Natural and Historical Overview of the Animal Wildlife-Livestock Interface

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Introduction

Epidemiological and ecological connections among host species and pathogens are continuously evolving as host contact rates and ecological interactions drive cross-species transmission of pathogens. The previous chapter discussed that in such communities, epidemiological ecotones, or interfaces are spaces of transition and contact among different compartments, becoming "experimental scenarios" where

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pathogens have evolved to adapt, taking the opportunity to jump to new hosts. In more recent geological times, domestication of animals led to an epidemiological transition from human–wildlife interactions to human-wildlife-livestock interactions. Since then, humans have served as the key drivers of pathogen spillover at these interfaces, influencing their distribution, intensity, and subsequent consequences. The observation of contemporaneous events indicates that the outcomes of interspecies transmission vary widely, from single-infection spillover transient outbreak events with no consequence in life history of hosts, to long-lasting outbreaks maintained in new hosts which greatly impact communities (e.g., the introduction of rinderpest virus in sub-Saharan Africa at the wildlife-livestock interface the late 1800s, Roeder et al. 2013). The complex nature of ecological, epidemiological, and socioeconomic factors that determined past events, though, are ineludibly interconnected and difficult to disentangle.

Over the last millennia, and accelerated in contemporaneous times, industry and urbanization have progressed exponentially and wild habitats have been dramatically altered into agricultural land, threatening biodiversity and provoking profound changes to interfaces among animals and humans. Only 1000 years ago, less than 4% of the world's ice-free (four million km^2) and non-barren land area was used for farming (Ellis et al. 2010), compared to this day, where half of all habitable area (70% of global land area) is used for agriculture. Livestock uses most of the world's agricultural land. However, the distribution of land use between livestock and crops for human consumption, and specific farming and husbandry practices are contextualized in very different environments and socioeconomic realities. *Human intervention, including cultural, political, and economic dimensions, has resulted in epidemiological interactions at the interfaces as human impact progressively intensified and expanded the wildlife-livestock interface over the world*, which is reviewed in this chapter. The pathogen communities shared by wild and domestic populations and the dynamics of these complex host–pathogen systems reflect the historical epidemiological interactions between them (Caron et al. 2020). We present how humans have coexisted in complex interdependent relationships, first with wildlife and later also with domestic animals, in a wide range of natural and human-impacted environments. This chapter illustrates how, from domestication, the interface has been a socio-ecological system where economies have influenced agricultural practices and the relationship with wildlife (management and use).

Human population growth, increasing demand for food and other goods, globalization, associated environmental changes (e.g., habitat alteration, urbanization, agricultural expansion, and intensification), and climate change are seriously impacting overall world health. We are experiencing a new epidemiological transitional period, characterized by emerging diseases and a globalization of disease ecology, reflected by the impacts of rapid changes in demographic, environmental, social, and technological aspects. O*ur capacity to modify and connect the interfaces has increased to the extent that improving health at the human, animal, and ecosystem interfaces* (One Health approach, a recent term for an old concept) *is the only option to successfully address the main global health challenges* (Godfroid et al. 2014; Cassidy 2015). *What we do during the next decades at ecosystem interfaces will determine our common future.*

Many questions arise from historical, ecological, and epidemiological perspectives. Which host interaction networks, composition, relative abundances occurred in past contexts, and how they interacted with and within their environment? What were the impacts of pathogens in past community assemblages and diversity? When and how did pathogens emerge in past multi-host systems, and particularly at wildlife-livestock-human interfaces? What were the consequences on transmission of novel species entering new host communities? How did virulence evolve after pathogens crossed to new host species? What were the interactions in the host assemblage? Host–pathogen–environment interactions have changed, but we can presume that the theoretical ecological framework that operated in the past is supported by the processes observed today (see Chapter "Host Community Interfaces: The Wildlife-Livestock"). We can probably identify parallels between the process of change of the wildlife-livestock interface over human history and the current gradient of characteristics of the interface from pristine to highly anthropized ecosystems (Fig. 1 of Chapter "Host Community Interfaces: The Wildlife-Livestock").

Understanding Previous Ecological and Epidemiological Contexts

Theoretical frameworks and technical advances (see Chapters "Host Community Interfaces: The Wildlife-Livestock", "Collecting Data to Assess the Interactions Between Livestock and Wildlife", "Characterization of Wildlife-Livestock Interfaces: The Need for Interdisciplinary Approaches and a Dedicated Thematic Field", and "Quantifying Transmission Between Wild and Domestic Populations") developed by different disciplines provide support to address the dynamics of current multi-host multi-pathogen systems, such as what the risks are for pathogen interspecific transmission and emergence. This scientific background can be applied to past assemblages of hosts, which have changed in terms of host community composition, the specific ecological relationships of their components, and the relative importance of the main drivers such as anthropogenic factors. As it happens for present systems, describing cross-species transmission processes that occur at varying levels of biological organization, especially in the past, is complicated by the many scales and data required (Becker et al. 2019), which are almost systematically absent for most past scenarios. Fortunately, research is providing clues on the characteristics and evolution of ecological animal networks and the prevalent interfaces of the past.

Unfortunately, our capacity to understand the ecology of past, often extinct, communities and their pathogens attenuates rapidly with time because the evidence for their functional characteristics become harder to discover and reconstruct. However, especially for recent communities in geological times, there may be some data, for instance, based on preserved fossil information (e.g., Poinar 2018) and evidence of habitat and climate conditions (Woodburne 2010). Different disciplines can help

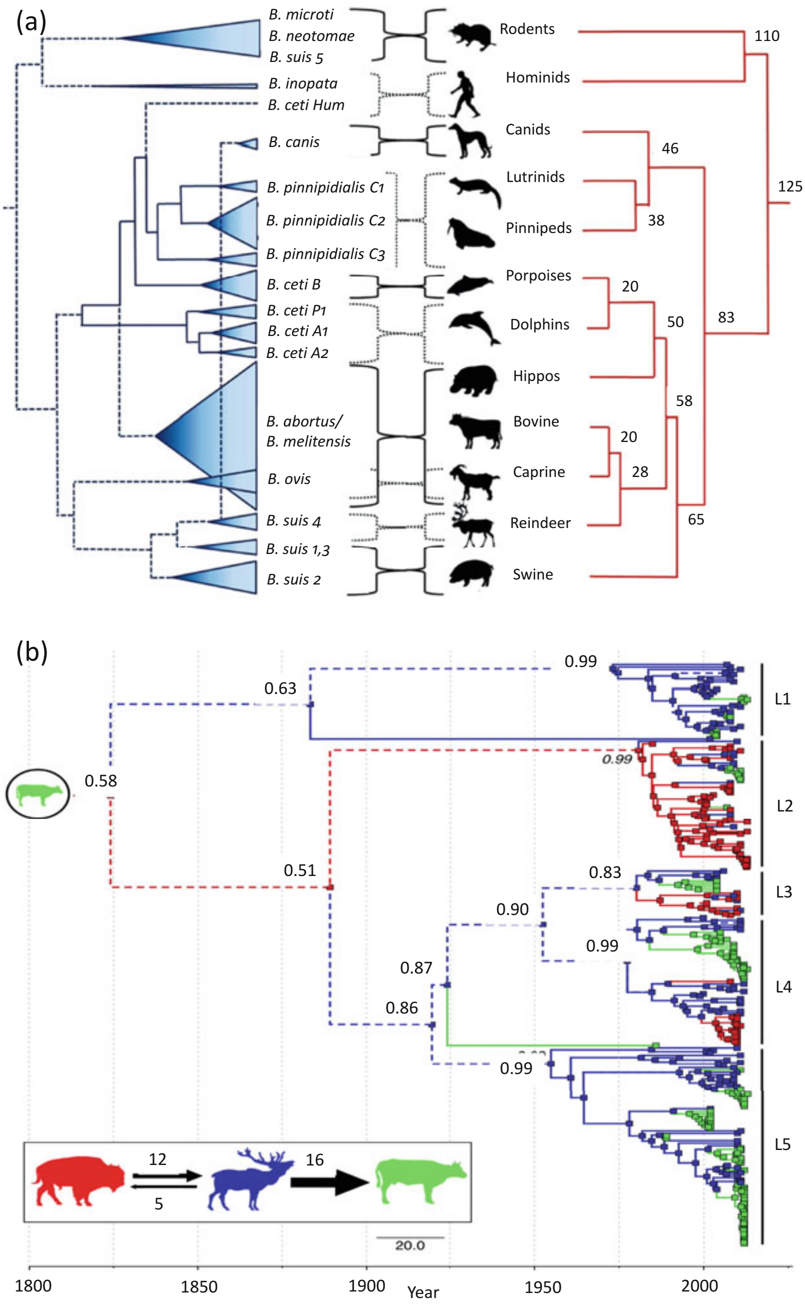

Fig. 1 The cophylogeny of hosts and *Brucella* pathogens. (**a**) The dispersion of *Brucella* species is confronted to the phylogeny of their preferred host mammal (cones proportional to the number of strains analyzed, modified from Moreno 2014 after Guzmán-Verri et al. 2012). Numbers in the mammal phylogenetic tree represent millions of years. (**b**) Shows a more contemporaneous approach, a reconstruction of *Brucella abortus* genealogies by Whole-genome sequencing for at the wildlife-livestock interface in the Greater Yellowstone Ecosystem (GYE, Kamath et al. 2016). It

Table 1 Comparison of disciplines potentially studying determinants of pathogen spillover in present and past host communities (inspired in Plowright et al. 2017)

Determinants for transmission	Disciplines studying past determinants of transmission	Disciplines studying current determinants of transmission
Reservoir host distribution, relative abundance, interactions between species	Paleontology, paleoecology, paleogeography, paleoclimatology, paleoethology, paleophilogenetics	Animal ecology, population biology, biogeography, behavioral ecology, landscape ecology, agricultural science
Pathogen prevalence	Paleogenetics, paleomicrobiology, paleoparasitology, paleopathology, paleoepidemiology, paleogenetics	Disease ecology, animal epidemiology, infectious disease dynamics, immunology, microbiology, veterinary medicine
Infection intensity		
Pathogen excretion from reservoir		
Pathogen survival and/or spread	Paleomicrobiology, paleoepidemiology	Microbiology, disease ecology, vector ecology, epidemiology, spatial ecology
Human factors	Archaeology, anthropology	Human epidemiology, medical anthropology, vector ecology, social sciences, behavioral ecology
Host–pathogen interaction	Paleomicrobiology, paleopathology, paleoepidemiology, evolutionary biology, paleogenetics	Microbiology, innate adaptive immunology, cell biology, pathology, genetics, evolutionary biology

to understand the structure of interaction networks in these preterit communities, such as paleoecology, paleoepidemiology, pathology, and genetics (Table 1). They address unknown ecological and historical contexts, can infer and speculate about the past based on (1) what the prevalent composition of host communities and their interactions were, (2) evidence of pathogens, and (3) evolutionary and phylogenetic studies of host and pathogens based on current and old samples. The introduction of improved molecular tools allowed the extraction of ancient DNA (aDNA, Marciniak 2016) and subsequent massive application of next-generation sequencing technologies. Paleogenetics and phylogenetic methods can be applied to situations where direct knowledge of the past is absent by the analysis of molecular sequences. In contrast to genetics, which studies individual genes and their roles in inheritance, paleogenomics aims at the collective characterization and quantification of all genes of an organism, their interrelations and influence on the organism. For instance, it is now possible to detect genetic drift, ancient population migrations and

Fig. 1 (continued) evidences cross-species transmission, and that brucellosis was introduced into wildlife in this region at least five times (authors estimated 12 host transitions from bison to elk, and 5 from elk to bison). These results support that free-ranging elk is currently a self-sustaining brucellosis reservoir and the source of livestock infections. The predicted date of the ancestral root of the tree was approximately 1769 (the time to most recent common ancestor for all GYE isolates) interrelationships, their association with pathogen spread and evolution, the evolutionary history of extinct species, and even the identification of phenotypic features across geographic regions (e.g., Huerta-Sánchez et al. 2014; Barlow et al. 2018). Scientists can also use paleogenomics to compare ancient ancestors (wildlife, domestic species, and their ancestors, pathogens) against modern-day species and provide insights as to when and by what means traits evolved, and how extinct organisms are related to living species and populations.

The *genomics revolution* (population genomics and paleogenomics) has increasingly provided insight regarding patterns of pathogen evolution and spatiotemporal epidemiological dynamics (Dearlove and Wilson 2013; Orton et al. 2013) and is continually developing. New findings and hypotheses continually arise, which are supported or rejected, and therefore examples must be considered in that context. Bacterial microbiomes (the genetic component of a microbiota) have been partially reconstructed from ancient remains in prehistoric humans using coprolites (Tito et al. 2008, 2020), and from Mammoth *Mammuthus primigenius* and woolly rhinoceros *Coelodonta antiquitatis* from frozen preserved intestinal contents (Mardanov et al. 2012). The evolutionary history of pathogens is closely linked with that of their hosts (Clayton and Moore 1997). Researchers, by using phylogenetic trees and networks of evolutionary relationships, can explain evolutionary paths (e.g., using pathogen samples from different times), how closely organisms are related to each other (e.g., samples from current pathogens so distance is a proxy to time of evolutive separation), and the study of cophylogeny (concordance between the phylogenies and interactions of different groups of species) of hosts and pathogens. Fig. 1 shows the case of bacteria *Brucella* (Moreno and Moriyón 2002), a monophyletic genus with high DNA similarity (Verger et al. 1985). *Brucella* species can be distinguished by single nucleotide polymorphism analysis and host preference (Foster et al. 2012). *Brucella* divergence seems linked to the evolution of the host (Moreno 2014), but these organisms are also able to breakdown the species barrier and "jump" from one mammal order to a very different one (Figs. 1a and 2). The fine spatial and temporal dynamics of pathogens, such as the transmission among wildlife and livestock of *Brucella abortus* (Fig. 1b) can also be approached by highly resolved time-calibrated phylogenies, evidencing cross-species transmission and the introduction history as well as identifying current maintenance reservoirs as source of infection to livestock hosts (Kamath et al. 2016). An interesting case is that of the *Mycobacterium tuberculosis* complex (MTBC). *M. tuberculosis, stricto* sensu, is the causative agent of tuberculosis (TB) and has caused more deaths in humans than any other infectious disease, likely infecting more people than any pathogen has at any other time in human history (Gagneux 2018). Most evidence to date supports an African origin for the human-adapted MTBC (the closest living relatives of the common ancestor of the MTBC are almost exclusively found in the Horn of Africa). *M. bovis,* which has a broader host range than *M. tuberculosis*, and humans were originally thought to have acquired TB from domestic animals during the Neolithic period. Later, the availability of the first full bacterial genome sequences revealed that *M. bovis* contains a smaller genome than *M. tuberculosis*, and this may indicate that the latter was unlikely to have evolved from *M. bovis* (Brosch et al. 2002).

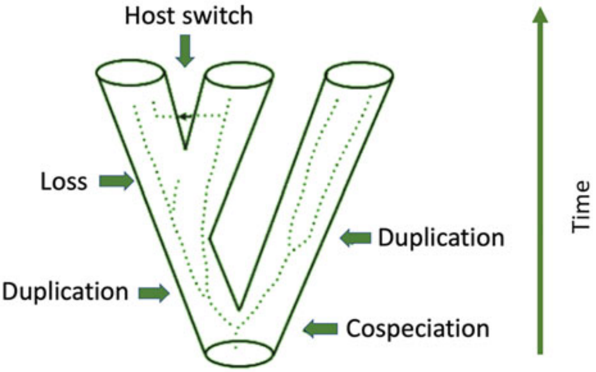

Fig. 2 Schematic representation of the possible different coevolutionary events among host and pathogens (modified from Baudet et al. 2015). The tube represents the host tree and the dotted lines the pathogen tree

Several studies showed that the order of gene loss across the various members of the MTBC supported an evolutionary scenario in which humans transmitted TB to animals (Mostowy et al. 2002; Dippenaar et al. 2015). In addition, multiple host jumps might have occurred in the evolution of certain MCT lineages, both from humans to animals and back. Another interesting example is the old lineage of protozoan parasites. Molecular paleoparasitology on mammalian trypanosomes has clarified that *Trypanosomatid* divergences can be dated prior to the origins of both current insect vectors (30–60 million year ago, Ma, for tse-tse fly), and placental mammalian hosts (<85 Ma) (Fernandes et al. 1993). Finally, as for viruses (Tao et al. 2017), phylogenetics provides evidence for natural recombination between distantly related African bat coronaviruses that resulted in ancestor viruses of certain Human Coronaviruses (HCoV), suggesting that past interspecies recombination played an important role in CoV evolution and the emergence of novel CoVs with zoonotic potential. As indicative, close correlations between Italian bat CoVs belonging to the genus *Betacoronavirus* and SARS-related CoV that emerged far in Asia have been shown (Balboni et al. 2010).

Pathogens, Host Communities, and the Time Scale of Evolution

Pathogens have been ubiquitous in ecosystems, affect evolutive forces upon populations, and are commonly regarded as factors that co-participate in fluctuations or declines in wild populations with consequences at the wildlife-livestock interface (Dobson and Hudson 1992; Kilpatrick and Altizer 2010; Pybus et al. 2013). Pathogens and host communities (wild and domestic) evolve in response to one another and changing environments, leading to co-evolutionary dynamics that modulate their genetic composition and diversity, and even co-speciation events. The immense diversity of hosts in natural communities, including domestic animals and humans has resulted in a large diversity of current pathogens, where *evolutive processes have shaped the biology of hosts and pathogens*. However, outcomes of pathogen–host relationships, such as immune escape and changes in virulence, are diverse and system-specific. Today, evolutionary questions underlying the emergence of pathogens in novel hosts are particularly challenging. The extent to which *pathogens have evolved toward generalists or specialists* following transmission into a novel host depends on their level of adaptation to dealing with different environments, their rates of molecular evolution and their ability to recombine (Bonneaud et al. 2019). Crucial mutations may also occur in reservoir or novel environments (Pepin et al. 2010). An *evolutionary arms race between hosts and pathogens* begins when pathogens impose a selective process in hosts, which leads to a strong selection pressure for a pathogen to evade the host immune response (Meyerson and Sawyer 2011). The evolutionary dynamics of pathogens and hosts is characterized by a *trade-off between transmission rate and virulence* (i.e., transmission time prior to host death limits pathogen adaptation). Current research on how pathogens are able to breach species barriers and evolve as emergent is providing insight on how pathogen strains arise in response to selective pressures from past environments (e.g., the role of adaptation in host jumps of viruses such as CoVs at the interfaces; Park et al. 2013) and why some pathogens (e.g., influenza) constantly evolve to evade antigenic recognition (Restif and Graham 2015) or adapt to new hosts (e.g., CoVs and host cell receptors; Park et al. 2013).

Viruses illustrate the strong selection pressures exerted by pathogens on hosts, which has led to the development of effective responses against pathogens. Viruses present high mutation rates (especially RNA viruses) and have been subject to selection pressure for millions of years, acting on virus proteins by amino acid changes (Demogines et al. 2013). However, successful evolutionary pathways for viruses are limited, as evidenced by convergent evolution of different viruses (Stern et al. 2017). In turn, host alleles in genes participating in antiviral response have a major selective benefit that spreads rapidly through host populations (Fernández-de-Mera et al. 2009). However, this spread can be disrupted by various factors, including biogeographical reasons (see Chapter "Natural and Historical Overview of the Animal Wildlife-Livestock Interface").

Viruses also offer good examples of evolutionary transitions leading to emergence of relevant pathogens at the wildlife-livestock interface, which can be seen when extrapolating from genetic diversity among extant viral species. They can inform us about the long-term "arms races" between hosts and viruses, characterized by events of selection and counterselection, and increasing depths of ancient viral lineages. In this respect, endogenous virus elements (EVEs) are a common component of the eukaryotic genome (Holmes 2011), there are even sequences from RNA viruses that have no DNA stage in their life cycle. The discovery and research of EVEs have contributed to a better understanding of the time scale of virus evolution (Emerman and Malik 2010) in contrast to molecular clock studies using "heterochronous" samples (sampled at different time points during epidemiological history) from a single virus (Gilbert and Feschotte 2010). The presence of EVEs in related host species integrated into the same genomic position (like "fossilized" genetic prints within host DNA) indicates that this integration event occurred prior to the divergence of these species. If it is known when species diverged, then the minimum age of the insertion event can also be estimated (Katzourakis and Gifford (2010). Although there are different dating estimates, recent reconstruction of the evolutionary history of retroviruses indicates they likely emerged between 450 and 550 Ma in the early Palaeozoic Era, coinciding with the origin of jawed vertebrates (Aiewsakun and Katzourakis 2017). This is currently the oldest inferred date estimate for any virus group and indicates that these viruses evolved within the marine environment. Other pathogens, such as bacteria, may display key differences in processes underlying their evolutive history. For instance, the jump of a pathogen into a novel host species followed by the specialization on that host and the loss of infectivity of previous host(s) is commonly observed in viruses but less often in bacteria. Bacterial pathogens typically exhibit high levels of phenotypic plasticity, low rates of evolution, and decreased ability to recombine, which should reduce their propensity to specialize on novel hosts. Thus, bacterial infections could be more likely to result in transient spillovers or increased host ranges than in host shifts.

Coevolution occurs when two or more species exert a reciprocal influence on one another's evolutionary trajectories (Vermeij 1994), and synchronous development of pathogen lineages with those of their hosts occurs. Cophylogeny is the reconstruction of ancient relationships among ecologically linked groups of organisms from their phylogenetic information. Cophylogenetic reconstructions for tracking host–parasite pathways normally use event-based models, including cospeciation, duplication (divergence), loss, and host switch (Fig. 2), and approaches that identify lateral gene transfers for the gene tree(s)/species tree problem (Hallett and Lagergren 2001). Pathogens that do not show complete fit with the phylogeny of their hosts are also interesting and may evidence their ability to jump between host species and establish on novel hosts. In fact, most pathogens seem to be able to switch hosts (Kossida et al. 2000). For instance, co-phylogenetic analyses revealed that cross-species transmission (host switch) may have been more common than co-divergence across coronavirus evolution, and cross-species transmission events were more likely between sympatric bat hosts (Leopardi et al. 2018).

The extent to which pathogens and their hosts codiverge remains an open question in most systems. However, cases of both cospeciation and horizontal switching have recently been documented, especially for RNA viruses (e.g., phylogeny for Hantavirus is significantly similar to its host trees, whereas Lyssavirus seems to display no significant congruence; Jackson and Charleston 2004). Numerous examples illustrate different cophylogenies where the timing, evolutionary mechanisms, nature of the pathogen, involved host compartments, and directional relationships vary:

- Herpesviridae, a large family of DNA viruses (McGeoch et al. 2000), have mammals and other vertebrates as their natural hosts (and in one described case, an invertebrate). Phylogenetic analysis of herpesviruses (HV) found in mammals and birds clearly evidence descent from a common ancestor. Each of the subfamilies of the Herpesviridae shows tree-branching features that can be explained by coevolution of HV lineages, as well as other features that require non-coevolutionary explanations. For instance, herpesviruses show weak correlations with the phylogenies of primates, rodents, ungulates, and carnivores. There are cases representing clear recent interspecies transfer of viruses, such as certain herpesvirus of wallaby (macropodid marsupials) and bovine.

- The Hepadnaviridae family of DNA viruses comprises two genera: Orthohepadnaviruses (including the Human Hepatitis B virus HBV that infect mammals), and Avihepadnaviruses (that infect avian species). Hepadnaviruses also have the ability of endogenization into the host genome (Gilbert and Feschotte 2010; Littlejohn et al. 2016) and phylogenetic analysis suggests that the integration events occurred at least 19 Ma (and a more recent study estimated to have occurred during a period of bird evolution from 12 to 82 Ma, Suh et al. 2013). Comparative phylogenetic analysis on endogenous and existing exogenous avian hepadnaviruses indicates multiple genomic integration events, and birds have been proposed as the ancestral hosts of Hepadnaviridae, while mammalian HBVs probably emerged after a bird–mammal host switch (Suh et al. 2013). Frequent cross-species transmissions have resulted in their widespread distribution in the animal kingdom and, as a result of a series of recombination events with other HBVs, for instance, both primate and human, resulted in at least 10 genotypes of human HBVs that are recognized today. Several theories (reviewed by Littlejohn et al. 2016) have been proposed to explain the origins of HBV, including cospeciation, coevolution, and cross-species transmission (even a bat origin). However, HBV evolution probably involved cospecies evolution within birds, rodents, and bats, followed by a series of cross-species transmission events to explain the close relationship between human and nonhuman primate HBVs observed today.
- In the particular case of adeno-associated virus (AAV)-derived endogenous viral element (mAAV-EVE1; Smith et al. 2016), a time-scaled cladogram using previously published estimates of divergence among marsupials represents a speciation history spanning an estimated 30 million years. This possibly suggests that the exogenous ancestor of mAAV-EVE1 could have been introduced to the island continent of Australia by migratory birds, evidencing a host jump (which probably was a complex process) among very different hosts.
- The Hepeviridae family (RNA viruses) includes two genera, *Orthohepevirus* and *Piscihepevirus* (Kelly et al. 2016; Cagliani et al. 2019). The *Orthohepevirus* genus is divided into four species of viruses infecting mammals and birds (*Orthohepevirus A–D*). Hepatitis E virus (HEV, an *Orthohepevirus A*) is a common cause of hepatitis worldwide. Human-infecting HEV strains are genetically heterogeneous. HEV-1 and HEV-2 only infect humans, primarily in tropical and subtropical regions. Genotypes 3 and 4 account for the majority of HEV human cases in industrialized countries and infect several domestic (mainly swine) and wild animals (e.g., ungulates and small carnivores). Phylogenetic analyses (Fig. 3; Cagliani et al. 2019) showed that HEV-3 and HEV-4 sequences derived from human cases are interspersed within those isolated from swine, indicating that pig-infecting HEV-3 and HEV-4 can easily cross the species barrier and infect humans. The wild boar *Sus scrofa*–domestic pig–human interfaces are interesting ecological, epidemiological, and evolutionary scenarios to study HEV-3, -4, -5, and -6. The remaining genotypes HEV-5/HEV-6 and HEV-7/HEV-8 have been detected in wild boars and camels, respectively. Phylogeny approaches have revealed that humans were the most likely hosts of the

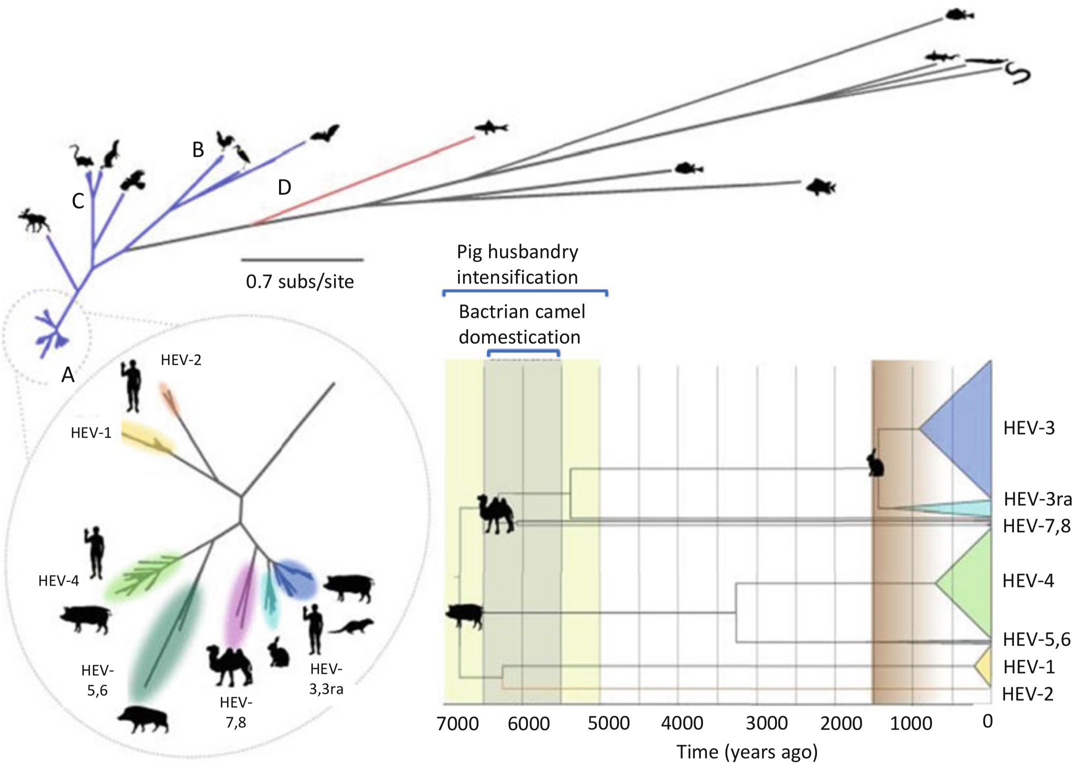

Fig. 3 Hepevirus phylogeny and time-scaled phylogenetic tree (modified from Cagliani et al. 2019, see reference for more details). Left: a maximum-likelihood phylogeny of the RdRp domain of known hepeviruses. The Piscihepevirus branch is in red, Orthohepevirus branches are in blue. The enlargement below shows phylogenetic relationships for viruses belonging to the Orthohepevirus A species (HEV), with representative hosts. Right: time-scaled phylogenetic tree of a non-recombining ORF1 region. Branch lengths represent evolutionary time. The timeframes of historical events mentioned in the text are reported. The rabbit and camel silhouettes mark the split of the rabbit- and camel/dromedary-infecting genotypes. The pig silhouette marks the human-restricted/enzootic genotype split

ancestor of extant orthohepeviruses, which is in concordance with the observation that most HEV genotypes can infect humans, whereas other animals are differentially susceptible to distinct HEV genotypes. Origins of the *Orthohepevirus* genus was recently dated to be at least 21 Ma. The Orthohepevirus A species originated in Asia, most likely from a human-infecting ancestor that existed approximately 4500 to 6800 years ago (Fig. 3 right), coinciding with the appearance of large human settlements that probably facilitated HEV emergence and spread (see below). The earliest events involved the separation of the enzootic (animal) and human-restricted genotypes, as well as the split of the camel-infecting genotypes occurring during the timeframe of camel domestication (Fig. 3 right). More recently, the place and timing of HEV-3ra divergence also corresponded to the period of rabbit domestication (Fig. 3 right). Today, humans may have acquired HEV through cross-species transmission from other animals, and the wildlife-livestock interface is crucial as a bridge for transmission.

- Species in the genus *Plasmodium* cause malaria in humans and infect a variety of mammals and other vertebrates. Mammalian *Plasmodium* parasites may have originated over 64 Ma (Silva et al. 2015). Cophylogeny reconstruction at the human-wildlife-livestock interface ecologically was applied to clarify the relationships for the most virulent human malaria, caused by the protozoan parasite *Plasmodium falciparum*. This parasite was at once thought to have arisen as a result of a host switch from birds to humans, at the time of the domestication of chickens (e.g., Waters et al. 1991). However, more recent work has shown that there is a close evolutionary relationship between *P. falciparum* and *P. reichenowi*, the chimpanzee malaria parasite, indicating codivergence events with respect to primate and *Plasmodium* evolution (Rich and Ayala 2010). Research supports the hypothesis that the last common ancestor of *P. falciparum* and *P. reichenowi* occurred around the time of the human–chimpanzee divergence and that current *P. falciparum* infections of African apes are most likely derived from humans and not the other way around, although *P. falciparum*-related pathogens can naturally circulate in some monkey populations in Africa (Prugnolle et al. 2011; Silva et al. 2011). On the other hand, *P. vivax*, split from the monkey parasite *P. knowlesi* in the much more distant past, during the time that encompasses the separation of the Great apes and Old-World monkeys. Overall, mammalian-infecting *Plasmodium* evolved contemporaneously with their hosts, with little evidence for parasite host-switching on an evolutionary scale, as evidenced by research on the timeframe within which to place the evolution of *Plasmodium* species (Silva et al. 2015).
- Different *Brucella* species (Fig. 1) cause brucellosis in domestic animals, terrestrial wildland animals, and sea mammals (dolphin, whales, seals, and walruses; Guzmán-Verri et al. 2012). The only species that are linked to human brucellosis are *B. melitensis*, *B. suis*, *B. abortus*, and to a minor extent *Brucella canis* (Moreno and Moriyón 2002). As mentioned above, *Brucella* divergence appears to be linked to the evolution of the host. One interesting feature of the genus is the absence of plasmids and lysogenic phages, which prevent horizontal transference of genes (Moreno 1998). It has been proposed that the extant *Brucella* species

expand clonally within the host environment and that genetic drift depends almost exclusively on mutation and internal genetic rearrangements (Moreno 1998). *Brucella* divergence seems linked to selective forces within the host environment, and consequently, to the evolution of the host (Moreno 1998). However, these organisms are capable of breaking down the species barrier and moving from one mammal order to a very different one (Fig. 1), which might favor the persistence of a distinct *Brucella* clone in a different "preferred" host.

- Changes in complex life cycles and pathogenicity of pathogens can occur rapidly, and this can be tracked by phylogeny and biogeographical approaches. The parasite *Toxoplasma gondii* protozoan infects warm-blooded vertebrates and also causes zoonotic disease in humans (Dubey 2010). There is a global predominance of three clonal *T. gondii* lineages, which suggests they have exceptional characteristics responsible for their current parasitism of nearly all warm-blooded vertebrates. The study of its genetic polymorphism analyses indicates that these clonal lineages emerged within the last 10,000 years after a single genetic cross. Comparison with ancient strains (approximately one million years) suggests that the success of the clonal lineages resulted from the concurrent acquisition of direct oral infectivity (Su et al. 2003). This key adaptation bypassed sexual recombination (only occurring in Felid species) and promoted transmission through successive hosts, thereby leading to clonal expansion. This radiation to transmission emergence through carnivorism (i.e., oral infectivity of tissue cysts) between intermediate hosts manifested itself in clonal strains 10,000 years ago (Su et al. 2003). It is hypothesized that such oral infectivity may have developed previously in South America where it was shown to be a trait of many *Toxoplasma* species before migrating to North America and then further north along the Bering Strait to colonize Asia, Europe, and Africa. The original genetic diversity of Old-World *T. gondii* may have been larger and the recent expansion of the domestic cat, an Old-World species until the sixteenth century, may have favored a specific subset of preadapted genotypes.
- It is thought that about 2 Ma, African hominids who scavenged for food or consumed bovids were exposed to tapeworm colonization (see Box 1). Supporting evidence was inferred from an examination of host and parasite evolutionary histories and evidence for the rate of molecular evolution between species of *Taenia* (Michelet and Dauga 2012). Humans probably transferred tapeworms to cattle and swine because the association between *Taenia* and hominids was established before livestock domestication. Only after the development of agriculture about 10,000 years ago, did cattle, swine, and domestic carnivores became intermediate hosts. Today, cysticercosis and echinococcosis due to tapeworm infection are relevant issues at the wildlife-livestock interface in developing countries (e.g., Miran et al. 2017).

From a biogeographical perspective, Brooks and Ferrao (2005) expressed that emerging infectious diseases are "evolutionary accidents waiting to happen." During periods of biotic expansion and exchange, pathogens and hosts may disperse from their areas of origin (Reullier et al. 2006; Hoberg and Brooks 2015). This, in conjunction with other ecological processes, may allow for host switching without evolving new host utilization capabilities. In fact, most of the recent host switches of emergent infectious diseases (EIDs) have been associated with events of biotic expansion (Hoberg and Brooks 2015). Over the course of natural history, either new hosts have moved into the area of origin of given pathogens, or the pathogen has moved out of its area of origin into an area where susceptible hosts live (Engering et al. 2013). Isolation of host populations, upon geographical or behavioral separation, likely resulted in isolation of pathogen populations and pathogen population bottlenecks, leading the way to further diversification (Van Blerkom 2003). Pathogens have probably been shared most commonly between species that are closely related and inhabited and/or used the same geographical region, habitats, and/or resources. However, this is challenged by globalization, which characterizes the ecological, epidemiological, social, political, and economic relationships of the modern world.

Pre-Domestication History

Pathogens rarely survive in the fossil record. Viruses could have originated 4 Ma, or "only" 2 billion years ago according to different theories and sources (Domingo 2016), and Bacteria probably arose on the planet more than 3.5 years ago (Schopf et al. 2018). Mutualism is probably as old as first life, however, the earliest fossil record of mutualism between microorganisms and animals are protists and bacteria from a fossil termite entombed in amber during the Mesozoic (by Poinar 2009, 2018). One of the oldest known instances of infectious agents is the case of spirochete cells that looked like the *Borrelia* genus (named *Palaeoborrelia dominicana*; genus *Borrelia* is today associated to Lyme disease) and were found in ticks that were also entombed in amber at least 15 Ma. This suggests Lyme disease-like and other tick-borne diseases may have been infecting animals long before humans were present on Earth (the oldest documented case of Lyme disease bacteria presence in humans comes from the famous 5300-year-old ice mummy discovered in the Eastern Alps; Keller et al. 2012). Additionally, the history of pathogen change (for adaptability within host populations and communities) from the behavior of current systems (Chapter "Host community Interfaces: The Wildlife-Livestock"), with continuous emergences (re-emergences) and extinctions also needs to be inferred.

Ecological and Environmental Changes Determining Host Diversity, Distribution, and Communities During the Pleistocene

Through processes of evolution, migration, colonization, and later, trade and travel, humans have impacted landscapes, other species, and the ways in which species have co-evolved, including pathogens. The very early origins of these processes, although accelerated during the last millennia and decades, were primarily forged during the Pleistocene. This is the geological epoch that approximately corresponds to the Paleolithic period in human prehistory (Toth and Schick 2007) and extends from the earliest known use of stone tools by hominins c. 3.3 Ma, to the end of the Pleistocene c. 11,650 years before present (BP). It is characterized by glaciations, relevant animal and human migrations, and colonizations. During the Pleistocene, key ecological and environmental changes determined the distribution and assemblages of animal communities (hosts) that later determined those giving rise to domestic species, and the evolution of anatomically modern humans. The appearance of *Homo sapiens* occurred about 200,000 years ago. This epoch is a key anteroom to a crucial change in human, animal, and pathogen history: domestication.

During the Pleistocene, climatic and environmental fluctuations resulted in successive events of north-south migration of animals, affected human dispersion, and produced the geographic shifting of many species, probably in many cases accompanied by absorption of part of the gene pools of local related species dispersing and sharing pathogens. Paleogenomics has demonstrated ancient gene flow between genomes of extinct species and existing recipient species (Huerta-Sánchez et al. 2014; Barlow et al. 2018), which probably also determined the flow of their respective guilds of pathogens. The case of wild boar during its expansion from Asia to Europe illustrates this (Liu et al. 2019), as a species that is widely distributed today and plays relevant epidemiolocal roles for animal- and human-shared pathogens. The genus *Sus* differentiated about 3 Ma and *S. scrofa* subsequently spread throughout Asia, Europe, and North Africa. This expansion (Schiffels and Durbin 2014; Fistani 1996) was highly efficient and similar to the great human expansion during the late Pleistocene (Frantz et al. 2013). It is thought that wild boar expansion could cause the disappearance of most suid species across Eurasia (wild boar appeared in Europe 1.5 to 0.4 Ma, depending on whether estimates are based on archaeological or molecular data. However, it is hypothesized that wild boar did not replace the other suid species it encountered, but instead exchanged genetic materials with them through admixture. These inter-specific/inter-generic admixtures likely led to the transfer of pathogens. Another example is the great American biotic interchange when the Neotropic (roughly South America) and Nearctic (roughly North America) ecozones joined, which resulted in land (its most evident effect was on the zoogeography of mammals) and freshwater fauna migrating from North America via Central America to South America and vice versa (accelerated about 2.7 Ma). This interchange ultimately determined the wildlife that humans would later discover and even domesticate during their expansion across the Americas.

Further (see above), it is hypothesized that an ancestral form of *T. gondii* was introduced in South America through the migration of Felidae after the emergence of the Panama isthmus and that the evolution of oral infectivity through carnivorism and the radiation of felids in this region enabled a new strain to outcompete the ancestral lineage and undergo a pandemic radiation (Webb 2006; Bertranpetit et al. 2017).

Pleistocene terrestrial ecosystems included a much greater diversity of megaherbivores (e.g., mammoths, mastodons, and giant ground sloths) and thus a greater potential for widespread habitat degradation if population sizes were not limited. The last ice age ended about 11,000 years ago, coinciding with the beginning of the Neolithic period. At this time, wild mammals on all continents underwent major changes, with a great impact in North and South America, where 33 (73%) and 46 (80%) genera of mammals became extinct, respectively. Australia also lost 55 species, but losses in Europe were not as severe, and extinctions during this time in Africa and Asia were similarly mild. Scientists attribute these extinctions to numerous causes, which primarily included climatic changes and overhunting by humans. What is clear is that humans during the Pleistocene were extremely efficient in exploiting natural resources and influenced animal community compositions, which probably conformed an intimate epidemiological human–wildlife interface until domestication.

Origins, Evolution, and Dispersal of Humanity and New Interfaces

No other living organism has influenced the current ecological and epidemiological scenarios on Earth like humans have. The genus *Homo* evolved during the lower Paleolithic age. Populations expanded and retreated due to glacial and interglacial periods, alternating fragmentation, and contiguous interbreeding, experiencing both bottlenecks and considerable intrapopulation divergence. These phenomena also increased the rate of diversification of many organisms (Lovette 2005). The superfamily Hominoid (including the ancestors of *Homo* species and Great apes) history dates up to 30 Ma in Africa and Eurasia and is characterized by many extinct genera and species. The evolutive history of humans begins at the end of the Miocene (approx. 6 Ma), a period characterized by a large diversity of primates inhabiting tropical forests of Africa. The common antecessor of humans and chimpanzees is still controversial (*Orrorin tugeniensis*, Senut et al. 2001; *Sahelanthorpus tchadensis*, one million older, Brunet et al. 2002). Australopithecines, which are supposed to be the bipedal ancestors (approximately 4–1 Ma) of the *Homo* branch, expanded their range from woodland to more open grassland savannah-like environments in East and South Africa. This scenario was probably the first actual human–animal interface and entailed changes in exposures to new vectors and risks associated with eating meat. However, most hominin evolution in eastern

Africa transpired in the context of faunal communities unlike any known today (large-bodied mammalian herbivores differed markedly from those today until ~700,000 years ago). Therefore, there is controversy whether what we observe at present is a sufficient analog for much of the past (Faith et al. 2019). The genus *Homo,* academically termed "human," emerged in Africa around 3 Ma and comprises a highly diverse group, which is still not completely disentangled. The earliest *Homo* found outside of Africa seems to be *Homo erectus* around 2 Ma, and when interpreted in the broad sense (there is some dispute over which fossils should be included within the species), spanned a very large geographical range in Eurasia. The subsequent expansion of such hunter-gatherers into unfamiliar environments would have exposed them to various new pathogens.

The first hominins were omnivorous (Thompson et al. 2019) and consumed meat and marrow from bones (first tools date back from at least 3.4 Ma). *Homo* probably accessed large mammal carcasses mainly through scavenging (Blumenschine and Pobiner 2006). However, evidence also suggests primary access to ungulate carcasses through hunting for those Early Pleistocene human populations (Domínguez Rodrigo et al. 2010) and replaced active scavenging. The carnivore guild composition and food web structure present as *Homo* expanded probably influenced their expansion and access to meat resources, especially large herbivores, for the earliest European hominins (Croitor and Brugal 2010). Interestingly, the transition from a predominantly herbivorous diet to an omnivorous diet and then eventually toward a strongly carnivorous diet shaped a *predator–prey interface*, with epidemiological consequences for the rest of human natural history (Michelet and Dauga 2012). The consumption of wild animals that also were prey to a variety of predators could be a relevant path of pathogen interspecific transmission in a natural environment. For example, it is thought that about 2 Ma, hominids who scavenged for food or preyed on bovids were exposed to *Taenia* infections (a cestode whose adult forms are intestinal tapeworms; Box 1). These worms were using hyena and large cats as definitive hosts and bovids as intermediate hosts. It is speculated that there may have been a role for anthropophagy during the middle and late Pleistocene in maintaining cross infections in humans, providing a possible disease transmission route for taeniids and allowing parasites to survive when animal hosts were rare (Rudolf and Antonovics 2007). The descendants of the African hominids spread and diversified tapeworms cysticercosis (the intermediate cyst is present in human tissues) and taeniasis (intestinal tapeworms present in humans) around the world through migrations, and later, following the development of farming and animal movement and trade. Another interesting example is *Trichinella* nematodes. The current species diversified during the age of modern placental mammals, and early hominids may have first acquired *Trichinella* on the African savannah several million years before swine domestication as their diets shifted from herbivory to facultative carnivory (Zarlenga et al. 2006). Transmission of *Trichinella* depended on carnivory and scavenging of carrion among Eurasian and African paleoguilds. Particularly, *Trichinella spiralis* appears to have commenced its independent evolutionary trajectory several million years before pigs were first domesticated, thus, the ecological setting in which hominids first acquired *trichinellosis* may parallel that of *Taenia* tapeworms.

The migration of *Homo* spp. out of Africa started as early as approximately 1.8 Ma, with evidence of the presence of *H. erectus* in the Middle East and as far as South-East Asia (Dennell and Roebroeks 2006). An ancient cultural shift much earlier than agriculture first appeared might have affected human evolution dramatically: the controlled use of fire. Early hominins may have used fire in an ad hoc manner by at least 1 Ma, but the controlled use of fire arose more recently (only 300,000–400,000 years ago; Gowlett 2016), or about 790,000 years ago (Goren-Inbar et al. 2004). This had a major effect on human host–pathogen relationships in sterilizing food (Wrangham et al. 1999). However, concomitant cultural changes associated with fire use by early humans exposed to smoke at campfires, which could contribute to the emergence of the *M. tuberculosis* complex (MTBC), the etiologic agent of tuberculosis (TB; Chisholm et al. 2016).

Homo sapiens appear in the Upper Palaeolithic (300–200,000 years ago) in Africa, together with relevant technological advances. The fact that a recently discovered species, *Homo naledi*, lived at the same time and in the same region as *H. sapiens* in Africa reveals the diversity of human forms that existed during the late Pleistocene (including *Homo rhodesiensis*), and therefore, epidemiological relationships. Neanderthals and modern humans both occupied the same areas in Europe for thousands of years prior to the spread of modern humans into the rest of Eurasia. The cause of Neanderthal extinction remains unknown as they were diverse and complex. Interestingly, it has been proposed that infectious-disease dynamics can explain the localization and persistence of the interspecies boundary during this time period and that modern human could overcome disease burden earlier than Neanderthals, giving them an advantage in their subsequent spread into Eurasia (Greenbaum et al. 2019).

Box 1 Shaping a New Predator–Prey Epidemiological Interface: The Origin of the Taeniasis/Cysticercosis Complex at Human–Wildlife Interface

A new predator–prey interface and ancient human migrations promoted the emergence and spread of pathogens around the world, creating new opportunities for pathogen transmission at the human–wildlife interface, some of which later found a niche at the wildlife-livestock interface. The taeniasis/cysticercosis complex are zoonotic diseases still endemic in many regions of the developing world and well established at the human–livestock interface, with secondary roles of the wildlife component today (wild bovids and wild boar). Based on the hypothesis that *Taenia* spp. and their hosts share a common history (Michelet and Dauga 2012; Wang et al. 2016), molecular and computational tools have enabled reconstruction an evolutionary history of the three species of *Taenia* currently known to parasitize humans, causing taeniasis and cysticercosis: *T. solium, T. saginata*, and *T. asiatica*. Pork and beef tapeworms are globally distributed, each infecting approximately 50–60 million people around the world. It is likely that two independent host switches

(continued)

Box 1 (continued)

from carnivorous species led to the occurrence of taeniids in human hosts. The emergence of *T. saginata* and *T. asiatica* is consistent with shifts from a felid host. The emergence of *T. solium* implies a shift from hyaenids (Hoberg 2006). The diversification of *T. asiatica* is estimated to have occurred 41,000 years ago (34,000–98,000), during the late Pleistocene. Thus, ancestors of modern-day human tapeworms emerged during the early to late Pleistocene, an epoch during which significant climatic fluctuations occurred. The arrival of *H. sapiens* in Asia coincided with the estimated time of emergence of *T. asiatica,* suggesting that new populations of wild boar and/or new breeding and husbandry practices imported by humans into Asia contributed to the emergence of this new species. Molecular chronologies also highlight correlations between evolutionary events and biotic factors, including secondary host switches and human migrations, long before the true development of agriculture and animal husbandry. Later, the development of animal husbandry, making livestock preferential intermediate hosts, led to the worldwide distribution of these parasites, where both domestic and sylvatic cycles were able to meet at the wildlife-livestock interface. A recent comparative genomics study reveals that high rates of gene duplications and functional diversifications might have partially driven the divergence between *T. asiatica* and *T. saginata* already during the expansion of *H. erectus* in Asia.

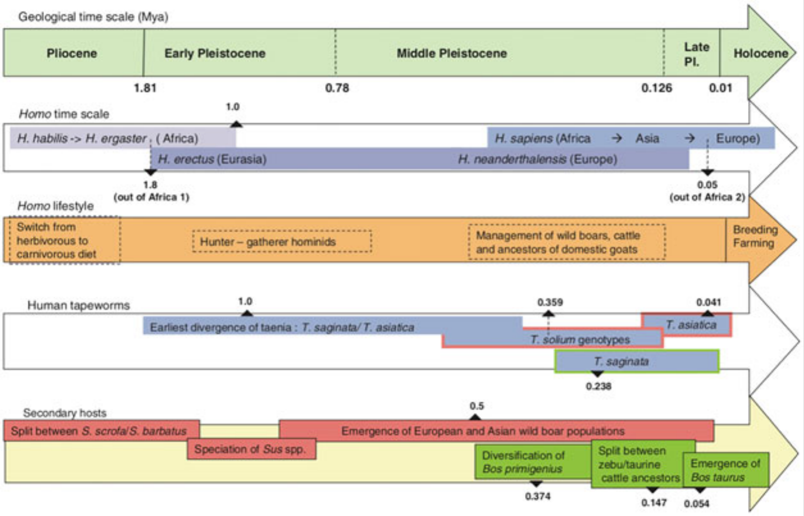

Figure Geological, human, and *Taenia* time scales (modified from Michelet and Dauga 2012). The length of the boxes for the time scale provides the 95% confident intervals. The arrow points represent the date of emergence.

During the Late Pleistocene (approx. 200,000 years ago), modern *H. sapiens* began dispersing out of Africa and into the rest of the world. The timing of the arrival of humans on each continent parallels the disappearance of many megafaunal genera (see above, the quaternary extinctions occurred 50,000–7000 years ago) and the extinction of larger carnivorans may also have provided niche space for dispersing humans. Interestingly, the late quaternary extinctions likely reduced the dispersal of pathogens by megafauna (Doughty et al. 2020). The migration of *Homo* spp. out of their African homeland similarly led to contact with new species and opportunities for cross-species transmission of zoonotic pathogens (Barrett et al. 1998). At this time, carrying capacity greatly depended on natural resources as the main driver of human and wildlife population sizes, and resource availability and distribution, and interspecific relationships (predation, competence, commensalism, etc.) determined community composition and interspecific opportunities for different species to interact and share pathogens. The influence of predators (e.g., lions) or prey (e.g., aurochs) on early humans was a force that caused humans to form cooperative groups or “tribes.” These small nomadic groups of hunter-gatherers, probably no more than 30–50 individuals, were highly mobile. These groups were likely too small and dispersed to support many of the acute pathogens that are/were typical of more densely populated sedentary communities (such as upper respiratory infections, and smallpox, measles, or mumps; Burnet 1962; Barrett et al. 1998; Düx et al. 2020).

Domestication: Origins and Diversity of Infectious Diseases at Animal Interfaces

Since the domestication process, human activities have promoted the emergence of new epidemiological spaces due to new interfaces created between domestic animals, wildlife, and humans. Animal domestication was a gradual process of intensification of the relationships between humans and animals over time, which culminated in relevant biological modifications observed in domesticates (Zeder 2015). This process was probably prompted by the demographic pressure of increasing human populations. Increased dependence of Neolithic humans on domesticated animals and plants led to semipermanent settlements, which later became permanent villages. Neolithic agriculture was independently developed several times and provided a new source of food and other goods to humans, which made increases in population density possible, and most habitable areas of the world were colonized around 12,000-years ago. Correspondingly, the human-livestock-wildlife interface plausibly started to serve a role as an epidemiological amplifier and source of pathogen emergence (Morand et al. 2014). New interfaces between domestic animals, wildlife, and humans were also introduced into new geographical areas or new host species during human travel and migrations. For example, rabies virus (Rhabdoviridae family) could be disseminated as dogs were brought to new continents long before the domestication of other species (Reperant et al. 2012).

Wildlife were the original hosts for most livestock pathogens, sharing them with domesticated species over centuries of coevolution and domestication. Domesticated animals then served as the source for many novel human pathogens, such as measles and smallpox (Pearce-Duvet 2006). However, domestication led to greater pathogen transmission between humans and domestic animals than other pairs of the complex human-wildlife-livestock interface, and many present-day human infections originated from zoonoses of domesticated animals (Wolfe et al. 2007). Additionally, the frequency of contact between humans (within and between communities), and the accumulation of infective material from human and animal waste increased. This favored denominated crowd diseases, which are now caused by more virulent and shorter lived infections predominate in large and densely settled populations (Zuckerman et al. 2014). Vectors also developed dependent relationships with human habitats. During the expansion of farming into new regions, the transmission of diseases such as malaria and yellow fever was favored (e.g., the yellow and dengue fever-carrying mosquito *Aedes aegypti* breeds preferentially in artificial containers; Thompson and O'Leary 1997).

Domestication and First Pastoralism

Over thousands of years (for most relevant species in Eurasia and Africa for 5000–12,000 years), animal domestication occurred following a sequence from the control of captive wildlife, to extensive livestock breeding, and finally, leading to intensive breeding (including pets). It is now clear that dogs were the first domesticated animal and originated from gray wolf (*Canis lupus*) before the development of agriculture (Larson and Fuller 2014). The intrusion of carnivores as secondary consumers of carcass remains (both cooked and raw) at abandoned human camps was a source of hominin–animal interactions and could have favored the domestication of wolves (Arilla et al. 2020). Apart from dogs, the earliest domestication of animals and plants most likely occurred in the Near East when hunting and gathering tribes began to domesticate goats and sheep at least 12,000 years ago. However, questions about the timing, location, and number of domestication centers remain unknown and recent genetic findings have proposed earlier domestication, up to 40,000 years ago (Freedman et al. 2014; Germonpré et al. 2017). The process of early domestication occurred in separate locations, including the Near East, Southeast Asia, eastern North America, highland Mexico, and Peru (Diamond 1987). For example, sheep (*Ovis aries*) were probably domesticated at least three separate times in the Fertile Crescent approximately 10,500 years ago and involved at least three different subspecies of the wild mouflon (*Ovis gmelini*). Genetic evidence suggests chickens were domesticated multiple times in Southeast Asia, China, and perhaps India (Liu et al. 2006; Kanginakudru et al. 2008).

Livestock and other domesticated animals have interacted with their wild counterparts and other wildlife since domestication began. Long-term contact and gene flow between wild and domestic stocks was common during the process of animal domestication and selective breeding of females was probably absent during the early phases of animal domestication (Marshall et al. 2014). In many cases, gene flow has not ceased until recent historic times. For instance, *Sus scrofa* exhibited significant introgression and gene flow between wild boar and domestic pig populations after domestication, indicating that initial domestication was probably not limited to a reduction of the number of wild boar from some local populations and subsequent genetic isolation, and new local wild boar lineages could rapidly replace "founding" lineages (e.g., Dzialuk et al. 2018). Another example of genetic flow, even hybridization, with potential epidemiological consequences at the first wildlife-livestock interfaces, or even before, is that of the European bison (or wisent, *Bison bonasus*; Fig. 4a, b), which is thought to be the result of hybridization between extinct bison and ancestors of modern cattle (aurochs, *Bos primigenius*) before 12,000 years ago (Węcek et al. 2017). Up to 10% of genomic ancestry in European bison today is from aurochs. Nuclear DNA sequences and morphology of wisent show close similarities to American bison (*B. bison*), but wisent mitochondrial DNA (mtDNA) indicates a closer relationship with cattle. This suggests some form of introgression from cattle or a related *Bos* species. The precise identity of the introgressor (aurochs or domestic cattle) is less certain, given the lack of knowledge of population structure in aurochs. Additionally, the European bison has no recognized Pleistocene fossil record and seems to suddenly appear in the early Holocene (<11,700 years ago). Taurine and zebu cattle from Asia also contain domestic cattle genes, descending from other bovine species with many combinations of mixed-species origin.

There is overall agreement on the common ancestors of domestic species. However, many details on the domestication process (beyond the scope of this book) and its consequences are still missing. The transition to domestication was a complex gradual process leading to the intensification in the relationship between wildlife and human societies (Vigne 2011), rather than an intentionally directed strategy. For each species, there were time periods of significant pre-domestication human–animal interactions (McHugo et al. 2019). However, multiple origins and the domestication process is relevant to the epidemiological role of the first wildlife-livestock interfaces. Vigne (2011) and Zeder (2012) grouped the phases of domestication into three general scenarios that seem to account for the full spectrum of animal domesticates: (1) commensal pathway, (2) prey pathway, and (3) directed pathway. The commensal pathway applies to animals, like dogs, that had initial contact with humans to feed on refuse or to prey on other animals attracted to human settlements. It is also possible that wild boar were drawn to human settlements to scavenge off refuse dumps and waste about 12,000 years ago (Ervynck et al. 2001). Epidemiological consequences of the commensal pathway included shared parasites. The prey pathway was probably followed by major livestock species because they were primary species that humans had hunted for thousands of years. Humans developed hunting strategies designed to increase prey availability when they became scarce over hundreds or thousands of years. The initial management of animals would consist in the rational control of animal resources which developed into herd management and finally, the controlled breeding of managed animals. For

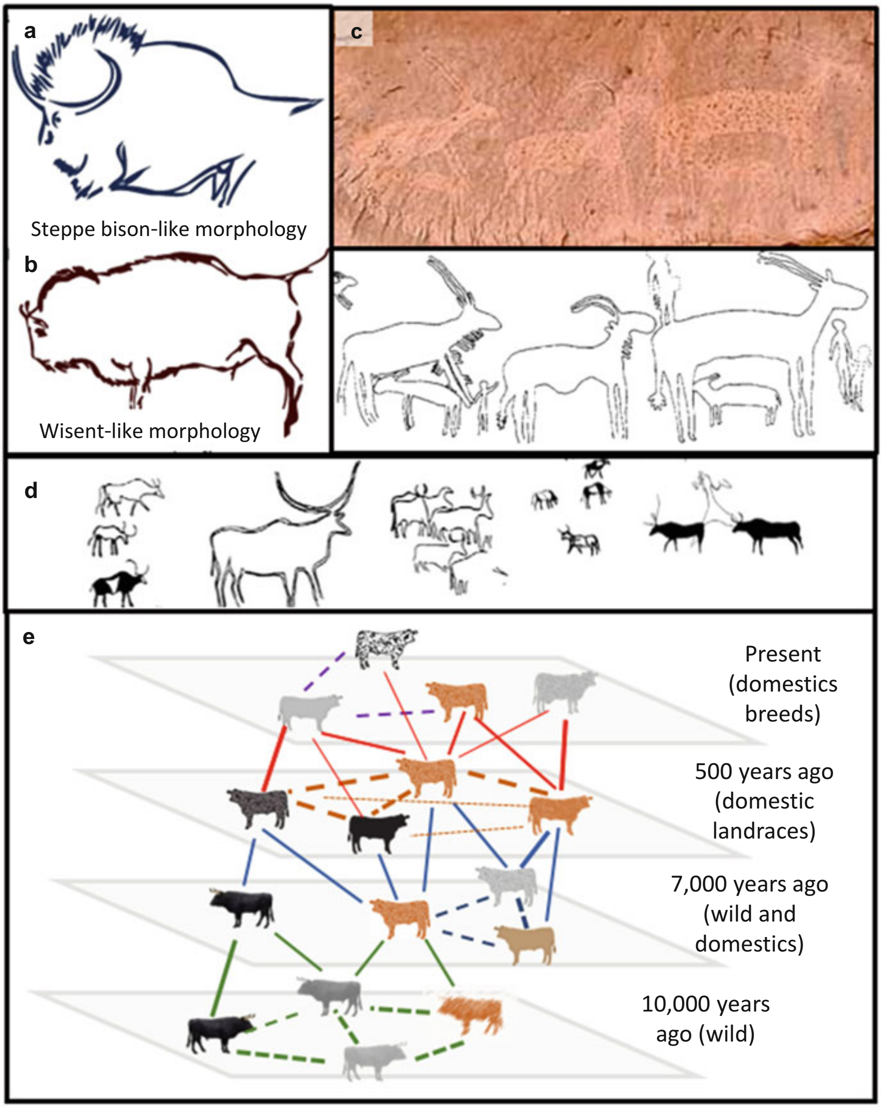

Fig. 4 Early cave artists recorded distinct morphological of ancient bison indicative of the replacement of the steppe bison (**a**) by the hybrid form (**b**) in Western Europe: reproductions (**a**) from Lascaux (France approximately 20,000 years ago) and Pergouset (wisent type, France <17,000 years ago, adapted from Lorblanchet 2001 and Soubrier et al. 2016). The combination of genomic, paleoenvironmental reconstructions, and cave paintings suggest that the hybridization of steppe bison with an ancient aurochs lineage during the late Pleistocene could have led to morphologically and ecologically distinct forms of bison (**b**). (**c**) Paintings at In-Taharin (central Tadrart Acasus) (After Sansoni 1994). This species was never actually domesticated but archeological remains suggest an intermediate domestication stage process occurred (Di Lernia and Cremaschi 1996). (**d**) Rock paintings from Tassili n'Ajjer in southwest Algeria showing putative domesticated cattle and a human figure, possibly a herder (Reproduced from

instance, baiting by means of the cultivation of wild plants in food plots was one of the first strategies. Reindeer (*Rangifer tarandus*) may be the most recent species to follow a prey pathway to domestication, and there is evidence for multiple independent reindeer domestication events (Røed et al. 2008). Interestingly, Barbary sheep (*Ammotragus lervia*) were never actually domesticated. However, archeological remains suggest an intermediate stage where "wild livestock" were kept, as an intermediate and necessary step to domestication, but fully domesticated sheep and goats arriving from the near East in the Neolithic probably interrupted the domestication process (Di Lernia and Cremaschi 1996; Fig. 4c). Finally, the directed pathway (fast track) to domestication begins when humans use the knowledge gained from the management of already domesticated animals to domesticate the next desirable wild species. This is likely the pathway followed in the domestication of the horse (*Equus caballus*) from wild horses (*E. ferus*) or donkeys (*E. asinus*) from wild Nubian ass (*E. a. africanus*; Rossel et al. 2008).

During the first transitional period, the Neolithic foraging economy still relied on hunting, while farming and pastoralism were progressively adopted. For example, between 12,000 and 11,000 years ago, goats were heavily exploited in the highlands of Lebanon and Syria, while Nubian ibex (*Capra nubiana*) was the target of intensive hunting. Over time, a primarily agropastoralist economy evolved (the change was appreciated mainly in the mid-10 millennium before present) where hunting was steadily "replaced" by herding. This facilitated a more constant and recurrent exposure to pathogens and possibly, the expansion and emergence of pathogens at the new interfaces. As Neolithization progressed, domesticated animals were introduced to other areas. The movement of managed herds outside the range of wild populations increased contact with other wild species and/or pathogen guilds, which furthered pathogen spread at the wildlife-livestock interface. As livestock became more globally distributed, the contact with close phylogenetic related wildlife and the opportunities for cross-species pathogen transmission intensified. Some ancestors during the expansion of domestic species become extinct, for example, aurochs, some wild Bactrian camel populations and wild horses. Predation, disease, competition for space and resources, and hybridization were inherent to the first wildlife-livestock interfaces. These interactions were not necessarily considered as conflicts by first pastoral societies, and there are regions where livestock and wildlife have coexisted for hundreds, even thousands of years with relatively few problems (e.g., some parts of Africa; Bourn and Blench 1999).

Early animal management involved herding, building shelters, and pens and the collection of fodder. Since these first steps, maintaining healthy animals and problems associated with inbreeding were recurrent. Herds were small and retained wild phenotypes due to regular restocking from the wild population, which probably resulted in significant disease issues. However, as a result of increased technical

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Fig. 4 (continued) Grigson 1991). (**e**) Spatiotemporal model of historical admixture and gene flow in European cattle populations (McHugo et al. 2019, reproduced under the terms of the Creative Commons Attribution 4.0 International License, http://creativecommons.org-licenses/by/4.0) competence and the availability of large, regional populations of domestic stock, and productivity progressively increased. The gradual development of systems of animal husbandry took place over several millennia and followed markedly different trajectories in different regions (Zeder 2012; Makarewicz and Tuross 2012; Vigne 2011; Arbuckle and Atici 2013). The Neolithic, Chalcolithic, and Bronze Age (c. 11,000–3200 years ago) periods encompass the major innovations in pastoral technologies in the ancient Near East, including:

- The earliest forms of pastoralism were characterized by a wide array of local, diverse, experimental pastoral economies, and relatively low herd productivity that evolved over a period of several millennia. Prehistoric pastoral nomads in southwest Asia were strongly associated with sedentary communities that practiced intensive plant cultivation, but there is no evidence to support the notion of a "dimorphic society" characterized by separate and specialized agriculturists and mobile pastoralists.
- By mid-to-late 8500–9000 BP, the organization of pastoralism shifted toward increased pastoral mobility, dispersed settlements, and greater emphasis on the exploitation of livestock for secondary products (dairy and fiber), and probable importation of new pathogens from other regions.
- During the late Chalcolithic (6000–5000 BP) period, changes in the pastoral economy are thought to have played an important role in the rise of the first complex urban societies in Mesopotamia, including increasing use of secondary products (wool and animal traction). Appearance of the domestic donkey and horse, as well as wheeled vehicles in southwest Asia, increased pastoral mobility, the expansion of sheep pastoralism into interior grasslands, and the development of mobile steppe regions, which intensified contact with new wildlife, pathogens, and vectors.
- A westward expansion of agricultural societies brought domestic taurine cattle, together with other livestock and crops, to central Anatolia around 10,000 BP. An eastward migration reached northern China or Mongolia between 5000 and 4000 BP. Cattle remains from Egypt and green Sahara have been dated from 5000 BP, and the earliest signs of livestock in Europe were found in Thessaly, Greece around 8500 BP.
- The fifth millennium BP is characterized by the proliferation of urban societies based on complex agropastoral economies. Pastoralists were highly integrated with cities, which intensified contact among animals (also peri-domestic) and with humans. Presence of urban markets for both primary and secondary animal products emerged. In the fourth and third millennia, BP mobile forms of pastoralism became more widespread, including specialized mobile pastoralists supplying settlements with animal products.

Consequences of Domestication and First Pastoralism at Wildlife-Livestock-Human Interfaces

Domestication created a new scenario for emergent pathogens, which adapted well to new conditions of multiple human–livestock–wildlife interfaces. This transition from human–wildlife to human–wildlife–domestic interactions was characterized by the maintenance of "crowd diseases" (both by humans and/or animals), the continuous presence of a domestic reservoir, and anthropophilic animals and vectors, which not only increased contact and exposure to pathogens, but provided space (interfaces) for evolution and adaption of pathogens to specific conditions. During the first stages of pastoralism, animals were reared in lower densities than today, and they could even be less prone to disease epidemics than those in high-density wild populations. However, wildlife and livestock cohabited and environmental or direct exposure to wildlife pathogens was common. Wildlife contacted escaped domestic animals, which already had developed more or less resistance to given pathogens, as still occurs today. Increased crowding without significant intervention measures to control disease during millennia of coexistence could select pathogens favored by high transmission rates, pathogenicity, or zoonotic potentials, both in livestock and in humans. Progressively, the development of husbandry practices created animal colonies or herds that were generally isolated from other wildlife but contained in crowded facilities. These conditions may have favored the spread of preexisting animal viruses and their divergence into specific genotypes, which later could spill over to wildlife. The history that accompanied the emergence of camel-infecting genotypes of hepatitis E viruses (Cagliani et al. 2019; Fig. 3) is an informative example. Authors dated the split of HEV-7 and HEV-8 from other genotypes ranging from 6300 BP to 3400 BP.

The development of animal husbandry also made livestock preferential intermediate hosts for many parasites capable of infecting humans (e.g., *Taenia*; Box 1) and led to their subsequent spread and worldwide distribution. For example, *Brucella* seems to have evolved through selection during the domestication of animals. The most virulent *Brucella* species with higher zoonotic spectrum are those from domesticated animals, while those that display lower pathogenicity and zoonotic potential are from wild animals (Moreno 2014; Fig. 1). The exception is *B. ovis*, which remains non-pathogenic for humans or for other animals (Blasco 1990) and it is speculated to be an earlier adaptation of *B. ovis* to sheep because it was already selected toward a higher affinity for venereal transmission in sheep before domestication of ovine (Moreno 1992).

Human migrations and trade favored the increase of livestock spatial ranges and the expansion of pathogens at the wildlife interface across the world. This first occurred within the domestic and/or human compartment, creating subsequent opportunities for pathogen transfer to wildlife. Many spillover events have probably occurred in which pathogens were eventually lost from the host without repeated reintroductions via cross-species transmission. However, the pathogen could be maintained at the wildlife-livestock-human interface and lead to the emergence of the disease in the new host species. In tropical areas, shared diseases at the wildlife-livestock interface prevented the expansion of pastoralism (e.g., gammaherpesviruses in ruminants, such as malignant catarrhal fever viruses) that keep certain regions seasonally off-limits for livestock. The opposite could also be possible because wild ungulates would be absent from human settlements due to diseases. For example, locally domesticated species (e.g., tropical bovids such as the mithan (*Bos frontalis*) of South Asia and the Bali cattle) performed better than ruminant species first domesticated in the Fertile Crescent (Felius et al. 2014).

As the final desiccation of the Sahara set in about 4500 BP, pastoralists gradually abandoned the Saharan region, shifting southward to the Sahelian biome, which were most suitable for their herds. However, they entered areas that exposed their herds to new disease challenges in more closed habitats of western Africa, where endemic tsetse flies transmitted trypanosomes from wild hoofed animals. Indigenous wild bovids are tolerant to this protozoan as the result of their long coevolution with the infection, but domestic livestock develops acute symptoms that often result in death. Similarly, African buffalo (*Syncerus caffer*) was probably the original host of the protozoan parasite *Theileria parva parva* (causing theileriosis or East coast fever transmitted by ticks), that infected cattle as pastoralists moved their herds into eastern Africa and zones of theileriosis for the first time (Gifford-Gonzalez 2000). This slow spread of domesticated animals south between 4000 and 3000 BP could also be attributed to diseases such as malignant catarrhal fever, Rift Valley fever, or foot-and-mouth disease. Even when agriculture and animal farming became more relevant, the ecological, cultural, and epidemiological relationship of humans and wildlife still were largely mediated by hunting. Hunter-gatherer societies persisted, even when increasingly confined to marginal areas. Within agricultural systems, farmers hunted in response to conflicts caused by predation upon domestic animals and to reduce competition for resources, such as water or pasture. Wild animals and their products could also be a source of pathogen entrance in livestock systems. However, as societies evolved, the balance of the wildlife-livestock interface progressively fell on the domestic side as the predominant host reservoir community, which continued and geographically expanded in the ages to come, where spillback and spillover roles have often changed.

The Neolithic transition toward an agricultural and pastoralist economy also facilitated the emergence of human-adapted pathogens due to the abovementioned factors (increased and closer contact between humans and animals, higher populations, higher densities in settlements, and mobility). For instance, when humans began to farm and live with their livestock, the evolution of a more virulent form of *Salmonella* was fostered. The analysis of the genetic material of old *Salmonella enterica* genomes (Key et al. 2020) provides evidence in support of the hypothesis that the cultural transition from foraging to farming facilitated the emergence of human-adapted pathogens that still persist today. The reconstruction of ancient *S. enterica* genomes from western Eurasia reveals how this bacterial pathogen evolved over a period of 6500 years. All *Salmonella* genomes recovered from foragers, pastoralists, and agropastoralists are progenitors to the strain *Paratyphi C* that specifically infects humans but is rare today. Those ancient *Salmonella*, however, probably did not display host specificity and instead infected humans and animals alike. It was previously suggested that old strains of *Salmonella* spread from domesticated pigs to humans around 4000 years ago, but the discovery of progenitor strains in humans more than 5000 years ago suggests they might have spread from humans to pigs. However, a possibility is that both human- and pig-specific *Salmonella* evolved independently from unspecific progenitors. Measles is another example of how pathogens crossed over to humans (Düx et al. 2020). There is controversy about when measles emerged in humans, because the historical descriptions of measles are relatively recent (late ninth century CE). However, recent research evidenced that measles virus diverged from rinderpest virus in the sixth century BCE, indicating an early origin for measles possibly associated with the coinciding rise of large cities (Düx et al. 2020). Düx et al. (2020) postulate that a bovine virus, the common ancestor of modern strains of rinderpest and measles, circulated in large populations of cattle (and possibly wild ungulates) since its divergence from peste des petit ruminants virus around the fourth millennium BCE. As a typically fast-evolving RNA virus, it may have produced variants that were able to cross the species barrier on several occasions, but small human populations could only serve as dead-end hosts. Then, as contiguous settlements reached adequate sizes to maintain the virus' continuous transmission, it emerged as a human pathogen.

The (1) establishment of local settlements, agriculture, and domestication of livestock spurred a large epidemiological change for human and animal health, which, during different times over the world, continued with (2) an intensification of regional contacts through trade and their epidemiological consequences. From a human perspective, the (3) first intercontinental explorations, imperialism and industrialization and more recently, (4) globalization, rapid urbanization, and climate, are primary transitional events determining changes in the wildlife-livestock-human interfaces.

Domination of the Land by First Civilizations and Regional Spread of Animal Epidemics

Over the course of human history, our impact on the natural environment has magnified, including our ability to alter, shape, and reshape nature. One notable effect was the creation of local interfaces established among domestic animals, wildlife, and humans. The alteration of environments and landscapes, such as clearing of trees to plant cereals, began from early Neolithics, and from the first civilizations, humans accelerated the decline of natural resources and wildlife. The development and expansion of trade with other regions, and the rapid growth of populations and concentrations of humans and animals in towns and cities permitted the spread of human and animal pathogens. This process, very relevant from the perspective of shared diseases at the livestock-wildlife interface, can be historically encompassed from the first civilizations that emerged in the Eastern Crescent to the development of intercontinental exploration, which provided the first glimpse of current globalization.

The earliest civilizations were characterized by complex divisions of labor and increasingly depended on trade with subsequent exploration and conflict. As a consequence, there was an increase in regional (continental) contact through trade and movement of livestock during approximately 5000 to 3000 BP (the first long-distance trade would occur between Mesopotamia and the Indus Valley in Pakistan around 5000 BP; McMichael 2004), promoting human and animal interactions. For instance, trade and animal movement fostered contact between domestic and wild Bactrian camels due to immigration of domestics from Iran (where wild camels were extinct) eastward to Mongolia, where native wild Bactrian camels still roam (Ming et al. 2020). Human actions significantly increased dispersal of hosts, pathogens, and vector species, enabling host switches (Rogalski et al. 2017). However, trade and movement effects on the history of animal disease dispersion were complex, as indicated by recent genomics and paleogenomics. For instance, after substantial evolutionary divergence between *B. taurus* (taurine) and *B. indicus* (zebu) cattle, it is evident that extensive zebu-taurine admixture occurred in African and Middle Eastern cattle populations (see Fig. 4d, e); which also may also be applicable to other areas or domestic livestock as they and their pathogens migrated, first with early agriculturalists, and later with traders and conquerors as they encountered related domestic or wild species.

Ancient civilizations had an impact on wildlife abundance, diversity, and distribution as wildland habitats were converted to agriculture (Angelakıs et al. 2020). Since then, many species have shown relatively high tolerance to humans and have adapted well to anthropized environments (e.g., roe deer and wild boar in Europe). Some species have greatly benefitted from peri-domestic habitats (urban or agricultural environments), even becoming pests in some localities. The dependence on natural resources made it such that the depletion of natural resources accompanied the decline in the power of old civilizations (e.g., Eastern Crescent, northern Africa, Mediterranean basin). Later, human civilizations progressively accelerated the transformation of landscapes over other regions of Eurasia and the rest of the inhabited world (Kaplan et al. 2009). The most important initial anthropogenic alterations of the natural environment that impacted wildlife-livestock interfaces was forest clearing to establish cropland and pasture, and the exploitation of forests for fuelwood and construction materials (Kaplan et al. 2010).

Following the case of Europe, the first detailed reports on livestock husbandry came from Greek and Roman civilization, with detailed contemporary accounts.

Transhumance, the seasonal migration of humans to provide pasture to their herds, was well established during the Classic period. This mobile pastoralism was associated with well-defined spatiotemporal interfaces occurring between livestock in wintering (e.g., lowlands in Mediterranean areas) and estivation (mountainous areas where open pastures were shared with wildlife and maintained with fire) quarters, where pathogens were also transported. Cattle from ancient Greece could be exported to several regions of western Europe, and Roman conquest further expanded the social, economic, and agricultural organization, including animal farming strategies (Colominas et al. 2014). The collapse of the Roman Empire was followed by periods of large-scale migration of Germanic and eastern European peoples and their livestock during the fifth and sixth century AD (Trentacoste et al. 2018). The migrations probably led to a considerable mixing of livestock, particularly cattle and horse populations from various European regions and their pathogens. It has been suggested that numerous concurrent human–bovine epidemics in the early medieval period (sixth to tenth centuries AC) were caused by an immediate ancestor (now extinct) of measles and rinderpest that was pathogenic to both cattle and humans (Newfield 2015), and even earlier concurrent human–bovine mortality events may have occurred before in Rome (Spinage 2003). During the following centuries, introduction of measles into naive human populations and/or flare-ups of the disease might have caused some ancient epidemics whose etiology remains uncertain.

About half of western European forests are estimated to have been cleared prior to the Middle Ages and deforestation increased gradually but steadily during 1000 years of medieval European history, alternating periods of increase and decrease due to historical and climatic contexts (Kaplan et al. 2009). For instance, collapse of the European human population due to the bubonic plague in the mid-fourteenth century may have resulted in the abandonment of up to 25% of all croplands (Yeloff and van Geel 2007). Forests returned in many areas, some to their previous levels within a hundred years.

Livestock diseases affected local populations in the Middle ages and importing animals from neighboring regions for restocking is likely to have caused both intensive gene and pathogen flow (Felius et al. 2014). There were also remarkable cultural and technological developments produced by the renaissance society and increasing urbanization. Fencing of pastures and cultivation of animal feed became common and storage methods improved, allowing for the survival of larger numbers of livestock during the winter. The export of animal products was of considerable importance and large numbers of animals were exported to surrounding countries (Felius et al. 2014). In most of western Europe, cattle were still kept as part of a mixed farming system (for the purpose of traction and dairying), but a thriving and highly organized cattle ranching economy developed in Spain where large herds of 1000–15,000 work and beef cattle were kept under extensive management and in close interaction with wildlife.

Worldwide Expansion of Wildlife-Livestock-Human Interfaces, Industrialization and First Glimpses of Globalization

The growing interdependence of the world's economies, cultures, and populations brought not only by regional, but also intercontinental trade and transportation, included animals, their pathogens, and vectors, which impacted current interfaces and created new ones. This period is characterized by *intercontinental exploration, colonization/imperialism, and the agriculture and industrial revolutions.* All these events provided opportunities for animal pathogens to cross considerable geographic boundaries and influenced modern agricultural practices and the characteristics of modern wildlife-livestock interfaces.

In general, agriculture inevitably transformed the land. Removal of natural vegetation impacted wildlife abundance, distribution, and behavior. Concurrently, the number of livestock husbandry practices have been increasing ever since pre-industrial times and have determined wildlife-livestock interfaces. Overall, wildlife is becoming less abundant, and populations are more fragmented and isolated (Kaplan et al. 2009). As for most large mammals, the cumulative impact of human activities had driven most species into severe declines and regional extinctions by the end of the Holocene (i.e., late nineteenth and early twentieth centuries), a trend that has continued for many of the planet's wild ungulates (Ripple et al. 2015). As landscape changes progress, the interface has become more local and occurs at smaller spatial and more fragmented scales. From the Old-World perspective, transformation of the natural landscape of Europe by deforestation continued from the Middle Ages until the nineteenth century. The rate of deforestation remained high during the early decades of the industrial revolution so that by 1800 AD most European countries were largely deforested. This habitat change influenced an important regression of the wildlife component of the interface. By the seventeenth century, growing human populations resulted in an ever-increasing demand for animal products (meat and dairy) and the expansion of cultivation has greatly reduced the forests which once covered so much of medieval Europe. When changes in agricultural practices improved productivity and slowed the clearing of forests for crops, and later, when fossil fuels replaced wood as the main source of industrial energy, wildlife populations, mainly ungulates and later carnivores, slowly recovered. We are still witnessing this recovery process and during the last several decades some wildlife populations in developed countries, such as ungulates, have adapted and are thriving and creating serious concerns at the interface (Gortazar et al. 2006).

In other regions, China's population reached 413 million and forest cover was 17% by 1840 (Liu and Tian 2010). The forests of southern Asia were cleared to provide cropland to support the rapidly expanding human population (FAO 2016). In 1500, the population of India was 100 million, more than twice that of Europe. It is probable that more than half of southern Asia's historic forest area has been lost in the last 500 years. Unfortunately, deforestation and forest degradation are still increasing in our globalized world (see below). Latin America was probably about 75% forested before European settlement (Sponsel et al. 1996), but today it is about 50% forested. European livestock occupied the space and replaced the role of native wild herbivores (e.g., big rodents in Llanos of Venezuela) in introduced ranching practices. In North America, as populations increased and settlers pushed westward in the nineteenth century, the rate of forest clearing and opportunities for interfaces with wildlife increased rapidly. By the early twentieth century, however, deforestation had largely stopped in North America (McCleery 1992). Forests in Africa are extremely diverse and over the centuries, in sub-Saharan Africa, deforestation and human populations have gradually increased together, with the greatest forest losses coming in areas where wood is needed for fuel or where forest land is needed for growing crops (FAO 2012b).

In Europe, the export of local livestock from areas characterized for their production to neighboring countries was well established during the sixteenth century. Movement of large herds of livestock to big cities for consumption occurred within and among countries. Livestock production increased in response to the demand of urban populations and the higher density of animals fostered the dissemination of infectious diseases such as the cattle plague, which in the eighteenth century devastated continental Europe. Livestock types that existed in Europe were regionally adapted and only since the late eighteenth century has selection for certain traits began to be practiced. Overall, the history of livestock on other continents during this period is not as dynamic as it was in Europe. However, on the Indian subcontinent, several zebu breeds have a history dating back to the late 16th century.

At the end of the nineteenth century, a devastating rinderpest (a morbillivirus, family Paramyxoviridae) epidemic spread throughout the African continent. The epidemic started in Eritrea in 1887, possibly introduced by Indian cattle brought by the Italians, and reached the Atlantic Ocean in 1893 and South Africa in 1898. According to some accounts, it killed 90% of all African cattle and devastated wild ungulates (i.e., buffalo, giraffe, and wildebeest). Rinderpest probably had their origins in an environment where cattle and humans were living in close proximity, likely from the cattle herds of Central or South Asia some 10,000 years ago at the time of domestication of the wild aurochs. Although rinderpest was eliminated from southern Africa shortly after the turn of the twentieth century, it became enzootic in other parts of the continent, often in wildlife, until eradicated globally in 2011. The partial resistance of zebu to rinderpest with a mortality of only 10–30% led to a drastic replacement of many taurine populations, and zebu is now the dominant species in West and East Africa. They are not, however, kept in the coastal regions infested with tsetse flies, where the trypanotolerant African taurine cattle have remained the primary domestic cattle breed.

Domestic animals, particularly ruminants and swine, were essential components of European colonial projects around the globe during this period of expansion. The exploration and colonization of North and South America resulted from the so-called Columbian exchange, i.e., the respective introduction of crops, livestock, and their associated pathogens into Europe and America. American domesticated animals (like llamas and guinea pigs), compared with European livestock, had a reduced potential for zoonotic disease. Therefore, Americans lived relatively free of animal-borne diseases. However, they faced severe risk when novel Old-World pathogens were introduced. It is estimated that livestock-derived zoonotic diseases contributed to the loss of as much as 90% of the native American population of humans (Jones 2004). For example, in 1493, an outbreak of what is now thought to have been swine influenza struck Native Americans in Hispaniola. There is some evidence to suggest that the infection source was pigs from Columbus's ships. Europeans also took measles and smallpox to the New World, where it caused devastating epidemics in the early sixteenth century. Native Americans were not exposed to smallpox or measles until the arrival of Europeans to North America and their genome had not experienced selection pressure by these pathogens. There is evidence that the immune-related genes of the ancient American were well-adapted to local diseases but not to novel infections (Lindo et al. 2016). On the other hand, the exchange resulted in the introduction of treponemal infections to Europe (Baker and Armelagos 1988). Horses, pigs, cattle, goats, sheep, and several other species adapted readily to conditions in the Americas, where broad expanses of grassland where available. By 1525, more than 1000 Spanish cattle populated the Caribbean colonies, from where they spread to Spanish colonies in America (Felius et al. 2014); bringing along their associated pathogens, including Texas fever, caused by *Babesia*. In South America, wild camelids (vicunas and guanacos rapidly following the Spanish conquest due to hunting and competition with sheep and cattle (Acebes et al. 2012; FAO 1996). Today remaining wild camelid populations are either endangered or extremely threatened (Wheeler 2012). The spread of European settlers and their domestic animals throughout northern Europe and North America during the past four centuries was followed by the deliberate extermination of large predators, including seven subspecies of wolf (*Canis lupus*; Day 1981). Livestock also caused serious damage to inlands ecosystems (e.g., New Zealand and Pacific). Some introduced livestock or domestic animals, like pigs, horses, and ferrets, easily became feral and constitute part of the present wildlife-livestock interface (Long 2003). For instance, in North America a large proportion of wild ungulates in the Great Plains were exterminated. An estimated 30–60 million plains bison (*Bison bison*) roamed North America in 1500 and were reduced to their lowest point in 1884 (425 bison; Lott 2002). Today, there are thousands of woods and plains bison, however, bovine tuberculosis and brucellosis are of serious concern in some populations that interface with livestock (Shury et al. 2015).

Agriculture and Industrial Revolutions

The agricultural revolution, initiated in Britain, led to modern farming, and stimulated an increase in agricultural production between the mid-17th and late 19th centuries. Advancements were attributed to new agricultural practices such as crop rotation, selective breeding, and a more productive use of arable land (Williamson 2002). Selective breeding for desired traits was established as a scientific practice (mating of related animals with similar traits) to fix certain characteristics in animals, including cattle breeds used primarily for beef (Molne 2010). Certain practices displaced the wildlife-livestock interface in newly industrialized countries, such as by converting some pastureland into arable land and increasing habitat more appropriate for wildlife, such as fenlands.

Almost in parallel, the industrial revolution started in England in the second half of eighteenth century and led to further urbanization and increased demand from cities for agricultural products (Molne 2010). Since then, developed countries of the world have all gone through the process of industrialization, with important consequences for agriculture. First, industrialization was always accompanied by rapid population growth, which increased the demand for food and subsequent need for crops and livestock. This encouraged the decline of subsistence farming and increased use of machinery, which decreased the demand for farm workers and influenced others to move to industrial cities. The industrial revolution marks a historical transition in late modern history that eventually led to the globalization we know today. It is considered the second epidemiological transition from the human perspective since pandemics receded and resulted in a shift in patterns of disease and mortality from primarily infectious diseases to what are referred to as "chronic" diseases (McKeown 2010). The massive growth of livestock production was possible due to increased farming intensification and trade of animals. A new model of dimorphic wildlife-livestock interfaces began to emerge in developed countries, characterized by significant encroachment of natural habitats by agriculture (especially from the late nineteenth century). This caused more complex disease dynamics and compartmentation of the relationships between domestic animals and wildlife. Options for disease control are more difficult, for example, when wild reservoirs are present. Phylogenetic analyses indicate that the emergence of human metapneumonia ancestors some 150–200 years ago coincides with the industrialization of the poultry industry (de Graaf et al. 2008), and the massive expansion of strain diversity of influenza viruses in swine and poultry correlates with the increase in industrial populations of swine and poultry worldwide. In the second half of the nineteenth century, a highly infectious respiratory disease with a high mortality rate affected cattle herds around the world, though it is difficult to distinguish the exact cause by just clinical symptoms it was likely a contagious bovine pleuropneumonia caused by *Mycoplasma mycoides mycoides* (Caswell and Williams 2016). Interestingly, the dating of the most recent common ancestor of bovine coronavirus BCoV and human coronavirus HCoV-OC43 is around 1890 (based on the spike of gene sequences; Vijgen et al. 2005; Bidokhti et al. 2013). During the slaughtering of affected herds, there was ample opportunity for culling personnel to contact bovine respiratory secretions, which could have contained BCoV, either as the causal agent or as a coinfecting agent. It can be hypothesized that the bovine respiratory disease in the second half of the nineteenth century might have been similar to the coronavirus-associated shipping fever disease.

One World, One Interface

The total number of livestock declined dramatically during the First and Second World War in most countries involved, especially in developed regions. However, the numbers of pigs, cattle, and poultry have increased considerably since. Food animal production in much of the world, beginning in the USA, has been transformed from traditional small-scale methods to industrial-scale operations that are vertically integrated, in which most aspects of production are controlled by a single entity (Graham et al. 2008). Industrial animal production includes high-tech animal husbandry, increased veterinary oversight, and formulated feeding, often with the addition of antibiotics to increase growth rates and feed conversion efficiency. About 60% of all mammals on Earth are livestock, mostly cattle and pigs, and 36% are human (globally, livestock and people constitute 97% of the world's mammal biomass; Thomas 2017; Berger et al. 2020). Wild mammals account for just over 4% of mammal biomass on Earth today. For example, the biomass of chickens is approximately over double the total mass of all other birds combined on Earth. The destruction of wild habitat for farming, logging, and development has resulted in the start of what many scientists consider the sixth mass extinction of life to occur in the Earth's four-billion-year history. However, some pastoral systems are biodiverse (e.g., savannah-like habitats in Spain called Dehesas; Gaspar et al. 2009). Humans represent just a hundredth of a percent of the Earth's biomass but have driven down the biomass of land animals by 85% and marine mammals by about 80% since the beginning of the last major extinction approximately 50,000 years ago. Wildlife on Earth have overall been reduced by humans to their lowest level in history. This impact is variable based on taxa, capacity of wild species to adapt to perturbed (anthropized) environments, geographical region, and recent history. However, disease issues at the wildlife-livestock-human interfaces are of increasing concern and far from being solved, but why?

During the twentieth century, significant epizootics of diseases at the wildlife-livestock interface occurred worldwide, such as foot-and-mouth disease, rinderpest, avian influenza, and African and classical swine fever. In certain cases, such as cattle rinderpest, measures that included vaccination were able to progressively reduce the prevalence of disease. Rinderpest reached the Americas in the nineteenth century by imported livestock and was eradicated in 1929 in the USA. In 1994, the Food and Agriculture Organization (FAO) launched a Global Rinderpest Eradication Programme and it was announced that rinderpest had been eliminated from the world in May 2011 (FAO 2012a). Another example is influenza viruses, which have evolved into numerous strains, posing threats to their natural hosts, pigs and birds, and jumping to humans (Taubenberger and Kash 2010). Migratory patterns of numerous wild bird species have spread influenza across continents throughout the ages, and in recent outbreaks has also affected the interface with poultry. Pandemic influenza viruses have caused significant mortality in humans. In the twentieth century, 3 influenza viruses caused major pandemics: the 1918 H_1N_1 virus, the 1957 H_2N_2 virus, and the 1968 H_3N_2 virus. These pandemics were initiated by the introduction and successful adaptation of a novel hemagglutinin subtype to humans from an animal source, resulting in antigenic shift (Smith et al. 2009). There is no empirical evidence that swine played a role in the emergence of human influenza pandemics in 1918, 1957, or 1968, but swine-to-human transmission occurs periodically and can trigger pandemics, as in 2009. Swine are not the only species capable of mediating the establishment of avian viruses in humans (Nelson and Worobey 2018). The virus that caused the 1918 influenza pandemic probably emerged from North American domestic and wild birds. While this last topic remains a point of discussion (Worobey et al. 2014), the message, as Rudolf Virchow stated in 1856, is that "between animal and human medicine there are no dividing lines," nor should there be. The wildlife-livestock interface term should equally be used for the term wildlife-livestock-human interface. Today, we estimate that almost 77% of livestock pathogens infect multiple host species, including wildlife (Cleaveland et al. 2001). This final section of the chapter offers a general perspective of the globalization of the wildlife-livestock-human interface. We note that brief introductions to current situations and specific characteristics of the interfaces in different regions are provided in successive chapters.

The Globalization of the Wildlife-Livestock-Human Interfaces

After numerous historical events (world wars, protectionism periods, and economic depressions), a definitive wave of globalization has occurred, with enormous consequences for the interfaces and their connections. Globalization has resulted in enhanced trade in livestock, other animals and their products, the relocation of farming centers, industrialization of farming, and unprecedented speed, volume, and reach of global air travel. Altogether, leading to increased risk for diseases to emerge at the wildlife-livestock-human interfaces, and spill back to wildlife (e.g., foot-and-mouth disease, peste des petits ruminants, African swine fever, Newcastle disease, highly pathogenic avian influenza, and zoonotic diseases like Ebola, West Nile fever, severe acute respiratory syndromes caused by coronaviruses, Nipah, Hendra, swine flu). From the human perspective, it has been proposed that this is a new epidemiologic transition (third), which combines the effects of globalization and ecological disruption (McKeown 2010). This transition is characterized by the emergence and re-emergence of an unprecedented number of diseases, most of which include a wildlife and/or domestic component, such as Ebola virus, Hantavirus, leishmaniasis, West Nile virus, Lyme disease, and human pathogenic coronaviruses. Although most of the global population now lives in urban environments, globalization has linked the health problems of impoverished communities with other populations throughout the globe (Neiderud 2015). Correspondingly, all humans and animals tend to be more frequently share a common global infectious disease ecology.

Over the last century, livestock evolved from highly localized production, often in mixed systems, where animals were typically born, fattened, and slaughtered in the same region, to *relocated intensive animal production*, where the number of live animals traded for food among regions and countries has exponentially increased. This long-distance live animal or product transportation amplifies risks derived from the concentrated and intensive nature of current industrial farming practices. In the past, pathogens would have simply emerged and died out; instead of being transmitted to livestock and amplified. For example, outbreaks of the highly pathogenic avian influenza virus H_5N_1 were reported across eight countries in Southeast Asia nearly simultaneously in 2004 (Tiensin et al. 2005). The pattern and timing of outbreaks suggested that the transport of live birds reared for human consumption was the primary cause in the rapid spread (FAO 2007). The long-distance transport of live animals was also related to the spread of swine influenza viruses in the USA, a large country where livestock may travel hundreds or thousands of miles (Greger 2007). The possibility of fast spread is a relevant concern for human and animal health. During the last several decades, sequencing of viral genomes evidenced triple reassortment of human, avian, and porcine influenza virus gene segments (Zhou et al. 1999). Apart from livestock, animals translocated for other human uses, such as exotic pets captured in the jungles have also been implicated in the spread of diseases affecting human and other animals (Chomel et al. 2007). For instance, pet bird shipments have likely been involved in the introduction of West Nile virus from the Middle East (Lanciotti et al. 1999) into the Western hemisphere (Rappole et al. 2000). Another example is the movement of hares from central and eastern Europe for hunting purposes that led to several outbreaks of tularemia (Godfroid et al. 2005).

The so-called “Livestock Revolution” initiated in the 1970s, in response to world population increase, urbanization, higher incomes, and demand for animal products expanded rapidly to developing countries. The world’s meat production nearly doubled from 1980 to 2004 (FAO 2006). This revolution implied a progressive replacement of traditional systems by intensive systems, where large numbers of genotypically similar animals are farmed under concentrated confinement with rapid population turnover (Pearson et al. 2005). Efficient and productive industrial animal production poses environmental concerns due to the large amount of waste, gas emissions, and elevated need for feed (e.g., soy and alfalfa), most of which is produced far away from industrial farms. There are also associated disease risks for animals and humans. High concentrations of genetically homogeneous animals kept indoors allows for the rapid selection, amplification, and dissemination of pathogens (Delgado and Narrod 2003; Pearson et al. 2005). Crowding of increasingly greater numbers of animals into increasingly smaller spaces has been identified as a critical factor in the spread of disease (Delgado and Narrod 2003). In the USA, the average number of animals in each chicken, pig, and cattle operation approximately doubled between 1978 and 1992 (Tilman et al. 2002), and a small proportion of farms produce most of the pigs or poultry.

The wildlife-livestock-human interface is more interconnected than ever. Wildlife-livestock-human interface is increasing as a result of human encroachment into wilderness, especially in tropical ecosystems (see Chapter “Host community Interfaces: The Wildlife-Livestock”). This increased population pressure on land use is also mediated by hunting and consumption of “bush meat,” capture of wildlife that is shipped to live animal markets (e.g., wet markets), and farming of game animals in proximity to traditional livestock and humans, which increases cross exposure to new pathogens originating from wildlife (e.g., bat coronaviruses). Mix farming, or the integration of crop and animal production, is well developed in developing countries, together with small-scale agriculture. There are a vast range of modalities and practices (Devendra and Thomas 2002) and opportunities for interaction with wildlife and there is increased exposure to new pathogens often in areas recently encroached. Additionally, the intensification of animal production favors increasing livestock-to-human contact, and in certain cases, with peri-domestic animals. Design and operational requirements of large-scale farming often result in compromises of biosecurity, and multiple pathways are available for exchange among wildlife (e.g., birds), other livestock, and other animals, as well as humans. Certain bridge hosts, such as "peri-domestic animals" (rodents, pets, birds) commonly associated with industrial animal agriculture (Slingenbergh et al. 2004), may vector pathogens from the outdoors to indoors. For instance, wild birds in proximity to farms and backyard productive systems with low biosecurity measures and close contact among several animal species are considered risk factors for the emergence and spread of influenza A virus. The confinement of thousands of animals requires controls to reduce heat and regulate humidity, and high-volume fans that result in a considerable movement of materials into the external environment. Waste and manure may also become a pathogen transmission route, particularly transmission of food-borne pathogens such as verotoxigenic *E. coli* and S*almonella* (Newell et al. 2010; Fig. 5). Intensification also requires greater frequency of movement of people and vehicles on and off farms, which further increases the risk of pathogen transmission. Effective management and biosecurity measures can mitigate between-herd and wildlife interactions (see Fig. 6). Due to increased poverty, the proximity of increasingly concentrated smallholder farming communities to intensified, industrial farming systems is growing, creating conditions conducive for disease emergence and entrenchment. Often, diverse types of production, ranging from free-range to outdoor paddocks and finally, intensive production, are epidemiologically connected, which make it difficult to control pathogens within compartments and at the interfaces established between livestock, wildlife, and humans (see Fig. 2b of Chapter "Host community Interfaces: The Wildlife-Livestock").

Antimicrobials are often used in industrial systems for growth promotion, disease prevention, or therapeutically, but can promote the evolution of antimicrobial-resistant pathogens that later can be transmitted to humans and wildlife. Paradoxically, 10,000 years ago, domestication of animals gave human populations zoonotic infections, but interactions with domesticated animals are now conferring drug-resistant infections. Drug resistance is even a growing concern in wildlife populations.

As a common determinant at the global level, climate change, particularly global warming, has changed ecosystems in many regions and has subsequently extended the distribution of several vectors that transmit diseases such as Rift Valley Fever, West Nile Fever, and Bluetongue. The, establishment, development, phenology, survival, and transmission of many pathogens depend on environmental conditions

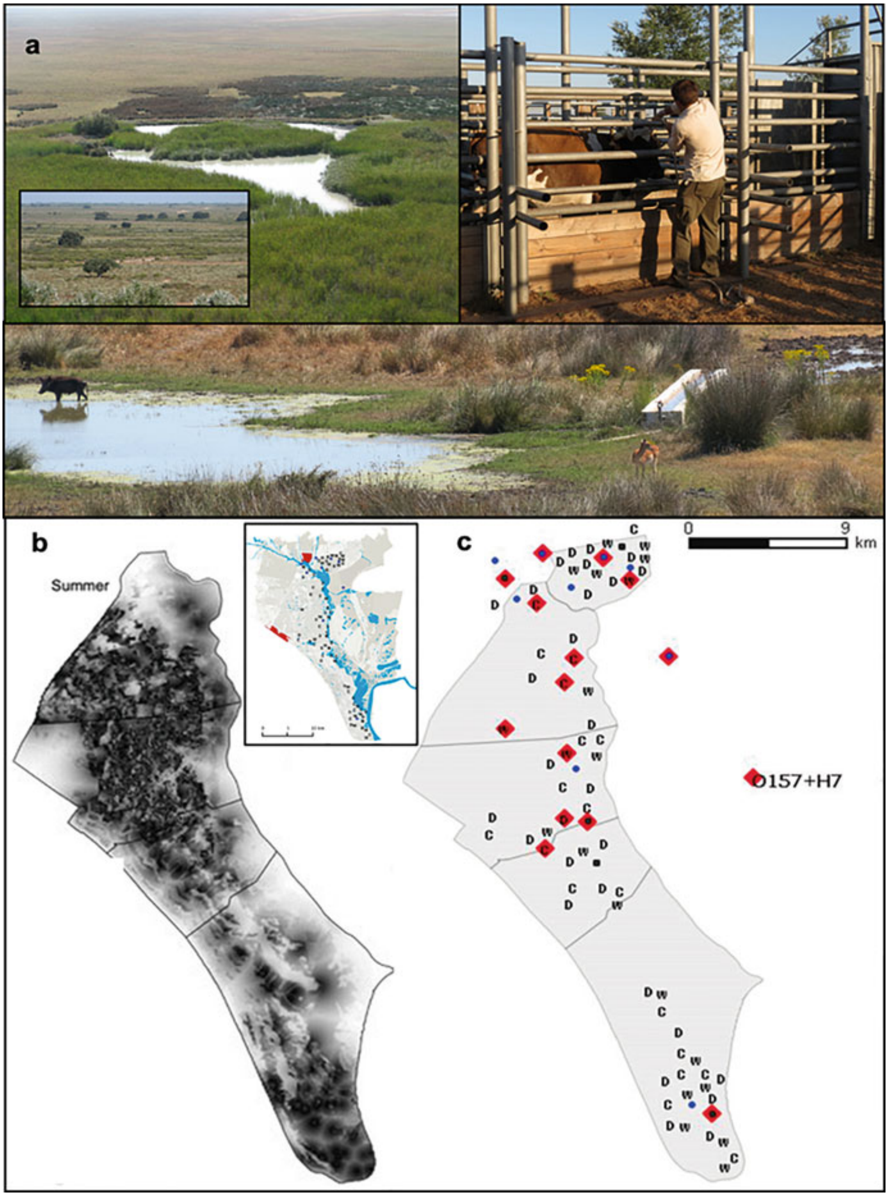

Fig. 5 Representation of the biotic homogenization at the wildlife-livestock-human interfaces. In relation to the distribution of *Escherichia coli* virulence genes in natural habitats (reproduced from Cabal et al. 2017). (**a**) Doñana National Park (South Spain) is considered one of the most important European wetlands in terms of biodiversity where extensive livestock (cattle, horses) and wild ungulates (red deer, fallow deer, and wild boar) share habitat. (**b**) As indicative, it represents the map of interactions (in gray tones) between wild boar and cattle based on telemetry (Barasona et al. 2014). (**c**) Spatial distribution (positive samples in red) of selected *E. coli* genes (rfb_{O157} + $fliC_{H7}$) detected in pooled fecal samples (*C* cattle, *D* deer, *W* wild boar), surface water (blue dots), and septic tanks (black squares) collected in DNP, Spain. The small map in between indicates urban nucleus (red) and surface waters (blue)

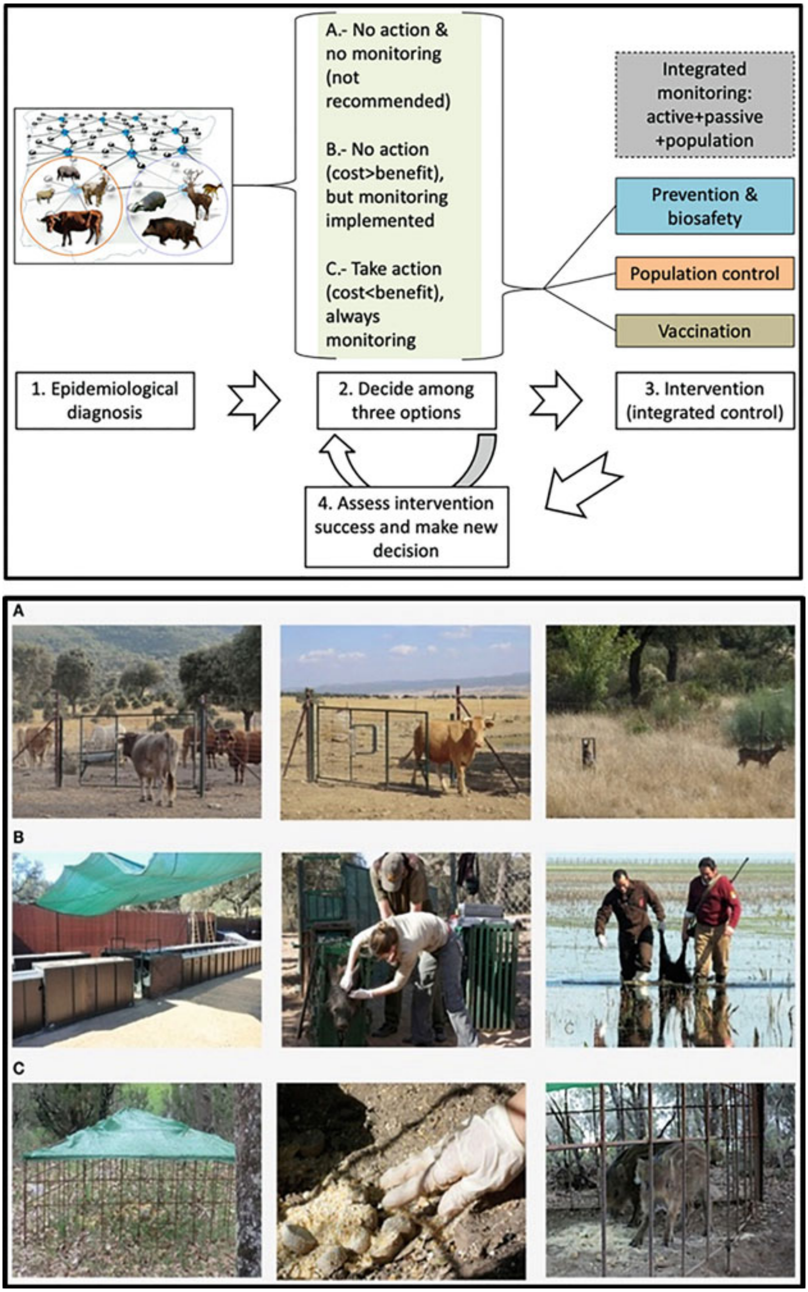

Fig. 6 The recent impacts of diseases on the wildlife-livestock interface have contributed significantly to shaping the current patterns of pathogen emergence, and therefore a better scientific understanding is essential to identify and manage risks. Top: Flowchart of the available disease control options and result assessment in diseases shared with wildlife. Bottom: Examples of some disease control options currently applied: (**a**) Farm biosecurity by segregating wildlife and cattle

(e.g., Rose et al. 2014). As a consequence of the environmental perturbations caused by climate (and associated anthropogenic change), the distribution, abundance, behavior, and population dynamics of pathogens and hosts have been impacted, so as transmission dynamics (Altizer et al. 2013; Molnár et al. 2014). “Warming of the climate system is unequivocal, and since the 1950s, many of the observed changes are unprecedented over decades to millennia” (concluded by the Intergovernmental Panel on Climate Change, IPCC 2013). However, the pattern of global warming is not spatially homogeneous, and therefore, the impacts we will observe at the wildlife-livestock interface. For, instance, the reduction of a population of moose (*Alces alces andersoni*) between 1960 and 2000s in Minnesota occurred in parallel to an increase in temperatures and lengthening of the annual growing season, which could interact with nutritionally deficient habitat at the edge of the species range (Murray et al. 2006). Multiple factors may participate together with climate change to determine epidemiological impacts at the wildlife-livestock interface, particularly in multiple host/vector systems, and we are just starting to understand the interactions between climate and host/pathogen responses (Rohr et al. 2011; Altizer et al. 2013).

Increasing biotic homogenization, including the spread of pathogens across interfaces, is likely a process that is increasingly characterizing many current ecosystems, and is anchored in processes driven by humans over recent history. Biotic homogenization consists of invasions and extinctions increasing the taxonomic, genetic, or functional similarity of multiple locations over a specified time interval (Olden 2006). As an example, Fig. 5 represents a process currently taking place on the *Escherichia coli* community in Doñana National Park (South Spain). This is a natural area that has been influenced by humans since the Paleolithic, with an old history of extensive farming (cattle and horses), while also being a hotspot of biodiversity in western Europe. This research has identified the effects of anthropic pressure and wild and domestic ungulate abundance on the distribution and diversity of the main human *E. coli* pathotypes and 9 of their representative virulence genes (VGs). One example has shown, *E. coli* was detected everywhere and there were no big differences among host species or among DNP zones. However, the distribution of genes characteristic of the described pathotypes was not random and VGs were more diverse and abundant where surface waters are more contaminated by human waste and farms. This exemplifies that human influence, in this case, was more relevant than host species in shaping the *E. coli* VGs spatial pattern and diversity in DNP.

Fig. 6 (continued) using fences [Source: Barasona et al. (2013); (**b**) Facilities for selective and random culling; (**c**) Vaccination against TB in wild boar using oral baits. Reproduced from Gortazar et al. (2014)]

Scientifically Based Management of the Interface in Modern Times

Species distributions and community structures have fluctuated dramatically during the Holocene, which has been accelerated during the so-called Anthropocene (the twentieth century's transition) and driven by climate, human exploitation, and human land use (Boivin et al. 2016). While a negative trend has continued for many wildlife species in most parts of the planet, the status of most wild ungulates and carnivores in developed countries has improved during the Anthropocene (Linnell and Zachos 2010). In some cases, species such as the Alpine (*Capra ibex*) and Iberian (*Capra pyrenaica*) ibexes were reduced to a few individuals but have now expanded over large areas (Stüwe and Nievergelt 1991), even causing conflicts in some cases as disease reservoirs (i.e., *Brucella*). Overall, the complete domination of the landscape by humans has contributed to the collapse of wildlife populations in most parts of the world and unprecedented biodiversity loss is a reality. Environmental problems arising from livestock production are particularly severe in developing nations, like deforestation for rearing livestock, overgrazing, land degradation, and particularly, diseases. Fences and other barriers interfere with wildlife migrations or natural movements and impede access to ephemeral resources. Modern wildlife management is an essential component of current interfaces with livestock and humans. While we are addressing in some cases catastrophic species extinction periods, wildlife use is increasingly regulated, and wildlife are managed and appreciated for their ecological, economic, social, and cultural value. Wildlife management must balance the needs of wildlife with the needs of people using the best available science (Leopold 1933). The apparent increase in severity of what we call conflict (from the human perspective) has a complex nature and is due to a number of factors (expansion of human activities into wildlife habitats, recovery, and expansion of some wildlife populations and large-scale environmental changes; Treves 2008). While human–wildlife conflict was previously considered a "rural or agricultural problem" (Messmer 2000) that mainly affects communities in proximity to forests, conflicts are now common both in urban and in suburban areas (Soulsbury and White 2015), as well as in remote areas newly encroached by humans. Urban/ suburban human conflict incidents typically involve wildlife species that have a history of coexistence with humans or the ability to survive in human-dominated environments, where infectious diseases are also involved. For example, *Leishmania* in wild lagomorphs has been recognized as the origin of a leishmaniasis outbreak in humans and domestic animals in central Spain in peri-urban environments (de Paixão Sevá et al. 2017).

There is currently much discussion regarding models of wildlife management and conservation, considering human–nature interactions, which will surely affect the wildlife-livestock-human interface. These include questions about land protection vs. land sharing (Fischer et al. 2014), what the role of protected areas is and how multiuse landscapes must be managed (including farming; Sayer 2009), and sustainable use vs. protectionist ideals (Cretois et al. 2019). Contrary to the science of spared landscapes (i.e., protected areas) the science of coexistence promotes the presence of wildlife in multiuse landscapes, remains ad hoc and fragmented, but the strategic utility and practicality of the whole approach are being contested (Linnell et al. 2020). Definitively, shared diseases at the wildlife-livestock-human interfaces are a crucial component to be included in the formulation of modern wildlife management. Today, human connections with ecological and epidemiological systems are increasingly driven by expanded and intensified agriculture, the use of environmental resources (e.g., forestry and mining in developing countries and remote areas) and impacts on climate. The subsequent alteration in habitats, changes in host communities, diversity, and functional interactions are favoring increased contact rates, susceptibility, and/or exposure of pathogens at the interfaces with wildlife, many of which are shared with livestock and/or zoonotic. The subsequent spread and maintenance of emergent pathogens are favored by the growing worldwide human population, global trade and ease of travel, and the existence of altered host communities (involving interfaces) that provide ecological niches. Consequently, as discussed earlier, the wildlife-livestock interface is becoming global. More than ever, today it is challenging to analyze the complex ways with which wildlife interact with livestock and humans and how those interactions are relevant to emerging diseases at the interfaces.

Comprehensive and continuing epidemiological studies at the wildlife-livestock-human interface are required in different scenarios (e.g., countries, farming systems, pathogens, degree of anthropization) to better understand the infection and transmission dynamics in wildlife and domestic components. It is essential to understand local, regional, and international social, economic, and cultural systems to better focus strategic control programs. Population and disease monitoring will improve the overall understanding of the role of wild hosts and the mode of transmission and emergence of new infections. This must enable countries and international organizations to better target their disease control programs and move toward eradication. Strategic research in collaboration with the medical sector is also needed to better understand the factors that contribute to interspecies pathogen transmission among all species. African swine fever (ASF) in Europe provides an interesting example. ASF was eradicated in domestic pig populations in Europe (except Sardinia) after decades of significant effort (Gavier-Widen et al. 2015). In 2007, the current outbreak of ASF, which severely affects wild boar and domestic pig populations, reached the Caucasus region via contaminated waste arriving in ships from Africa. Since then, the virus has spread into eastern Europe and some places in central and western Europe through wild boar, domestic pigs, and human activities. The virus has raised serious concerns in countries with large pork industries, which may suffer economic losses due to trade restrictions. To control the outbreak, national authorities have taken drastic, but not always effective measures, which disregard the science of wildlife management (Vicente et al. 2019). Poland, for example, has massively increased the culling of wild boar to minimize ASF spread and the risk of transmission to domestic pigs, despite opposition by experts, because the policy does not include population monitoring that could evaluate its effectiveness. It also does not limit wild boar access to agricultural crops and game feed, which is a key driver of population growth. Meanwhile, countries are building large border fence to exclude cross-border migration of wild boar, which will disrupt wildlife habitats, but it will not stop the virus from spreading through the transportation of live pigs, wild boar, or pig- and wild boar-derived tissues and products or through the movement of other objects carrying the virus, such as human clothing. Instead of haphazard policies, efforts coordinated by governments that adhere to the principles of modern wildlife management are required. Adaptive wildlife management strategies consider the human dimension and prevent unsound reactive management. Improved wildlife population monitoring and analysis are the best ways to determine which approaches to wildlife management are successful ecologically, economically, and socially. Sustainable management will depend on local circumstances and national wildlife management regulations, but science-based strategies can be implemented at the continental scale. Legislators should consult scientists and wildlife and animal health agencies before making decisions about wildlife policy. Countries should coordinate population monitoring and management. Shared responsibility for wildlife management among countries should also enable funding for research that can critically evaluate its success. The crisis associated with disease emergence at the wildlife-livestock interface, including zoonotic diseases, can serve as a chance to develop a science-based wildlife management plan.

Finally, we remark that establishing a proper surveillance and monitoring scheme (for disease and population) is the absolute priority before deciding whether or not to intervene. Disease control can be achieved by different means, including: (1) preventive actions, (2) arthropod vector control, (3) host population control through random or selective culling, habitat management or reproductive control, and (4) vaccination. Alternative options of zoning or no-action should also be considered, particularly in view of a cost-benefit assessment. Ideally, tools from several fields should be combined in an integrated control strategy. The success of disease control in wildlife depends on many factors, including disease ecology, natural history, characteristics of the pathogen, availability of suitable diagnostic tools, characteristics of the domestic and wildlife host(s) and vectors, geographical spread of the problem, and scale of the control effort and stakeholders' attitudes. The control of wildlife disease often consists of an intervention in natural ecosystems and is, as such, often controversial. Figure 6 schematizes the options that are available for disease control at the wildlife-livestock-human interface, including preventive measures, population control, and vaccination, with some examples provided.

Final Remarks

- Through processes of evolution, migration, domestication, colonization, trade, travel, harvest, erasure, and fragmentation of habitat, disease, introduction of alien species, humans have greatly and irreversibly impacted the planet and most life forms on it. This includes pathogens of humans and animals. As the human population approaches eight billion today, human impact is continuously shaping, creating, expanding, and interconnecting new wildlife-livestock-human and their subsequent epidemiological interactions all over the world.

- Pathogen communities and the dynamics of complex multiple host multiple pathogen systems (interfaces) reflect this history of epidemiological interactions among them, where evolutive processes in this human-driven system have influenced the biology of both hosts and pathogens.
- Wildlife were the original hosts for most pathogens of livestock, sharing them with domesticated species over centuries of coevolution and domestication. Domestic animals subsequently transmit pathogens to humans and today many human infections originated from zoonoses of domesticated animals.
- The initial stages of animal domestication were probably characterized by frequent interaction of first forms of livestock with their wild counterparts and constant and/or recurrent exposure to pathogens. The gradual development of animal husbandry took place over several millennia and followed markedly different trajectories in different regions. Domestication determined a new scenario for emergent pathogens that adapted well to the new conditions of the multiple human–livestock–wildlife interface, characterized by the maintenance of "crowd diseases" (both by humans and/or by animals), the continuous presence of domestic reservoirs, anthropophilic animals and vectors. This provided niches for the evolution and adaption of pathogens to specific conditions.
- Agricultural activities by humans inevitably transformed different parts of the world at different rates, varying by epochs, civilizations, and regions. The removal and change of natural vegetation, the impacts on the abundance, type, distribution, and behavior of wildlife, the number of livestock and husbandry practices have been increasing and expanding since pre-industrial times and have determined the wide diversity of wildlife-livestock interfaces. Overall, wildlife is becoming less abundant and distributed and more fragmented and isolated, but interfaces have become more interconnected.
- The growing interdependence of world economies, human population growth, intercontinental trade, and transportation (including animals, their pathogens, and vectors) has provided opportunities for animal pathogens to cross considerable geographic boundaries and determined modern agricultural practices and characteristics of wildlife-livestock interfaces.
- The wildlife-livestock interface is more interconnected than ever. On the one hand, the wildlife-livestock-human interface is increasing as a result of human encroachment into wilderness, especially in tropical ecosystems. On the other hand, the intensification of animal production also favors increasing livestock-to-human contact, and occasionally, with other animals.
- Overall, wildlife has been reduced by humans to their lowest levels ever. Disease issues at the wildlife-livestock-human interfaces, though, are of increasing concern as they are leading to global pandemics and are far from being efficiently controlled or managed. The capacity to modify and connect the interfaces that characterize humans has increased to the extent that improving health at the

human, animal, and ecosystem interfaces is required to successfully address the main global health challenges.

- Climate and associated anthropogenic and environmental change impact the distribution, abundance, behavior, and population dynamics of pathogens and hosts, determining transmission dynamics, and threats to human health and livelihoods. The global warming impacts on the wildlife-livestock-human interface will be diverse, and the pattern not spatially homogeneous. However, multiple factors may participate together with climate change to determine epidemiological impacts at the interface, particularly in complex host/pathogen/vector systems. This context requires a better understanding of the interactions between climate change and host/pathogen responses.
- More than ever, it is challenging to analyze the complex ways in which wildlife interact with livestock and humans, and how it is relevant to emerging diseases. Comprehensive and continuing epidemiological studies at the wildlife-livestock-human interface are required in different scenarios (e.g., countries, farming systems, pathogens, and degree of anthropization) to better understand the infection and transmission dynamics in wildlife and domestic components. Population and disease monitoring of wildlife will improve the overall understanding of the roles of wild hosts, modes of transmission, and emergence of new infections. This would enable countries and international organizations to better target their disease control programs and move toward eradication. Legislators and animal and human health policy makers must base decisions on wildlife and animal health science and countries should coordinate responsibility and management.

References

Acebes P, Traba J, Malo JE (2012) Co-occurrence and potential for competition between wild and domestic large herbivores in a south American desert. J Arid Environ 77:39–44

Aiewsakun P, Katzourakis A (2017) Origin of retroviruses in the early Palaeozoic era. Nat Commun 10:8

Altizer S, Ostfeld RS, Johnson PTJ, Kutz S, Harvell CD (2013) Climate change and infectious diseases: from evidence to a predictive framework. Science 341:514–519

Angelakıs AN, Zaccaria D, Krasilnikoff J, Salgot M, Bazza M, Roccaro P, Jimenez B, Kumar A, Yinghua W, Baba A, Harrison JA, Garduno-Jimenez A, Fereres E (2020) Irrigation of world agricultural lands: evolution through the millennia. Water 12:1285

Arbuckle BS, Atici L (2013) Initial diversity in sheep and goat management in Neolithic southwestern Asia. Levant 45:219–235

Arilla M, Rosell J, Blasco R (2020) A neo-taphonomic approach to human campsites modified by carnivores. Sci Rep 10:6659

Baker BJ, Armelagos GJ (1988) The origin and antiquity of syphilis: paleopathological diagnosis and interpretation. Curr Anthropol 29:703–738

Balboni A, Palladini A, Bogliani G, Battilani M (2010) Detection of a virus related to betacoronaviruses in Italian greater horseshoe bats. Epidemiol Infect 139:216–219

Barasona JA, VerCauteren KC, Saklou N, Gortazar C, Vicente J (2013) Effectiveness of cattle operated bump gates and exclusion fences in preventing ungulate multi-host sanitary interaction. Prev Vet Med 111:42–50

Barasona JA, Latham MC, Acevedo P, Armenteros JA, Latham AM, Gortazar C, Carro F, Soriguer RC, Vicente J (2014) Spatiotemporal interactions between wild boar and cattle: implications for cross-species disease transmission. Vet Res 45:122

Barlow A, Cahill JA, Hartmann S, Theunert C, Xenikoudakis G, Fortes GG, Paijmans JLA, Rabeder G, Frischauf C, Grandal-d'Anglade A, García-Vázquez A, Murtskhvaladze M, Saarma U, Anijalg P, Skrbinšek T, Bertorelle G, Gasparian B, Bar-Oz G, Pinhasi R, Slatkin M, Dalén L, Shapiro B, Hofreiter M (2018) Partial genomic survival of cave bears in living brown bears. Nat Ecol Evol 2:1563–1570

Barrett R, Kuzawa CW, McDade T, Armelagos GJ (1998) Emerging and re-emerging infectious diseases: the third epidemiologic transition. Annu Rev Anthropol 27:247–271

Baudet C, Donati B, Sinaimeri B, Crescenzi P, Gautier C, Matias C, Sagot MF (2015) Cophylogeny reconstruction via an approximate Bayesian computation. Syst Biol 64:416–431

Becker DJ, Washburne AD, Faust CL, Pulliam JRC, Mordecai EA, Lloyd-Smith JO, Plowright RK (2019) Dynamic and integrative approaches to understanding pathogen spillover. Philos Trans R Soc Lond B Biol Sci 374:20190014

Bennett M, Begon ME (1997) Virus zoono. Bridge University Press

Berger J, Wangchuk T, Briceño C, Vila A, Lambert JE (2020) Disassembled food webs and messy projections: modern ungulate communities in the face of unabating human population growth. Front Ecol Evol 8:128

Bertranpetit E, Jombart T, Paradis E, Pena H, Dubey J, Su C, Mercier A, Devillard S, Ajzenberg D (2017) Phylogeography of toxoplasma gondii points to a south American origin. Infect Genet Evol 48:150–155

Bidokhti MR, Tråvén M, Krishna NK, Munir M, Belák S, Alenius S, Cortey M (2013) Evolutionary dynamics of bovine coronaviruses: natural selection pattern of the spike gene implies adaptive evolution of the strains. J Gen Virol 94:2036–2049

Blasco JM (1990) *Brucella ovis*. In: Nielsen K, Duncan JR (eds) Animal brucellosis. CRC Press, Boca Raton, FL, pp 351–382

Blumenschine RJ, Pobiner BL (2006) Zooarchaeology and the ecology of Oldowan hominin carnivory. In: Ungar P (ed) Early hominin diets: the known, the unknown, and the unknowable. Oxford University Press, Oxford, pp 167–190

Boivin NL, Zeder MA, Fuller DQ, Crowther A, Larson G, Erlandson JM, Denham T, Petraglia MD (2016) Ecological consequences of human niche construction: examining long-term anthropogenic shaping of global species distributions. PNAS 113:6388–6396

Bonneaud C, Weinert LA, Kuijper B (2019) Understanding the emergence of bacterial pathogens in novel hosts. Philos Trans R Soc Lond Ser B Biol Sci 374:20180328

Bourn D, Blench R (1999) Can livestock and wildlife co-exist? An interdisciplinary approach. Overseas Development Institute, The Environmental Research Group Oxford, Oxford

Brooks DR, Ferrao AL (2005) The historical biogeography of co-evolution: emerging infectious diseases are evolutionary accidents waiting to happen. J Biogeogr 32:1291–1299

Brosch R, Gordon V, Marmiesse M, Brodin P, Buchrieser C, Eiglmeier K, Garnier T, Gutierrez C, Hewinson G, Kremer K, Parsons LM, Pym AS, Samper S, van Soolingen D, Cole ST (2002) A new evolutionary scenario for the *Mycobacterium tuberculosis* complex. Proc Natl Acad Sci U S A 99:3684–3689

Brunet FG, Pilbeam D, Mackaye HT, Likiusm A, Ahounta D, Beauvilain A, Blondel C, Bocherens H, Boisserie JR, De Bonis L, Coppens Y, Dejax J, Denys C, Duringer P, Eisenmann V, Fanone G, Fronty P, Geraads D, Lehmann T, Lihoreau F, Louchart A, Mahamat A, Merceron G, Mouchelin G, Otero O, Pelaez Campomanes P, Ponce De Leon M, Rage JC, Sapanet M, Schuster M, Sudre J, Tassy P, Valentin X, Vignaud P, Viriot L, Zazzo A, Zollikofer C (2002) A new hominid from the upper Miocene of Chad, Central Africa. Nature 418:145–151

Burnet FM (1962) Natural history of infectious disease manual. Am. Tious disease, Washington, DC/Cambridge Public Health Association, Cambridge, UK

Cabal A, Vicente J, Alvarez J, Barasona JA, Boadella M, Dominguez L, Gortazar C (2017) Human influence and biotic homogenization drive the distribution of *Escherichia coli* virulence genes in natural habitats. Microbiology 6(3):1–10

Cagliani R, Forni D, Sironi M (2019) Mode and tempo of human hepatitis virus evolution. Comput Struct Biotechnol J 17:1384–1395

Caron A, Morand S, de Garine-Wichatitsky M (2020) Epidemiological interaction at the wildlife-livestock-human Interface: can we anticipate emerging infectious diseases in their hotspots? A framework for understanding emerging diseases processes in their hot spots. New Front Mol Epidemiol Infect Dis 11:311–332

Cassidy A (2015) Humans, other animals and 'one health' in the early twenty-first century. In: Woods A, Bresalier M, Cassidy A, Mason Dentinger R (eds) Animals and the shaping of modern medicine one health and its histories. Springer, New York

Caswell JL, Williams KJ (2016) Respiratory system. In: Jubb K, Palmer's Pathology of Domestic Animals (eds) Pathology of domestic animals, vol 2, 6th edn. Elsevier, St. Louis, MO, pp 465–591

Chisholm RH, Trauer JM, Curnoe D, Tanaka MM (2016) Controlled fire use in early humans might have triggered the evolutionary emergence of tuberculosis. Proc Natl Acad Sci U S A 113:9051–9056

Chomel BB, Belotto A, Meslin F (2007) Wildlife, exotic pets, and emerging Zoonoses. Emerg Infect Dis 13:6–11

Clayton DH, Moore J (eds) (1997) Host-parasite evolution: general principles and avian models. Oxford University Press, London

Cleaveland S, Laurenson MK, Taylor LH (2001) Diseases of humans and their domestic mammals: pathogen characteristics, host range and the risk of emergence. Philos Trans R Soc Lond Ser B Biol Sci 356:991–999

Colominas L, Schlumbaum A, Saña M (2014) The impact of the Roman empire on animal husbandry practices: study of the changes in cattle morphology in the north-east of the Iberian Peninsula through osteometric and ancient DNA analyses. Archaeol Anthropol Sci 6:1–16

Cretois B, JDCl L, Kaltenborn BP, Trouwborst A (2019) What form of human-wildlife coexistence is mandated by legislation? A comparative analysis of international and national instruments. Biodivers Conserv 28:1729–1741

Croitor R, Brugal JP (2010) Ecological and evolutionary dynamics of the carnivore community in Europe during the last 3 million years. Quat Int 212:98–108

da Paixão Sevá A, Martcheva M, Tuncer N, Fontana I, Carrillo E, Moreno J, Keesling J (2017) Efficacies of prevention and control measures applied during an outbreak in Southwest Madrid, Spain. PLoS One 12(10):e0186372

de Graaf M, Osterhaus AD, Fouchier RAM, Holmes EC (2008) Evolutionary dynamics of human and avian Metapneumoviruses. J Gen Virol 89:2933–2942

Dearlove B, Wilson DJ (2013) Coalescent inference for infectious disease: meta-analysis of hepatitis C. Phil Trans R Soc B 368:20120314

Delgado CL, Narrod CA (2003) Policy, technical, and environmental determinants and implications of the scaling-up of livestock production in four fast–growing developing countries: a synthesis. International Food Policy Research Institute, Washington, DC

Demogines A, Abraham J, Choe H, Farzan M, Sawyer SL (2013) Dual host-virus arms races shape an essential housekeeping protein. PLoS Biol 11(5):e1001571

Dennell R, Roebroeks W (2006) An Asian perspective on early human dispersal from Africa. Nature 438:1099–1104

Devendra C, Thomas D (2002) Crop-animal interactions in mixed farming systems in Asia. Agr Syst 71:27–40

Di Lernia S, Cremaschi M (1996) Taming barbary sheep: wild animal management by early Holocene hunter-gatherers at Uan Afuda (Libyan Sahara). Nyame Akua 46:43–54

Diamond J (1987) The worst mistake in the history of the human race. Discover 8:64–66

Dippenaar A, Parsons SDC, Sampson SL, van der Merwe RG, Drewe JA, Abdallah AM, Siame KK, van Pittius NCG, van Helden PD, Pain A, Warren RM (2015) Whole genome sequence analysis of *Mycobacterium suricattae*. Tuberculosis 95:682–688

Dobson AP, Hudson PJ (1992) Regulation and stability of a free-living host-parasite system – *Trichostrongylus tenuis* in red grouse. 2. Population models. J Anim Ecol 61:487–498

Domingo E (2016) Long-term virus evolution in nature. In: Virus as populations composition, complexity, dynamics, and biological implications. Academic Press, Elsevier, San Diego, CA, pp 227–262

Domínguez Rodrigo M, Pickering R, Bunn HT (2010) Configurational approach to identifying the earliest hominin butchers. Proc Natl Acad Sci U S A 107:20929–20934

Doughty CE, Prys-Jones Y, Faurby S, Abraham A, Hepp C, Leshyk V, Fofanov VY, Nieto JNC, Svenning C, Galetti M (2020) Megafauna decline have reduced pathogen dispersal which may have increased emergent infectious diseases. Ecography 43:1107. https://doi.org/10.1101/2020.01.21.914531

Dubey JP (2010) Toxoplasmosis of animals and humans. CRC, Boca Raton, p 313

Düx A, Lequime S, Patrono LV, Vrancken B, Boral S, Gogarten JF, Hilbig A, Horst D, Merkel K, Prepoint B, Santibanez S, Schlotterbeck J, Suchard MA, Ulrich M, Widulin N, Mankertz A, Leendertz FH, Harper K, Schnalke T, Lemey P, Calvignac-Spencer S (2020) Measles virus and rinderpest virus divergence dated to the sixth century BCE. Science 368:1367–1370

Dzialuk A, Zastempowska E, Skórzewski R, Twarużek M, Grajewski J (2018) High domestic pig contribution to the local gene pool of free-living European wild boar: a case study in Poland. Mammal Res 63:65–71

Ellis EC, Klein Goldewijk K, Siebert S, Lightman D, Ramankutty N (2010) Anthropogenic transformation of the biomes, 1700 to 2000. Glob Ecol Biogeogr 19:589–606

Emerman M, Malik HS (2010) Paleovirology—modern consequences of ancient viruses. PLoS Biol 8(2):e1000301

Engering A, Hogerwerf L, Slingenbergh J (2013) Pathogen–host–environment interplay and disease emergence. Emerg Microbes Infect 2(2):e5

Ervynck A, Hongo H, Meadow R (2001) Born free? New evidence for the status of *Sus scrofa* at Neolithic Cayonu Tepesi (southeastern Anatolia, Turkey). Paleorient 27:47–73

Faith JT, Rowan J, Du A (2019) Early hominins evolved within non-analog ecosystems. PNAS 116:21478–21483

FAO (1996) Wildlife utilization in Latin America: current situation and prospects for sustainable management. (FAO conservation guide – 25). Food and Agriculture Organization of the United Nations – FAO, Rome

FAO (2006) World agriculture: towards 2030/2050 – interim report. FAO, Rome

FAO (2007) Wild birds and avian influenza: an introduction to applied field research and disease sampling techniques. Edited by D. Whitworth, S.H. Newman, T. Mundkur and P. Harris. FAO animal production and health manual, no. 5, Rome. www.fao.org/avianflu

FAO (2012a) Lessons learned from the eradication of rinderpest for controlling other transboundary animal diseases. Proceedings of the GREP Symposium and High-Level Meeting, 12–15 October 2010, Rome, Italy. FAO animal production and health proceedings, no. 15. Rome, Italy

FAO (2012b) State of the World's forests 2012. Food and Agriculture Organization of the United Nations, Rome

FAO (2016) State of the World's Forests 2016. Forests and agriculture: land-use challenges and opportunities, Rome

Felius M, Beerling ML, Buchanan DS, Theunissen B, Koolmees PA, Lenstra JA (2014) On the history of cattle genetic resources. Diversity 26:705–750

Fernandes AP, Nelson K, Beverley SM (1993) Evolution of nuclear ribosomal RNAs in kinetoplastid protozoa: perspectives on the age and origins of parasitism. Proc Natl Acad Sci U S A 90:11608–11612

Fernández-de-Mera IG, Vicente J, Naranjo V, Fierro Y, Garde JJ, de la Fuente J, Gortazar C (2009) Impact of major histocompatibility complex class II polymorphisms on Iberian Red Deer parasitism and life history traits. Infect Genet Evol 9:1232–1239

Fischer J, Abson DJ, Butsic V, Chappell MJ, Ekroos J, Hanspach J, Kuemmerle T, Smith HG, von Wehrden H (2014) Land sparing versus land sharing: moving forward. Conserv Lett 7:149–157

Fistani AB (1996) *Sus scrofa priscus* (Goldfuss, de Serres) (Mammalia, Artiodactyla, Suidae) from the middle Pleistocene layers of Gajtan 1 site, southeast of Shkoder (North Albania). Ann Palıontologie 82:177–229

Foster JT, Price LB, Beckstrom-Sternberg SM, Pearson T, Brown WD, Kiesling DM et al (2012) Genotyping of Brucella species using clade specific SNPs. BMC Microbiol 12:110. https://doi.org/10.1186/1471-2180-12-110

Frantz LAF, Schraiber JG, Madsen O, Megens H, Bosse M, Paudel Y, Semiadi G, Meijaard E, Li N, Crooijmans RPMA, Archibald AL, Slatkin M, Schook LB, Larson GM, Groenen MAM (2013) Genome sequencing reveals fine scale diversification and reticulation history during speciation in *Sus*. Genome Biol 14:R107. 2013

Freedman AH, Gronau I, Schweizer RM, Ortega-Del Vecchyo D, Han E, Silva PM, Galaverni M, Fan Z, Marx P, Lorente-Galdos B, Beale H, Ramirez O, Hormozdiari F, Alkan C, Vilà C, Squire K, Geffen E, Kusak J, Boyko AR, Parker HG, Lee C, Tadigotla V, Siepel A, Bustamante CD, Harkins TT, Nelson SF, Ostrander EA, Marques-Bonet T, Wayne RK, Novembre J (2014) Genome sequencing highlights the dynamic early history of dogs. PLoS Genet 10:e1004016

Gagneux S (2018) Ecology and evolution of *Mycobacterium tuberculosis*. Nat Rev Microbiol 16:202–213

Gaspar P, Mesías FJ, Escribano M, Pulido F (2009) Sustainability in Spanish extensive farms (Dehesas): an economic and management indicator-based evaluation. Rangeland Ecol Manage 62:152–162

Gavier-Widen D, Gortazar C, Stahl K, Neimanis AS, Rossi S, Hard av Segerstad C, Kuiken T (2015) African swine fever in wild boar in Europe: a notable challenge. Vet Rec 176:199–200

Germonpré M, Fedorov S, Danilov P, Galeta P, Jimenez E, Sablin M, Losey RJ (2017) Palaeolithic and prehistoric dogs and Pleistocene wolves from Yakutia: identification of isolated skulls. J Archaeol Sci 78:1–19

Gifford-Gonzalez D (2000) Animal disease challenges to the emergence of pastoralism in sub-Saharan Africa. Afr Archaeol Rev 17:95–139

Gilbert C, Feschotte C (2010) Genomic fossils calibrate the long-term evolution of hepadnaviruses. PLoS Biol 8:e1000495

Godfroid J, Cloeckaert A, Liautard JP, Kohler S, Fretin D, Walravens K (2005) From the discovery of the Malta fever's agent to the discovery of a marine mammal reservoir, brucellosis has continuously been a re-emerging zoonosis. Vet Res 36:313–326

Godfroid J, DeBolle X, Roop RM, O'Callaghan D, Tsolis RM, Baldwin C, Santos RL, McGiven J, Olsen S, Nymo IH, Larsen A, Al Dahouk S, Letesson JJ (2014) The quest for a true one health perspective of brucellosis. Rev Sci Tech 33:521–538

Goren-Inbar N, Alperson N, Kislev ME, Simchoni O, Melamed Y, Ben-Nun A, Werker E (2004) Evidence of hominin control of fire at Gesher Benot Ya'aqov, Israel. Science 304:725–727

Gortazar C, Acevedo P, Ruiz-Fons JF, Vicente J (2006) Disease risk and overabundance of game species. Eur J Wildl Res 52:81–87

Gortazar C, Diez-Delgado I, Barasona JA, Vicente J, De La Fuente J, Boadella M (2014) The wild side of disease control at the wildlife-livestock-human interface: a review. Front Vet Sci 1:27

Gowlett JAJ (2016) The discovery of fire by humans: a long and convoluted process. Phil Trans R Soc B 371:20150164

Graham JP, Leibler JH, Price LB, Otte JM, Pfeiffer DU, Tiensin T, Silbergeld EK (2008) The animal-human Interface and infectious disease in industrial food animal production: rethinking biosecurity and biocontainment. Public Health Rep 123:282–299

Greenbaum G, Getz WM, Rosenberg NA, Feldman MW, Hovers E, Kolodny O (2019) Disease transmission and introgression can explain the long-lasting contact zone of modern humans and Neanderthals. Nat Commun 10:5003

Greger M (2007) The long haul: risks associated with livestock transport. Biosecurity and Bioterrorism: Biodefense Strategy, Practice, and Science 5:301–312

Grigson C (1991) An African Origin for African cattle? Some archaeological evidence. Afr Archaeol Rev 9:119–144

Guzmán-Verri C, González-Barrientos R, Hernández-Mora G, Morales JA, Baquero-Calvo E, Chaves-Olarte E, Moreno E (2012) *Brucella ceti* and brucellosis in cetaceans. Front Cell Infect Microbiol 2:3. https://doi.org/10.3389/fcimb.2012.00003

Hallett MT, Lagergren J (2001) Efficient algorithms for lateral gene transfer problems, RECOMB '01. ACM, San Diego

Hoberg EP (2006) Phylogeny of *Taenia*: species definitions and origins of human parasites. Parasitol Int 55:S23–S30

Hoberg EP, Brooks DR (2015) Evolution in action: climate change, biodiversity dynamics and emerging infectious disease. Philos Trans R Soc Lond Ser B Biol Sci 370(1665):20130553

Holmes EC (2011) The evolution of endogenous viral elements. Cell Host Microbe 10:368–377

Huerta-Sánchez E, Jin X, Bianba AZ, Peter BM, Vinckenbosch N, Liang Y, Yi X, He M, Somel M, Ni P, Wang B, Ou X, Huasang, Luosang J, Xi Z, Cuo P, Li K, Gao G, Yin Y, Wang W, Zhang X, Xu X, Yang H, Li Y, Wang J, Wang J, Nielsen R (2014) Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. Nature 512:194–197

IPCC (2013) Climate change 2013: the physical science basis. Contribution of Working Group I to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change. Cambridge University Press, Cambridge

Jackson AP, Charleston MA (2004) A Cophylogenetic perspective of RNA–virus evolution. Mol Biol Evol 21:45–57

Jones DS (2004) Rationalizing epidemics: meanings and uses of American Indian mortality since 1600. Harvard University Press, Cambridge, MA

Kamath PL, Foster JT, Drees KP, Luikart G, Quance C, Anderson NJ, Clarke PR (2016) Genomics reveals historic and contemporary transmission dynamics of a bacterial disease among wildlife and livestock. Nat Commun 7:11448

Kanginakudru S, Metta M, Jakati RD, Nagaraju J (2008) Genetic evidence from Indian red jungle fowl corroborates multiple domestication of modern day chicken. BMC Evol Biol 8:174

Kaplan JO, Krumhardt KM, Zimmermann N (2009) The prehistoric and preindustrial deforestation of Europe. Quat Sci Rev 28:3016–3034

Kaplan JO, Krumhardt KM, Ellis EC, Ruddiman WF, Lemmen C, Goldewijk KK (2010) Holocene carbon emissions as a result of anthropogenic land cover change. The Holocene Special Issue:1–17

Katzourakis A, Gifford RJ (2010) Endogenous viral elements in animal genomes. PLoS Genet 6 (11):e1001191

Keller A, Graefen A, Ball M, Matzas M, Boisguerin V, Maixner F, Leidinger P, Backes C, Khairat R, Forster M, Stade B, Franke A, Mayer J, Spangler J, McLaughlin S, Shah M, Lee C, Harkins TT, Sartori A, Moreno-Estrada A, Henn B, Sikora M, Semino O, Chiaroni J, Rootsi S, Myres NM, Cabrera VM, Underhill PA, Bustamante CD, Vigl EE, Samadelli M, Cipollini G, Haas J, Katus H, O'Connor BD, Carlson MR, Meder B, Blin N, Meese E, Pusch CM, Zink A (2012) New insights into the Tyrolean Iceman's origin and phenotype as inferred by whole-genome sequencing. Nat Commun 3:698

Kelly AG, Netzler NE, White PA (2016) Ancient recombination events and the origins of hepatitis E virus. BMC Evol Biol 16:210. Mol Biol Evol. 2015 May; 32(5): 1354–1364

Key FM, Posth C, Esquivel-Gomez LR, Hübler R, Spyrou MA, Neumann GU, Furtwängler A, Sabin S, Burri M, Wissgott A, Lankapalli AK, Vågene ÅJ, Meyer M, Nagel S, Tukhbatova R, Khokhlov A, Chizhevsky A, Hansen S, Belinsky AB, Kalmykov A, Kantorovich AR, Maslov VE, Stockhammer PW, Vai S, Zavattaro M, Riga A, Caramelli D, Skeates R, Beckett J, Gradoli

MG, Steuri N, Hafner A, Ramstein M, Siebke I, Lösch S, Erdal YS, Alikhan NF, Zhou Z, Achtman M, Bos K, Reinhold S, Haak W, Kühnert D, Herbig A, Krause J (2020) Emergence of human-adapted *Salmonella enterica* is linked to the Neolithization process. Nat Ecol Evol 4:324–333

Kilpatrick AM, Altizer S (2010) Disease ecology. Nat Educ Knowl 3(10):55

Kossida S, Harvey PH, Zanotto PMA et al (2000) Lack of evidence for Cospeciation between Retroelements and their hosts. J Mol Evol 50:194–201

Lanciotti RS, Roehrig JT, Deubel V, Smith J, Parker M, Steele K, Crise B, Volpe KE, Crabtree MB, Scherret JH, Hall RA, MacKenzie JS, Cropp CB, Panigrahy B, Ostlund E, Schmitt B, Malkinson M, Banet C, Weissman J, Komar N, Savage HM, Stone W, McNamara T, Gubler DJ (1999) Origin of the West Nile virus responsible for an outbreak of encephalitis in the northeastern United States. Science 286:2333–2337

Larson G, Fuller DQ (2014) The evolution of animal domestication. Ann Rev Ecol Evol Syst 66:115–136

Leopardi S, Holmes EC, Gastaldelli M, Tassoni L, Priori P, Scaravelli D, Zamperin G, De Benedictis P (2018) Interplay between co-divergence and cross-species transmission in the evolutionary history of bat coronaviruses. Infect Genet Evol 58:279–289

Leopold A (1933) Game management. Charles Scribner's Sons, New York

Lindo J, Huerta-Sánchez E, Nakagome S, Rasmussen M, Petzelt B, Mitchell J, Cybulski JS, Willerslev E, DeGiorgio M, Malhi RS (2016) A time transect of exomes from a native American population before and after European contact. Nat Commun 7:13175

Linnell J, Zachos F (2010) Status and distribution patterns of European ungulates: genetics, population history and conservation. In: Ungulate management in Europe: problems and practices. Cambridge University Press, Cambridge, pp 12–53

Linnell JDC, Cretois B, Nilsen EB, Rolandsen CM, Solberg EJ, Veiberg V, Kaczensky P, Moorter BV, Panzacchi M, Rauset GR, Kaltenborn B (2020) The challenges and opportunities of coexisting with wild ungulates in the human-dominated landscapes of Europe's Anthropocene. Biol Conserv 244:108500

Littlejohn M, Locarnini S, Yuen L (2016) Origins and evolution of hepatitis B virus and hepatitis D virus. Cold Spring Harb Perspect Med 6:a021360

Liu M, Tian H (2010) China's land cover and land use change from 1700 to 2005: estimations from high-resolution satellite data and historical archives. Glob Biogeochem Cycles 24(3)

Liu Y, Wu G, Yao Y, Miao Y, Luikart G, Baig M, Beja-Pereira A, Ding Z, Palanichamy MG, Zhang Y (2006) Multiple maternal origins of chickens: out of the asian jungles. Mol Phylogenet Evol 38:12–19

Liu L, Bosse M, Megens H, Frantz LA, Lee Y, Irving-Pease EK, Narayan G, Groenen MAM, Madsen O (2019) Genomic analysis on pygmy hog reveals extensive interbreeding during wild boar expansion. Nat Commun 10:1992

Long JL (2003) Introduced mammals of the world: their history, distribution and influence. CABI Publishing, Wallingford

Lorblanchet M (2001) La Grotte Ornée de Pergouset (Saint-Géry, Lot). Un Sanctuaire Secret Paléolithique Maison des Sciences de L'Homme

Lott DF (2002) American Bison: a natural history. University of California Press, Berkeley

Lovette IJ (2005) Glacial cycles and the tempo of avian speciation. Trends Ecol Evol 20:57–59

Makarewicz C, Tuross N (2012) Finding fodder and tracking transhumance: isotopic detection of goat domestication processes in the near east. Curr Anthropol 53:495–505

Marciniak S (2016) Hunting for pathogens: ancient DNA and the historical record. In: Mant M, Holland A (eds) Beyond the bones. Academic Press, New York, pp 81–100

Mardanov AV, Bulygina ES, Nedoluzhko AV, Kadnikov VV, Beletskii AV, Tsygankova SV, Tikhonov A, Ravin N, Prokhorchuk EB, Skryabin KG (2012) Molecular analysis of the intestinal microbiome composition of mammoth and woolly rhinoceros. Dokl Biochem Biophys 445:471–474

Marshall FB, Dobney K, Denham T, Capriles JM (2014) Evaluating the roles of directed breeding and gene flow in animal domestication. PNAS 29(111):6153–6158

McCleery DW (1992) American forests: a history of resiliency and recovery. USDA Forest Service and Forest History Society, Durham

McGeoch DJ, Dolan A, Ralph AC (2000) Toward a comprehensive phylogeny for mammalian and avian herpesviruses. J Virol 74:10401–10406

McHugo GP, Dover M, Machugh D (2019) Unlocking the origins and biology of domestic animals using ancient DNA and paleogenomics. BMC Biol 17:98

McKeown RE (2010) The epidemiologic transition: changing patterns of mortality and population dynamics. Am J Lifestyle Med 3(1 Suppl):19S–26S

McMichael J (2004) Environmental and social influences on emerging infectious diseases: past, present and future. Philos Trans R Soc Lond Ser B Biol Sci 359:1049–1058

Messmer TA (2000) The emergence of human wildlife conflict management: turning challenges into opportunities. Int Biodet Biodeg 45:97–102

Meyerson NR, Sawyer SL (2011) Two-stepping through time: mammals and viruses. Trends Microbiol 19:286–294

Michelet L, Dauga C (2012) Molecular evidence of host influences on the evolution and spread of human tapeworms. Biol Rev Camb Philos Soc 87:731–741

Ming L, Yuan L, Yi L, Ding G, Hasi S, Chen G, Jambl T, Hedayat-Evright N, Batmunkh M, Badmaevna GK, Gan-Erdene T, Ts B, Zhang W, Zulipikaer A, Hosblig, Erdemt, Natyrov A, Mamay P, Narenbatu MG, Narangerel C, Khongorzul O, He J, Hai L, Lin W, Sirendalai S, Aiyisi LY, Wang Z, Jirimutu (2020) Whole-genome sequencing of 128 camels across Asia reveals origin and migration of domestic Bactrian camels. Commun Biol 3(1):1

Miran MB, Kasuku AA, Swai ES (2017) Prevalence of echinococcosis and *Taenia hydatigena* cysticercosis in slaughtered small ruminants at the livestock-wildlife interface areas of Ngorongoro, Tanzania. Vet World 10:411–417

Molnár PK, Kutz SJ, Hoar BM, Dobson AP (2014) Metabolic approaches to understanding climate change impacts on seasonal host–macroparasite dynamics. Ecol Lett 16:9–21

Molne A (2010) Sentient genetics: breeding the animal breeder as fundamental other. J Eighteenth-Century Stud 33:584–597

Morand S, McIntyre KM, Baylis M (2014) Domesticated animals and human infectious diseases of zoonotic origins: domestication time matters. Infect Genet Evol 24:76–81

Moreno E (1992) *Brucella* evolution. In: Plommet M (ed) Prevention of brucellosis in mediterranean countries. Pudoc Scientific Publishers, Wageningen, pp 198–121

Moreno E (1998) Genome evolution within the alpha: why do some bacteria not possess plasmids and others exhibit more than one different chromosome? Figure 1. FEMS Microbiology Reviews 22(4):255–275

Moreno E (2014) Retrospective and prospective perspectives on zoonotic brucelosis. Front Microbiol 5:213

Moreno E, Moriyón I (2002) *Brucella melitensis*: a nasty bug with hidden credentials for virulence. Proc Natl Acad Sci U S A 99:1–3. https://doi.org/10.1073/pnas.022622699

Mostowy S, Cousins D, Brinkman J, Aranaz A, Behr MA (2002) Genomic deletions suggest a phylogeny for the *Mycobacterium tuberculosis* complex. J Infect Dis 186:74–80

Murray DL, Cox EW, Ballard WB, Whitlaw HA, Lenarz MS, Custer TW, Barnett T, Fuller TK (2006) Pathogens, nutritional deficiency and climate influences on a declining moose population. Wildl Monogr 166:1–30

Neiderud C (2015) How urbanization affects the epidemiology of emerging infectious diseases. Infect Ecol Epidemiol 5:27060. https://doi.org/10.3402/iee.v5.27060

Nelson M, Worobey M (2018) Origins of the 1918 pandemic: revisiting the swine “mixing vessel” hypothesis. Am J Epidemiol 187:2498–2502

Newell DG, Koopmans M, Verhoef L, Duizer E, Aidara-Kane A, Sprong H, Opsteegh M, Langelaar M, Threfall J, Scheutz F, van der Giessen J, Kruse H (2010) Food-borne diseases-the challenges of 20 years ago still persist while new ones continue to emerge. Int J Food Microbiol 139:S3–S15

Newfield TP (2015) Human-bovine plagues in the early middle ages. J Interdiscip Hist 46:1–38

Olden JD (2006) Biotic homogenization: a new research agenda for conservation biogeography. J Biogeogr 33:2027–2039

Orton RJ, Wright CF, Morelli MJ, Juleff N, Thébaud G, Knowles NJ, Valdazo-González B, Paton DJ, King DP, Daniel TH (2013) Observing micro-evolutionary processes of viral populations at multiple scales. Phil Trans R Soc B 368:20120203

Park M, Loverdo C, Schreiber SJ, Lloyd-Smith JO (2013) Multiple scales of selection influence the evolutionary emergence of novel pathogens. Philos Trans R Soc Lond Ser B Biol Sci 368:20120333

Pearce-Duvet JM (2006) The origin of human pathogens: evaluating the role of agriculture and domestic animals in the evolution of human disease. Biol Rev Camb Philos Soc 81:369–382

Pearson J, Salman MD, BenJabara K, Brown C, Formenty P, Griot C, James A, Jemmi T, King L, Lautner E, McCluskey BJ. Meslin FX, Ragan V (2005) Global risks of infectious animal diseases. Council for Agricultural Science and Technology, Issue Paper No. 28

Pepin KM, Lass S, Pulliam JRC, Read AF, Lloyd-Smith JO (2010) Identifying genetic markers of adaptation for surveillance of viral host jumps. Nat Rev Microbiol 8:802–813

Plowright RK, Parrish CR, McCallum H, Hudson PJ, Ko AI, Graham AL, Lloyd-Smith L-SJO (2017) Pathways to zoonotic spill over. Nat Rev Microbiol 15:502–510

Poinar G (2009) Description of an early cretaceous termite (Isoptera: Kalotermitidae) and its associated intestinal protozoa, with comments on their co-evolution. Parasit Vectors 2:12

Poinar G (2018) Vertebrate pathogens vectored by ancient hematophagous arthropods. Hist Biol 32:888. https://doi.org/10.1080/08912963.2018.1545018

Prugnolle F, Ollomo B, Durand P, Yalcindag E, Arnathau C, Elguero E, Berry A, Pourrut X, Gonzalez JP, Nkoghe D, Akiana J, Verrier D, Leroy E, Ayala FJ, Renauda F (2011) African monkeys are infected by *Plasmodium falciparum* nonhuman primate-specific strains. Proc Natl Acad Sci U S A 19(108):11948–11953

Pybus OG, Fraser C, Rambaut A (2013) Evolutionary epidemiology: preparing for an age of genomic plenty. Philos Trans R Soc Lond Ser B Biol Sci 368:20120193

Rappole JH, Derrickson SR, Hubálek Z (2000) Migratory birds and spread of West Nile virus in the Western hemisphere. Emerg Infect Dis 6:319–328

Reperant LA, Giuseppe Cornaglia G, Osterhaus AD (2012) The importance of understanding the human-animal interface: from early hominins to global citizens. Curr Top Microbiol Immunol 365:49–81

Restif O, Graham AL (2015) Within-host dynamics of infection: from ecological insights to evolutionary predictions. Philos Trans R Soc Lond B 370:20140304

Reullier J, Pérez-Tris J, Bensch S, Secondi J (2006) Diversity, distribution and exchange of blood parasites meeting at an avian moving contact zone. Mol Ecol 15:753–763

Rich SM, Ayala FJ (2010) Progress in malaria research: the case for phylogenetics. Adv Parasitol 54:255–280

Ripple W, Newsome TM, Wolf C, Dirzo R, Everatt KT, Hayward MW, Kerley GIH, Levi T, Lindsey PA, Macdonald DW, MY PLE, Sandom CJ, Terborgh J, Van Valkenburgh B (2015) Collapse of the world's largest herbivores. Sci Adv 1:e1400103

Røed KH, Flagstad Ø, Nieminen M, Holand Ø, Dwyer MJ, Røv N, Vilà C (2008) Genetic analyses reveal independent domestication origins of Eurasian reindeer. Proc Biol Sci 275:1849–1855

Roeder P, Mariner J, Kock R (2013) Rinderpest: the veterinary perspective on eradication. Philos Trans R Soc Lond Ser B Biol Sci 368:20120139

Rogalski MA, Gowler CD, Shaw CL, Hufbauer RA, Duffy MA (2017) Human drivers of ecological and evolutionary dynamics in emerging and disappearing infectious disease systems. Philos Trans R Soc Lond Ser B Biol Sci 372:20160043

Rohr JR, Dobson AP, Johnson PTJ, Kilpatrick AM, Paull SH, Raffel TR, Ruiz-Moreno D, Thomas MB (2011) Frontiers in climate change-disease research. Trends Ecol Evol 26:270–277

Rose H, Hoar B, Kutz SJ, Morgan ER (2014) Exploiting parallels between livestock and wildlife: predicting the impact of climate change on gastrointestinal nematodes in ruminants. Int J Parasitol Parasit Wildl 3:209–219

Rossel S, Marshall F, Peters J, Pilgram T, Adams MD, O’Connor D (2008) Domestication of the donkey: timing, processes and indicators. Proc Natl Acad Sci 105:3715–3720

Rudolf VH, Antonovics J (2007) Disease transmission by cannibalism: rare event or common occurrence? Proc R Soc Biol Sci 274:1205–1210

Sansoni U (1994) Lepiu antiche pitture del Sahara. Jaca Boo, Milano

Sayer J (2009) Reconciling conservation and development: are landscapes the answer? Biotropica 41:649–652

Schiffels S, Durbin R (2014) Inferring human population size and separation history from multiple genome sequences. Nat Genet 46:919–925

Schopf JW, Kitajima K, Spicuzza MJ, Kudryavtsev AB, Valley JW (2018) Archaea in the Archean. Proc Natl Acad Sci 115:53–58

Senut B, Pickfor M, Gommery D, Mein P, Cheboi K, Coppens Y (2001) First hominid from the Miocene (Lukeino formation, Kenya). Comptes Rendus de l’Academie des Sciences, Series IIA – Earth and Planetary Science 332:137–144

Shury TK, Nishi JS, Elkin BT, Wobeser GA (2015) Tuberculosis and brucellosis in wood bison (*Bison bison athabascae*) in northern Canada: a renewed need to develop options for future management. J Wildl Dis 51:543–555

Silva JC, Egan A, Friedman R, Munro JB, Carlton JM, Hughes AL (2011) Genome sequences reveal divergence times of malaria parasite lineages. Parasitology 138:1737–1749

Silva JC, Egan A, Arze C, Spouge JL, Harris DG (2015) A new method for estimating species age supports the coexistence of malaria parasites and their mammalian hosts. Mol Biol Evol 32:1354–1364

Slingenbergh J, Gilbert M, de Balogh KI, Wint W (2004) Ecological sources of’ zoonotic diseases. Rev Sci Tech Off Int Epiz 23:467

Smith GJD, Bahl J, Vijaykrishna D, Zhang J, Poon LLM, Chen H, Webster RG, Malik Peiris JS, Yi G (2009) Dating the emergence of pandemic influenza viruses. PNAS 106:11709–11712

Smith RH, Hallwirth C, Westerman M, Hetherington NA, Tseng Y, Cecchini S, Virág T, Ziegler M, Rogozin IB, Koonin EV, Agbandje-McKenna M, Kotin RM, Alexander IE (2016) Germline viral “fossils” guide in silico reconstruction of a mid-Cenozoic era marsupial adeno-associated virus. Sci Rep 6:28965

Soubrier J, Gower G, Chen K, Richards SM, Llamas B, Mitchell KJ, Ho SY, Kosintsev P, Lee MS, Baryshnikov G, Bollongino R, Bover P, Burger J, Chivall D, Crégut-Bonnoure E, Decker JE, Doronichev VB, Douka K, Fordham DA, Fontana F, Fritz C, Glimmerveen J, Golovanova LV, Groves C, Guerreschi A, Haak W, Higham T, Hofman-Kamińska E, Immel A, Julien MA, Krause J, Krotova O, Langbein F, Larson G, Rohrlach A, Scheu A, Schnabel RD, Taylor JF, Tokarska M, Tosello G, van der Plicht J, van Loenen A, Vigne JD, Wooley O, Orlando L, Kowalczyk R, Shapiro B, Cooper A (2016) Early cave art and ancient DNA record the origin of European bison. Nat Commun 7:13158

Soulsbury CD, White PCL (2015) Human-wildlife interactions in urban areas: a review of conflicts, benefits and opportunities. Wild Res 42:541–553

Spinage CA (2003) Cattle plague: a history. Springer, New York

Sponsel L, Headland T, Bailey R (eds) (1996) Tropical deforestation: the human dimension. Columbia University Press, New York

Stern A, Yeh MT, Zinger T, Smith M, Wright C, Ling G, Nielsen R, Macadam A, Andino R (2017) The evolutionary pathway to virulence of an RNA virus. Cell 169:35–46

Stüwe M, Nievergelt B (1991) Recovery of Alpine ibex from near extinction: the result of effective protection, captive breeding, and reintroductions. Ap Anim Behav Sci 29:379–387

Su C, Evans D, Cole RH, Kissinger JC, Ajioka JW, Sibley LD (2003) Recent expansion of *Toxoplasma* through enhanced Oral transmission. Science 299:414–416

Suh A, Brosius J, Schmitz J, Kriegs JO (2013) The genome of a Mesozoic paleovirus reveals the evolution of hepatitis B viruses. Nat Commun 4:1791

Tao Y, Shi M, Chommanard C, Queen K, Zhang J, Markotter W, Kuzmin IV, Holmes EC, Tong S (2017) Surveillance of bat coronaviruses in Kenya identifies relatives of human coronaviruses NL63 and 229E and their recombination history. J Virol 91(5):e01953–e01916

Taubenberger JK, Kash JC (2010 Jun 25) Influenza virus evolution, host adaptation and pandemic formation. Cell Host Microbe 7(6):440–451

Thomas CD (2017) Inheritors of the earth: how nature is thriving in an age of extinction. Hachette, London

Thompson CS, O'Leary JP (1997) The discovery of the vector for "yellow Jack". Am Surg 63:462–463

Thompson JC, Carvalho S, Marean CW, Alemseged Z (2019) Origins of the human predatory pattern: the transition to large-animal exploitation by early hominins. Curr Anthropol 60:1–23

Tiensin T, Chaitaweesub P, Songserm T, Chaisingh A, Hoonsuwan W, Buranathai C, Parakamawongsa T, Premashthira S, Amonsin A, Gilbert M, Nielen M, Stegeman A (2005) Highly pathogenic avian influenza H5N1, Thailand, 2004. Emerg Infect Dis 11:1664–1672

Tilman D, Cassman KG, Matson PA, Naylor R, Polasky S (2002) Agricultural sustainability and intensive production practices. Nature 418:671–677

Tito RY, Macmil S, Wiley G, Najar F, Cleeland L, Qu CM, Wang P, Romagne F, Leonard S, Ruiz AJ, Reinhard K, Roe BA, Lewis CM (2008) Phylotyping and functional analysis of two ancient human microbiomes. PLoS One 3(11)

Tito RY, Knights D, Metcalf J, Obregon-Tito AJ, Cleeland L, Najar F, Roe B, Reinhard K, Sobolik K, Belknap S, Foster M, Spicer P, Knight R, Lewis CM (2020) Insights from characterizing extinct human gut microbiomes. PLoS One 7(12):e51146

Toth N, Schick K (2007) Overview of Paleolithic anthropology. In: Henke HCW, Hardt T, Tatersall I (eds) Handbook of paleoanthropology. Springer, Berlin; Heidelberg; New York, pp 1943–1963

Trentacoste A, Nieto-Espinet A, Valenzuela-Lamas S (2018) Pre-Roman improvements to agricultural production: evidence from livestock husbandry in late prehistoric Italy. PLoS One 13(12): e0208109

Treves A (2008) The human dimensions of conflicts with wildlife around protected areas. In: Wildlife and society: the science of human dimensions. Island Press, Washington, DC. isbn 9781597264082

Van Blerkom LM (2003) Role of viruses in human evolution. Am J Phys Anthropol Suppl 37:14–46

Verger JM, Grimont F, Grimont PA, Grayon M (1985) Brucella, a monospecific genus as shown by deoxyribonucleic acid hybridization. Int J Syst Evol Microbiol 35:292–295

Vermeij GJ (1994) The evolutionary interaction among species: selection, escalation, and coevolution. Annual Review of Ecology and Systematics 25(1):219–236

Vicente J, Apollonio M, Blanco-Aguiar JA, Borowik T, Brivio F, Casaer J, Croft S, Ericsson G, Ferroglio E, Gavier-Widen GC, Jansen PA, Keuling O, Kowalczyk R, Petrovic K, Plhal R, Podgorski T, Sange M, Scandura M, Schmidt K, Smith GC, Soriguer R, Thulke H, Zanet S, Acevedo P (2019) Science-based wildlife disease response. Science 364:943–944

Vigne JD (2011) The origins of animal domestication and husbandry: a major change in the history of humanity and the biosphere. C R Biol 334:171–181

Vijgen L, Keyaerts E, Moës E, Thoelen I, Wollants E, Lemey P, Vandamme AM, Van Ranst M (2005) Complete genomic sequence of human coronavirus OC43: molecular clock analysis suggests a relatively recent zoonotic coronavirus transmission event. J Virol 79:1595–1604

Wang S, Wang S, Luo Y, Xiao L, Luo X, Gao S, Dou Y, Zhang H, Guo A, Meng Q, Hou J, Zhang B, Zhang S, Yang M, Meng X, Mei H, Li H, He Z, Zhu X, Tan X, Zhu XQ, Yu J, Cai J, Zhu G, Hu S, Cai X (2016) Comparative genomics reveals adaptive evolution of Asian tapeworm in switching to a new intermediate host. Nat Commun 22:12845

Waters AP, Higgins DG, MacCutchan TF (1991) *Plasmodium falciparum* appears to have arisen as a result of lateral transfer between avian and human hosts. Proc Natl Acad Sci U S A 88:3140–3144

Webb SD (2006) The great American biotic interchange: patterns and processes 1. Ann Mo Bot Gard 93:245–257

Węcek K, Hartmann S, Paijmans JLA, Taron U, Xenikoudakis G, Cahill JA, Heintzman PD, Shapiro B, Baryshnikov G, Bunevich AN, Crees JJ, Dobosz R, Manaserian N, Okarma H, Tokarska M, Turvey ST, Wójcik JM, Żyła W, Szymura JM, Hofreiter M, Barlow A (2017) Complex admixture preceded and followed the extinction of wisent in the wild. Mol Biol Evol 34:598–612

Wheeler JW (2012) South American camelids-past, present and future. J Camelid Sci 5:1–24

Williamson T (2002) The transformation of rural England: farming and the landscape 1700–1870. University of Exeter Press, Exeter

Wolfe ND, Panosian CP, Dunavan DJ (2007) Origins of major human infectious diseases. Nature 17:279–283

Woodburne MO (2010) The great American biotic interchange: dispersals, tectonics, climate, sea level and holding pens. J Mamm Evol 17:245–264

Worobey M, Han GZ, Rambaut A (2014) A synchronized global sweep of the internal genes of modern avian influenza virus. Nature 508:2454–2257

Wrangham RW, Jones JH, Laden G, Pilbeam D, Conklin-Brittain N (1999) The raw and the stolen. Cooking and the ecology of human origins. Curr Anthropol 40:567–594

Yeloff D, van Geel B (2007) Special paper: abandonment of farmland and vegetation succession following the Eurasian plague pandemic of AD 1347-52. J Biogeogr 34:575–582

Zarlenga DS, Rosenthal BM, La Rosa G, Pozio E, Hoberg EP (2006) Post-Miocene expansion, colonization, and host switching drove speciation among extant nematodes of the archaic genus *Trichinella*. PNAS 103:7354–7359

Zeder A (2012) In: Gepts P, Famula TR, Bettinger RL et al (eds) Pathways to animal domestication melinda biodiversity in agriculture: domestication, evolution, and sustainability. Cambridge University Press, Cambridge

Zeder MA (2015) Core questions in domestication research. Proc Natl Acad Sci U S A 112:3191–3198

Zhou NN, Senne DA, Landgraf JS, Swenson SL, Erickson G, Rossow K, Liu L, Yoon KJ, Krauss S, Webster RG (1999) Genetic Reassortment of avian, swine, and human influenza a viruses in American pigs. J Virol 73:8851–8856

Zuckerman M, Harper K, Barrett R, Armelagos G (2014) The evolution of disease: anthropological perspectives on epidemiologic transitions. Special issue: epidemiological transitions – beyond Omran’s theory. The evolution of disease: anthropological perspectives on epidemiologic transitions. Glob Health Action 7:23303