ILAR Journal, 2017, Vol. 58, No. 3, 315–318

doi: 10.1093/ilar/ilx035
Article

Changing Patterns of Emerging Zoonotic Diseases in Wildlife, Domestic Animals, and Humans Linked to Biodiversity Loss and Globalization

A. Alonso Aguirre

A. Alonso Aguirre is Department Chair of Environmental Science and Policy, George Mason University, Fairfax, Virginia 22030.

Address correspondence to A. Alonso Aguirre, Environmental Science and Policy, George Mason University, 4400 University Drive, MSN: 5F2, Fairfax, VA 22030-4400, or email aaguirr3@gmu.edu.

Abstract

The fundamental human threats to biodiversity including habitat destruction, globalization, and species loss have led to ecosystem disruptions altering infectious disease transmission patterns, the accumulation of toxic pollutants, and the invasion of alien species and pathogens. To top it all, the profound role of climate change on many ecological processes has affected the inability of many species to adapt to these relatively rapid changes. This special issue, “Zoonotic Disease Ecology: Effects on Humans, Domestic Animals and Wildlife,” explores the complex interactions of emerging infectious diseases across taxa linked to many of these anthropogenic and environmental drivers. Selected emerging zoonoses including RNA viruses, Rift Valley fever, trypanosomiasis, Hanta virus infection, and other vector-borne diseases are discussed in detail. Also, coprophagous beetles are proposed as important vectors in the transmission and maintenance of infectious pathogens. An overview of the impacts of climate change in emerging disease ecology within the context of Brazil as a case study is provided. Animal Care and Use Committee requirements were investigated, concluding that ecology journals have low rates of explicit statements regarding the welfare and wellbing of wildlife during experimental studies. Most of the solutions to protect biodiversity and predicting and preventing the next epidemic in humans originating from wildlife are oriented towards the developed world and are less useful for biodiverse, low-income economies. We need the development of regional policies to address these issues at the local level.

Key words: climate change; coprophagous beetles; hantavirus; One Health; Rift Valley Fever; trypanosomiasis; wildlife welfare; zoonoses

This is not the first time that *ILAR Journal* departs from traditional research on animal welfare applied to laboratory and domestic animals. In 2016, it published a special issue titled “Insights Gained from Wildlife Research in the Context of Global Anthropogenic Change.” That issue focused on specific diseases affecting bats, raccoons, and elephants; a proactive response to zoonotic pathogens; and a brief history and the welfare policy needs of wildlife in the United States. The One Health approach is mentioned as key to have a better understanding of health across humans, animals, plants, and ecosystems (Bryan and Sikes 2016). This special issue, “Zoonotic Disease Ecology: Effects on Humans, Domestic Animals and Wildlife,” explores the complex interactions of emerging infectious diseases across taxa linked to the impacts of massive biodiversity loss and globalization.

The fundamental human threats to biodiversity include overexploitation of species, habitat destruction, and exotic species introduction (referred as the “evil trio”), and have led to ecosystem disruptions causing alteration of disease transmission patterns. Adding pathogen pollution, global toxification, and global environmental change linked to climate (the “savage sextet”) compound the pervasive biodiversity loss (Aguirre 2009). Perhaps from these, the most insidious factor is climate change, which has a profound effect on all ecological processes including increased precipitation in some regions and drought in others; increased erosion of the coastal zone with rising sea levels; increased tsunamis, hurricanes, and tropical storms; and the inability of many species to adapt to the relatively rapid changes in climatic regimes, potentially resulting in mass extinctions (Aguirre and Tabor 2008). A recent study documents that more than 700 threatened mammals and birds have been adversely affected by climate change (Pacifici et al. 2017). We have observed major geographic range changes of many species on land (to higher latitudes) and at sea (to colder waters); warmer temperatures lead to massive coral bleaching, marine dead zones, acidification of seawater, and decline of coastal wetlands.

It is difficult to estimate species numbers and extinction rates and how the latter have changed over geological frames since the arrival of humans; however, the International Union for Conservation of Nature (IUCN) has estimated extinction rates for several taxa. The primary threats to 8688 species listed in the IUCN Red Data Book include overexploitation (72%), agricultural activity (62%), and climate change (19%). More recently, Ceballos et al. (2017) estimated that rates of population loss in terrestrial vertebrates is staggering: 32% of 27,600 vertebrate species have decreased in population size and range. The authors refer to these massive declines as a “biological annihilation.” Linked to these factors, disease has been proven catastrophic to diminished and already stressed populations including amphibian chytridiomycosis; white nose syndrome of bats; Tasmanian devil facial tumors; nutrient-driven hypoxic dead zones impacting fish and shellfish; and mites, microbial pathogens, and neonicotinoids in honeybees. These are some examples of infectious and noninfectious agents becoming leading factors in species declines and extinctions. Disease has become a major threat to biodiversity jumping across species and taxa. For instance, the Ebola virus, which became a global pandemic in 2014, is pushing gorillas and chimps to extinction in western Africa with mortality rates of 95% and 77%, respectively. Current trends show that one-third of great ape populations in Africa have died of the disease since the 1990s (Alexander et al. 2015). Every year we have novel viruses spilling over from wildlife to humans or domestic animals in unexpected ways. Highly pathogenic H5N1 avian influenza surprised many epidemiologists’ rules by jumping from chickens straight to humans, calling world attention to a potential pandemic with the H1N1 outbreak in Mexico.

It is important to note that despite much anecdotal evidence, we still do not understand many of the potential effects that anthropogenic change might have on disease emergence (Patz et al. 2004). To be able to better predict disease emergence in the wake of urbanization, agricultural development, and a changing climate and thus make informed health-relevant policies, we need far more ecology and health analyses. For sound health policy, we must shift away from dealing primarily with specific risk factors and look “upstream” to underlying landscape determinants of disease and ultimately human behavior and established institutions that are detrimental to sustainable population health.

Infectious diseases in the human-wildlife-domestic animal interfaces are affected by a multitude of environmental factors including pollution, water management, putrescible waste management, vector ecology, urban microclimates, and human encroachment on wildlife habitats. The impact of anthropogenic change on ecosystem health is multi-faceted and therefore needs the transdisciplinary approach offered by One Health. For the development of policy based on research results, this transdisciplinary coalition is necessary to identify and address health issues at the local level. This coalition should be composed of local politicians, community representatives, economists, ecologists, public health workers, city planners (engineers and architects), social scientists, and educators (Aguirre et al. 2016).

While compelling, the human health justification for wildlife conservation is extremely anthropocentric, and an urgent need is to address how biodiversity depends on us. One Health collaborations in research, intervention, and education should consider coincidental health problems and risks in areas of spatial and temporal overlap among species and stressors including crowding, pathogens, metals, nutrients, biotoxins, anthropogenic chemicals, and climate change. Collectively countering such stressors can restore ecosystem services that protect humans and nonhumans alike. Transdisciplinarity, integrative research, and capacity building are core elements in establishing One Health interventions that address extant, emerging, and reemerging pathogens and toxicants that harm humans, wildlife, and other components of biodiversity. The One Health model requires practical, sustainable, and effective solutions with a keen understanding of local socio-economic factors as well as a solid grasp of complex regional, national, and international health and environmental policies. “Zoonotic Disease Ecology: Effects on Humans, Domestic Animals and Wildlife” includes selected examples of emerging pathogens and their impact across humans, species, and ecosystems. Tick-borne zoonoses, RNA viruses, Rift Valley fever (RVF), Chagas disease, hantavirus infection, the role of coprophagous insects on disease ecology, and the impacts of climate on disease emergence are discussed as vivid examples of these complex interactions.

Tick-Borne Zoonoses in the United States: Persistent and Emerging Threats to Human Health

The first article written by Eisen and colleagues (2017) overviews tick-borne zoonoses in the United States. Almost 30% of zoonotic diseases are vector-borne linked to a wild reservoir. The greatest diversity of arthropod-borne pathogens is transmitted by ticks. Prevalence and incidence of known and novel tick-borne diseases continues to increase as humans and their domestic animals continue to take over wildlife habitats. Eisen et al. provide a detailed review of the diseases, natural history of ticks, and spatial and temporal changes in vector and their disease distributions and occurrence in recent times. Notably, >40% of the pathogens described herein were discovered during the last two decades.

Coprophagous Insects and the Ecology of Infectious Disease of Wildlife

The second article of this special issue by Nichols and collaborators (2017) describes the role of one of the most biodiverse groups of insects and their role in transmission and maintenance of infectious agents. Over 7000 species of coprophagous dung beetles interact with a staggering diversity of macro- and microparasites with fecal-oral transmission. This close insect-pathogen association impacts host fitness, wildlife density, community structure, and ecosystem functioning. The authors discuss how these relationships interact and may change with environmental global change. Future efforts should focus on understanding the overall dynamics of disease ecology in wildlife and how parasites contribute to the maintenance of ecosystem structure and function and the wildlife evolutionary processes in motion.

Are RNA Viruses Candidate Agents for the Next Global Pandemic? A Review

RNA viruses are a diverse and important group of zoonotic agents that include 180 species, and 2 new species are discovered yearly. These pathogens are shared primarily between humans and mammals and sometimes birds and have been described as the most important viruses in zoonotic disease transmission, representing a challenge for global disease control. This group has rapid adaptive rates linked to anthropogenic-induced rates of interspecies contacts that may lead to a pandemic. Examples of RNA viruses include HIV, SARS, Hendra, Nipa, and MERS to name a few. Carrasco-Hernández and collaborators (2017), throughout different levels of complexity, cover the molecular mechanisms allowing RNA viruses to adapt to new host species and to develop resistance to specific pharmaceutical regimes. Known ecological processes involved in zoonotic transmission are also discussed.

RVF: Does Wildlife Play a Role?

Rift Valley fever (RVF) is an acute, mosquito-borne, zoonotic disease of domestic and wild ruminants in the Arabian Peninsula and the African continent. Outbreaks are associated with heavy rainfall and flooding. The disease causes abortions and perinatal mortality. Although the disease is subclinical or mild in humans, it manifests with flu-like symptoms. Sporadic large outbreaks are followed for 5- to 10-year intervals during drier years. Rostal and colleagues (2017) describe the eco-epidemiology of the virus during apparently quiescent, inter-epidemic periods. There is evidence for low-level circulation of the virus in livestock and wild ruminants; however, a specific reservoir host has not been identified. Vaccination remains the only effective way to protect livestock from RVF. The utilization of predictive tools to determine when outbreaks will occur has been unreliable, as these present a sudden onset. Further research should focus on these inter-epidemic periods and the search for a reservoir host.

The Animal Wildlife Act and the Conduct and Publishing of Wildlife Research in the United States

Paul et al. (2016) provided an overview of the regulations and policies applicable to research with wildlife and the resources available related to welfare policy. In addition, Sikes and Bryan (2016) provide the history and policy related to the evolution of wildlife welfare in the United States. The fifth article of this special issue by Mulcahy (2017) focuses on the research using wild animals covered by the Animal Welfare Act and its enabling regulations that must be reviewed and approved by an Animal Care and Use Committee (ACUC). He reviewed the instructions to authors and policy statements of 106 journals focusing on disease ecology both originating in the United States and produced internationally. Significant differences on ACUC requirements were identified in several journals. Interestingly, ecology journals had low rates of explicit statements for ACUC review regardless of geographic origins or sources.

Toward an Ecological Framework for Assessing Reservoirs of Vector-Borne Pathogens: Wildlife Reservoirs of *Trypanosoma cruzi* across the Southern United States

Hodo and Hamer (2017) reviewed 77 published reports of *Trypanosoma cruzi* infection in 26 wildlife species across 15 southern states in the United States. Many species of triatomine vectors and wildlife maintain the enzootic cycle, which with the right conditions increase the risk of spillover to humans, domestic dogs, and nonhuman primates and in turn may develop Chagas disease. Considering elements of reservoir competence and vector-host contact, the authors applied the conceptual framework of “reservoir potential.” Over 60% of studies reviewed identified raccoons (*Procyon lotor*) and striped skunks (*Mephitis mephitis*) among the most infectious wildlife reservoirs. This model could develop new research tools to reduce the risk of *T. cruzi* spilling over to populations at risk and better manage the enzootic cycle of Chagas disease.

The Impact of Global Environmental Changes on Infectious Disease Emergence with a Focus on Risks for Brazil

Global environmental change may be connected with ecological process disruption, which leads to infectious disease emergence in different biomes around the globe. Nava et al. (2017) provide an extensive review of the the anthropogenic and environmental drivers of infectious disease emergence using Brazil as a case study. The authors highlighted diseases of present public health importance in Brazil including Chikungunya, dengue fever, yellow fever, Zika, hantavirus pulmonary syndrome, leptospirosis, leishmaniasis, and Chagas disease. Analyzing the specific drivers considering factors such as biome type, reservoirs involved, country policy, and the pathogen involved is necessary to correctly evaluate the specific impact of each driver and implement preventive, control, and/or mitigation measures. The express aim of this review is to show that in order to develop a more realistic perspective on global environmental change and emergfing infectious disease ecology, a transdisciplinary approach of the problem is required. In addition, assessing biological, social, and economic contexts by developing forecasting tools needs to work with local health and environmental policy.

Species Identity Supersedes the Dilution Effect Concerning Hantavirus Prevalence at Sites across Texas and Mexico

The study addresses a research question centered in ascertaining if rodent assemblage structure differs between sylvan and disturbed sites at a given locality, and if so, disturbed habitats may support greater assemblage-wide hantavirus seroprevalence (Milholland et al. 2017). Furthermore, the authors questioned if there is a difference in relative abundance and numerical dominance of hantavirus reservoir species between these habitat types. Rodents were sampled from sylvan and disturbed habitats at 20 sites across northern Texas through southern Mexico and tested for hantavirus antibodies to establish assemblage seroprevalence at each habitat. Next, the differences between habitat types were compared, and inferences were made regarding assemblage structure, hantavirus prevalence, and the efficacy of dilution effect dynamics with data across a regional scale. Their findings did not support the hypothesis that “greater species richness is higher in sylvan habitats compared to disturbed areas,” suggesting that characteristics of assemblage structure do not adhere to current conceptions of species richness, and that the dilution effect is limited to site-/habitat-specific characteristics.

References

Aguirre AA. 2009. Biodiversity and human health. EcoHealth 6: 153–156.

Aguirre AA, Beasley VR, Augspurger T, Benson WH, Whaley J, Basu N. 2016. One Health—Transdisciplinary opportunities for SETAC leadership in integrating and improving the health of people, animals, and the environment. Environ Toxicol Chem 35:2383–2391.

Aguirre AA, Tabor GM. 2008. Global factors driving emerging infectious diseases: Impact on wildlife populations. Ann N Y Acad Sci 1149:1–3.

Alexander KA, Sanderson CE, Marathe M, Lewis BL, Rivers CM, Shaman J, Drake JM, Lofgren E, Dato VM, Eisenberg MC, Eubank S. 2015. What factors might have led to the emergence of Ebola in West Africa? PLoS Negl Trop Dis 9: e0003652. doi:10.1371/journal.pntd.0003652.

Bryan JA II, Sikes RS. 2016. Introduction to insights gained from wildlife research in the context of global anthropogenic change. ILAR J 56:272–274.

Carrasco Hernández R, Jácome R, López Vidal Y, Ponce de León S. 2017. Are RNA viruses candidate agents for the next global pandemic? A review. ILAR J 58:000–000.

Ceballos G, Ehrlich PR, Dirzo R. 2017. Biological annihilation via the ongoing sixth mass extinction signaled by vertebrate population losses and declines. Proc Natl Acad Sci USA 114: E6089–E6096. doi:10.1073/pnas.1704949114.

Eisen R, Kugeler K, Eisen L, Beard C, Paddock C. 2017. Tick-borne zoonoses in the United States: Persistent and emerging threats to human health. ILAR J 58:000–000.

Hodo C, Hamer S. 2017. Toward an ecological framework for assessing reservoirs of vector-borne pathogens: Wildlife reservoirs of *Trypanosoma cruzi* across the southern United States. ILAR J 58:000–000.

Milholland MT, Castro-Arellano I, Arellano E, Nava-García E, Rangel-Altamirano G, Gonzalez-Cozatl FX, Suzán G, Schountz T, González-Padrón S, Vigueras A, Rubio AV, Maikis TJ, Westrich BJ, Esteve-Gassent MD, Torres M, Rodriguez-Ruiz, ER, Hahn D, Lacher TE Jr. 2017. Species identity supersedes the dilution effect concerning hantavirus prevalence at sites across Texas and Mexico. ILAR J 58: 000–000.

Mulcahy D. 2017. The Animal Welfare Act and the conduct and publishing of wildlife research in the United States. ILAR J 58:000–000.

Nava A. 2017. The impact of global environmental changes on infectious disease emergence with a focus on risks for Brazil. ILAR J 58:000–000.

Nichols E, Alarcón NV, Forgie S, Gomez-Puerta LA, Jones MS. 2017. Coprophagous insects and the ecology of infectious diseases of wildlife. ILAR J 58:000–000.

Pacifici M, Visconti P, Butchart SHM, Watson JEM, Cassola FM, Rondinini C. 2017. Species’ traits influenced their response to recent climate change. Nat Clim Change 7:205–209.

Patz JA, Daszak P, Tabor GM, Aguirre AA, Pearl M, Epstein J, Wolfe ND, Kilpatrick AM, Foufopoulos J, Molyneux D, Bradley DJ and Members of the Working Group on Land Use Change and Disease Emergence. 2004. Unhealthy landscapes: Policy recommendations pertaining to land use change and disease emergence. Environ Health Perspect 112:1092–1098.

Paul E, Sikes RS, Beaupre SJ, Wingfield JC. 2015. Animal welfare policy: Implementation in the context of wildlife research -policy review and discussion of fundamental issues. ILAR J 56:312–334.

Rostal M, Liang JE, Zimmermann D, Bengis R, Paweska JT, Karesh WB. 2017. Rift Valley Fever: Does wildlife play a role? ILAR J 58:000–000.

Sikes RS, Bryan JA II. 2015. Institutional Animal Care and Use Committee considerations for the use of wildlife in research and education. ILAR J 56:335–341.