* provides the scientific basis to understanding disease from the standpoint of adaptation, but also improves our understanding of the mechanisms underlying current infectious disease transmission dynamics, context-dependent virulence, and more effective treatment and control strategies (Stearns and Koella 2008). For instance, the bacterial pathogen *Mycoplasma gallisepticum* has relatively recently and successfully jumped from poultry, its original host, to house finches (Hochachka et al. 2013). Evolutionary biology has integrated with traditional approaches to immunology and pathogen biology to address how new pathogens keep emerging as a result of evolution, driven by human activity, including ecological changes related to modern agricultural practices. Evolutionary biology and applied epidemiology can be used to detect adaptation in the case of pathogen emergence, such as host jumps. The increasing ease of large-scale genomic sequencing, together with advances in bioinformatics, molecular evolutionary theory, and new statistical tools for linking viral genetic variation with epidemiology and phylogeography (Pepin et al. 2010), is providing valuable means to visualize viral emergence and generate hypotheses about evolutionary mechanisms. This requires interdisciplinary teams (including field ecologists, microbiologists, immunologists, epidemiologists, bioinformaticians, and evolutionary biologists) using multiple approaches (field sampling, laboratory experiments, data analysis, and theoretical modelling).

In summary, a large body of developing theoretical frameworks have increased our understanding of transmission processes in complex host communities, especially relative to zoonotic situations but less so for the wildlife-livestock interface. The geographic diversity and complexity of the wildlife-livestock interface and any multi-host system require conducting local interdisciplinary research to find the best appropriate management. Also, research must adopt a holistic perspective to interpret pathogen dynamics at the wildlife-livestock-human interface considering biological, ecological, economic, and social drivers of pathogen emergence. What is the frequency and risks of pathogen flow between species at the wildlife-livestock interface? What mechanisms of amplification and persistence operate? What is the influence of different livestock production systems, socioeconomic context, and wildlife management? What possible interventions and more effective strategies can lead to reduced pathogen emergence and maintenance at the interfaces?

Final Remarks

- The different interfaces are “barriers” among human and animal (livestock and wildlife) compartments, which constitute opportunities for horizontal transmission between species, a new space for evolution, emergence, and maintenance of pathogens. The wildlife-livestock interface or ecotone often constitutes a proper ecological and epidemiological entity, with specific niches and epidemiological roles for wild, domestic, and environmental reservoirs, representing an important feature of pathogen transmission in the landscape. This allows for delineating the suitability for risk distribution of shared pathogens to identify a target for ecological and disease surveillance in these areas and allocating limited resources to improve and better understand and manage both human and animal health.
- Human activities have determined the appearance of new interfaces and opportunities for pathogen emergence and spread. Only the integrated understanding of ecological, epidemiological, social, cultural, and economic mechanisms that operate at wildlife-livestock-human interfaces will allow transdisciplinary integrative approaches to prevent and control disease. The wildlife-livestock interface term should equally be used for the term wildlife-livestock-human interface. This means different disciplines should increase their level of research cooperation and collaborative surveillance of animal and human pathogens to make the best coordinated decisions for similar problems of global concern.
- Recent disease emergence at wildlife-livestock-human interfaces, and their global spread, as exemplified in recent pandemics, illustrate the weaknesses of current wildlife disease and population monitoring and early warning systems acting at the origin of pathogen emergence, which need to be capable of detecting what is going on at the interface before pathogens spread and it becomes too late to prevent their impacts.
- These interfaces are interconnected centers for pathogen transmission giving rise not only to temporal, but spatial disease emergence. Local and regional drivers associated with risk for emergence of pathogens are connected worldwide, ranging from wildlife exclusive pathogens in the absence of livestock and local pastoralism systems to transcontinental-global interconnected food animal production systems and markets. Particular attention to the neglected wildlife-livestock interface is needed in complex ecosystems in developing regions, characterized by high biodiversity, a complex interplay of ecological and human factors, and increased opportunities for EIDs to arise and pathogen spillover to occur.
- The wildlife-livestock interface has been often neglected, and, consequently, disease spillover is largely underreported, even for zoonoses. Monitoring trends in wildlife populations, large-scale surveillance efforts, and addressing the ecological and epidemiological study of the wildlife-livestock interface to identify epidemiologically relevant animal reservoirs are warranted to understand and prevent diseases of animal relevance, but also those potentially spreading to

humans. Also, improved monitoring of livestock and large-scale trends are needed to depict interfaces and evaluate broad-scale risks.

- There are essential gaps, which prevent us from better understanding and managing disease dynamics at the wildlife-livestock interface. As the first step in many interfaces, it is necessary to describe the hosts and their pathogens, their distributions and behavioral characteristics with epidemiological consequences; and then, what the pathways and transmission rates are among these compartments, and which effects pathogens exert at both population and community levels. Also, the effect of disease management at the interface in given socioeconomic and cultural environments needs to be understood to develop successful mitigation strategies.

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