Wildlife: The Need to Better Understand the Linkages

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Abstract Wildlife are frequently a neglected component of One Health; however, the linkages between the health of wildlife and human, domestic animal, and environmental health are clear. The majority of emerging zoonotic diseases are linked to wildlife, primarily driven by anthropogenic land changes. Despite this risk, wildlife have important links to people as environmental indicators, food security and safety, and through human livelihoods. This chapter will describe these linkages and demonstrate the need to understand these linkages through targeted surveillance and understanding the ecology of wildlife diseases. While the management of wildlife diseases presents a significant challenge, such practices will greatly improve the health of people, domestic animals, wildlife and the environment.

Contents

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1 Introduction

One Health is the all-encompassing concept that recognizes the inextricable links between the health of people, animals (wild and domestic), and the environment. While the link between people and domestic animals is well recognized, as they have been used for food, work, and products for millennia, the link between the health of people and wildlife is often neglected. This may be due to a perceived distance between wildlife and people and a lack of understanding of the important linkages that unite human health with the health of all animals. In an ever more urbanized and globalized world, the distance between people and wildlife is shrinking and these linkages are becoming ever more evident. In this chapter, we will discuss the linkages between human health and wildlife from multiple perspectives. This includes direct linkages with human health, such as emerging and nonemerging zoonotic diseases, as well as linkages between wildlife health and the environment, food security and the health of domestic animals, and sustainable human livelihoods. Wildlife are an important component of One Health, but is often neglected due to difficulty in conducting health studies and limited data and funding. We will further discuss the importance of understanding these linkages with wildlife through targeted surveillance, understanding the ecology of wildlife diseases, and the management of wildlife diseases.

2 Linkages with Emerging Infectious Diseases

When wildlife are discussed in the context of One Health, it is frequently in terms of their role as hosts to emerging infectious diseases (EIDs). With the number of EIDs significantly increasing during the past 60 years, recent work has demonstrated that the majority are zoonotic (60 %) and approximately 70 % of those are of wildlife origin (Jones et al. 2008). An EID is frequently defined as a disease that has recently been jumped into a new host, has evolved a new pathogenicity, is increasing in incidence, or has expanded into a new geographic range (Lederberg et al. 1992; Jones et al. 2008). While outbreaks of EIDs may seem like rare events, as a group

they cause hundreds of thousands of deaths annually (Bogich et al. 2012) and a single event may cost US$10–50 billion to the global economy (Newcomb 2003).

The process of disease emergence is complex and often multifactorial, but it can be better understood using broadscale, ecological approaches in identifying these factors, or drivers. In the first attempt to classify the underlying drivers of disease emergence, the Institute of Medicine (IOM) identified six factors including: human demographics and behavior; technology and industry; economic development and land use; international travel and commerce; microbial adaptation and change; and breakdown of public health measures (Lederberg et al. 1992). In 2003, seven additional drivers were added to the IOM report including: human susceptibility to infection; climate and weather; changing ecosystems; poverty and social inequity; war and famine; lack of political will; and intent to harm (Smolinski et al. 2003). IOM's classification of the "factors in emergence" largely paved the way for current research investigating the underlying drivers of infectious disease emergence. It is important to note that these drivers are not mutually exclusive, and that factors may act in concert and will vary at different stages of the emergence process. For example, anthropogenic land use change has resulted in cross-species transmission of disease or initial emergence, from animal hosts to humans both directly by increasing human contact with animal populations, and in other cases indirectly by changing vector populations (Daszak et al. 2000; Patz et al. 2004). Climate and weather can augment these affects and modulate outbreak size; particularly with vector or waterborne diseases, and global trade and travel has facilitated the spread of those diseases (Hufnagel et al. 2004). These EID drivers function on a different scales, vary geographically (Keesing et al. 2010), and can be attributed to a combination of environmental, ecological, political, and social forces. Despite ongoing research investigating the role of EID drivers, additional studies and modeling approaches are needed to more fully understand the complex mechanisms of emergence (Bogich et al. 2012).

2.1 Wildlife Trade and Zoonoses

One important driver of zoonotic disease emergence that has often been overlooked by the One Health community is the wildlife trade. Trade in wildlife, both legal and illegal, can lead to the introduction of zoonoses and/or foreign animal diseases that may impact domestic animals or native wildlife species (Karesh et al. 2005). The illegal wildlife trade is estimated to be approximately US$20 billion, the second largest black market after narcotics (Karesh et al. 2012). It is likely that this estimate is overly conservative as a recent study found that within one tropical country, Venezuela, 1–10 million animals are traded annually at an estimated cost of US$321 million (Asmüssen et al. 2011). An estimated 1.5 billion live wild animals were legally imported into United States between 2000 and 2006. Nearly, 90 % of those animals were destined for the pet trade (Smith et al. 2009). With the magnitude of stressed, and possibly immune compromised, wild animals being

transported on a global scale, it is not surprising that this has resulted in the spread and transmission of diseases that affect native wildlife, domestic animals, and people.

Previous outbreaks of important zoonotic diseases have already been attributed to the wildlife trade; notable, among these in the twenty-first century are severe acute respiratory syndrome (SARS) and monkeypox. SARS is a novel coronavirus that shifted from bats into civets and humans causing severe morbidity and mortality (case fatality rate of 13.2–43.3 %) (Donnelly et al. 2003). Globalization and airline networks expidited the spread of SARS from its point of origin in Southern China to infect people in 28 countries, making it the first pandemic of the twenty-first century (Zhou and Yan 2003). The "wet market" where SARS emerged in Guangzhou, China had stalls where wild mammals, domestic animals, reptiles, and birds were sold in conditions of poor hygiene and in close proximity. After the SARS outbreak was traced back to these markets, the Chinese government reportedly confiscated 838,500 wild animals (Karesh et al. 2005). The most likely scenario of initial spillover and emergence was that rhinolophid bats harboring a SARS or SARS-like coronavirus were kept in cages in close proximity to civets that contracted and amplified the virus in the markets (Li et al. 2005). However, the evidence demonstrating bats as the original natural reservoir of SARS-like coronaviruses was not discovered until years after the initial outbreak (Li et al. 2005; Field 2009). Ongoing research has now revealed large numbers of novel coronaviruses from bats, and the hypothesis of SARS originating from these hosts has been further validated (Woo et al. 2009; Yuan et al. 2010). Monkeypox emerged under similar conditions through the legal pet trade in the US in 2003. It is hypothesized that prairie dogs (*Cynomys* spp.) were in contact with a shipment containing Gambian rats (*Cricetomys* spp.) and African dormice (*Graphiurus* spp.) at a wholesale pet store. The prairie dogs became ill, as did 37 people in contact with them (Guarner et al. 2004).

Despite the serious threat of EIDs from wildlife in the legal and illegal trade, few international programs exist to screen imported wildlife for pathogens of concern. A recent study analyzed wildlife products confiscated by the US Customs and Border Protection at John F. Kennedy Airport in Queens, NY as well as seizures from airports in Philadelphia, Washington, DC, Houston, and Atlanta (Smith et al. 2012). Smith et al. (2012) detected simian foamy virus (SFV) and several herpesviruses from bushmeat samples, including nonhuman primates, e.g., chimpanzees (*Pan troglodytes*), mangabeys (*Cercocebus* spp.), and guenons (*Cercopithecus* spp.), that were imported from Guinea, Liberia, and Nigeria. While SFV has not yet been shown to be pathogenic in people, approximately 1 % of bushmeat hunters in close contact with dead primates were found to be infected with SFVs (Wolfe et al. 2004). Wolfe et al. (2004) demonstrated sporadic transmission of SFVs to humans, and offered a better understanding of how human immunodeficiency virus/acquired immunodeficiency syndrome (HIV/AIDS) may have emerged from primates. We know that simian immunodeficiency virus (SIV) jumped several times into people hunting and consuming nonhuman primates before mutating into the pandemic HIV strains that are now circulating

(Heeney et al. 2006). This recent work by Smith et al. (2012) demonstrates that zoonotic pathogens can be transported in bushmeat and potentially could cause an outbreak in a location far from its endemic region, underscoring the need for better port surveillance and regulation of this trade. Left unregulated, legal and illegal wildlife trade can potentially have a large impact on human health, as well as direct impacts on wildlife and domestic animal health (discussed below).

3 Linkages with the Environment

The health of wildlife is closely linked to the health of the environment and can be extremely sensitive to anthropogenic changes. This includes direct physiological and behavioral responses to chemicals and pollution as well as competition and other effects from the introduction of nonnative wildlife and/or new pathogens.

3.1 Wildlife as Environmental Indicators

Animals have long been used as indicators of a toxic environment. The proverbial "canary in a coal mine", as later memorialized by Sting in a 1980 song, stems from the use of canaries to detect trace amounts of methane and carbon monoxide in mines since the early 1900s. Their death indicated to miners that they needed to evacuate the mine to prevent asphyxiation. Dichlorodiphenyltrichloroethane (DDT) was one of the first global acknowledgments of chemicals affecting non-target animals. DDT was found to reduce the eggshell thickness of multiple bird species (Porter and Wiemeyer 1969). It was later discovered that bioaccumulation of the chemical through the trophic levels had devastating effects on the populations of certain top predators and insectivorous birds (e.g., raptors such as peregrine falcons (*Falco peregrinus*) and bald eagles (*Haliaeetus leucocephalus*) (Grier 1982). These effects became widely distributed by Rachel Carson's "Silent Spring" (Carson 1962) and wildlife and plants were increasingly recognized as important indicators of man-made environmental health threats. During the 1990s, the US Environmental Protection Agency (EPA) began using ecological risk assessment (in addition to human risk assessment) to evaluate the risk of agrochemicals or other manufactured chemicals, superfund sites, as well as air and water pollution (EPA 1998). Ecological risk assessment depends on scientific assessment of the risk a chemical poses to a wide variety of plants and animals, including invertebrates, fish, birds, and small mammals (EPA 1998). While the system continues to be improved, risk assessments have been important in identifying the detrimental effect of acid rain (Beamish 1974), perfluorinated chemicals (Van de Vijver et al. 2003), and most recently endocrine disruptors (Kloas and Lutz 2006). These ecological risk assessments have contributed to several US national environmental laws that were created to protect the health of people.

In addition to top predators, small mammals are frequently used in ecological risk assessments and have been proposed as sentinels for heavy metal contamination. Talmage (1991) suggests that small mammals make good indicators of environmental pollution because of their abundance, widespread distribution, short dispersal distance, generalized food habits, short life span, high reproductive rate, and relative ease of capture. In particular, they can be used to assess the environmental contamination of landfills and mine areas (Torres et al. 2011). Insectivorous mammals appear to be the best indicators as they are exposed more directly through invertebrates that may consume soil (e.g., earthworms) (Hamers et al. 2002). In particular, small mammals have been used successfully to assess cadmium, fluoride, lead, and mercury exposures (Talmage 1991). One relatively recent study found that both rodents and children living around a mining site in Mexico had nearly twice the levels of lead and arsenic as the respective controls from the reference site (Jasso-Pineda et al. 2007). Despite the many studies that have successfully demonstrated that various rodent species can be used as environmental indicators for heavy metals and chronic pollution and the frequent use of rodents in risk assessments for new chemicals on the market, rodents are rarely used for regulatory purposes (e.g., for long-term monitoring of mining sites) (Handy et al. 2003). When used appropriately, environmental indicators could be a very valuable tool in long-term monitoring of the risk of pollution and contamination of both terrestrial and aquatic habitats (Lam and Gray 2003; Jasso-Pineda et al. 2007) and should be utilized more frequently.

3.2 Nonzoonotic Wildlife Diseases of Conservation Concern

As with zoonotic EIDs, emerging diseases of wildlife have increased during recent decades (Daszak et al. 2000) and have frequently been linked to anthropogenic ecological changes. Specifically, it is likely that trade, travel, invasive species, and poor biosecurity measures are driving many of these diseases. We highlight this with two emerging fungal pathogens that have caused devastating impact on two vertebrate groups, chytrid fungus in amphibians and white-nose syndrome (WNS) in bats, with indirect One Health consequences for human health and food security.

3.2.1 Chytridiomycosis

During the late twentieth century, amphibian populations began to decline on a global scale (Heyer et al. 1988; Young et al. 2001). Chytridiomycosis (*Batrachochytrium dendrobatidis*; chytrid fungus) was determined to be the causative agent in many of the declines (Daszak et al. 1999). This fungus caused multiple species declines (even local extirpation of multiple amphibian populations in some areas) in pristine habitats in the Americas and Australia (Daszak et al. 1999). It is believed that the chytrid fungus was spread through the trade of African clawed

frogs (*Xenopus laevis*), the original host, and the North American bullfrog (*Rana catesbeiana*) (Weldon et al. 2004; Schloegel et al. 2009). *R. catesbeiana* is frequently raised and traded for food, with greater than 270,000 kg of this species sold within Brazil every year (Schloegel et al. 2010). It has been suggested that out of more than 200 species of amphibians noted to be rapidly declining due to enigmatic causes (Stuart et al. 2004), a significant portion of them may have been due to chytrid (Skerratt et al. 2007). This fungus demonstrates how seemingly unrelated anthropogenic actions (wildlife trade) can have far-reaching effects on the environment and wildlife. Additionally, the loss of amphibians may disrupt ecological processes, such as a reduction in predation on mosquito larvae, resulting in consequent indirect impacts on human or animal health.

3.2.2 White-Nose Syndrome

WNS is an emerging disease of hibernating bats caused by the fungus *Geomyces destructans* (Blehert et al. 2009; Lorch et al. 2011). It was first documented in the US in 2006, and was most likely introduced accidentally by people traveling to and from Europe, where it is ubiquitous and causes no bat mortality (Puechmaille et al. 2011). This cold-loving fungus thrives in the winter environment of bat hibernacula and disrupts the hibernation and physiology of over-wintering bats. Bat mortality is frequently attributed to starvation and dehydration as the infection causes arousal during the winter leading to the depletion of the fat reserves of the hibernating animals (Cryan et al. 2010; Reeder et al. 2012). The fungus grows on the muzzle and wing membranes of susceptible bats. Mortality rates at many hibernacula are extremely high, commonly in the range of 80–100 % (Turner et al. 2011). WNS has rapidly spread south and west across the US, being confirmed in 19 US states and four Canadian provinces; and by early 2012, the US Fish and Wildlife Service estimated that over 5.5 million bats have died from the disease. WNS is predicted to cause the local extirpation or possibly the extinction of the little brown bat (*Myotis lucifugus*), which was once the most populous bat in the US (Frick et al. 2010). Once a wildlife disease such as WNS is established, control becomes very difficult. Researchers are currently working to understand the environmental and life-history variables that allow the fungus to persist and spread, with hopes that areas or microclimates can be set aside for management intervention ahead of the epidemic wave (Boyles and Willis 2010; Wilder et al. 2011; Langwig et al. 2012). Other unproven solutions being developed include antifungal treatment, maintaining rescue captive breeding colonies, and artificially heating caves. WNS, like chytrid, is an introduced fungal pathogen and arguably they are two of the most significant wildlife diseases—threatening a wide range of species with possible ecological and global extinction (Fisher et al. 2012). The value of bats in control of agricultural pests in North America alone has been estimated to US$3.4 billion annually, with a loss of bats translating into increased production costs (pesticides and other pest control methods) and smaller crop yields (Boyles et al. 2011).

4 Linkages with Food Safety and Security

As introduced above, food safety and security is an important component of One Health, especially as the FAO estimates that 1.02 billion people are undernourished worldwide (FAO 2009). Wildlife is linked with food security as wildlife can contaminate foodstuff with zoonotic diseases, bushmeat is a major protein source for people living in many tropical countries, and wildlife and domestic animals can share significant pathogens.

4.1 Foodborne Illnesses

Foodborne illnesses pose a serious threat to public health with growing economic and international trade ramifications. Standard epidemiological public health methods are frequently used to investigate foodborne outbreaks among people. However, foodborne diseases are good examples of the intricate link between human and animal populations, and the surrounding environment. In 2006, a virulent strain of *E. coli* O157:H7 was linked to spinach and affected approximately 200 people in 26 states (CDC 2006). A typical epidemiological investigation of this outbreak would have extended only to human morbidity, mortality, assessments of risk and probable source, laboratory diagnosis, and clinical treatment. However, when domestic and wild animal health and ecology were considered, Warnert (2007) found the same strain of *E. coli* O157:H7 isolates that caused the human outbreak in wild pig feces, the feces of several cows, and in a stream on one of the four spinach farms in the area. Thus, a One Health perspective integrating our knowledge of epidemiology, clinical diagnostics, the environment and ecology, was required to fully investigate and understand this outbreak and has great utility in understanding the foodborne illness outbreaks.

Foodborne pathogens from wildlife span the taxonomic spectrum from helminthes to viruses. Emerging foodborne diseases represent the majority of foodborne illnesses in the US and an even larger percentage of the foodborne illnesses are likely due to yet undescribed pathogens (Tauxe 2002). Many of the known foodborne pathogens and up to 70 % of foodborne EID events are zoonotic and many may be linked to wildlife. Commonly, both wild and domestic animals are implicated as sources of food contamination (Beuchat and Ryu 1997; Doyle and Erickson 2008; Newell et al. 2010; Gorski et al. 2011; Cima 2012). Despite this, definitive identification of a specific source animal or species is rare, particularly as epidemiological investigations often occur long after the index case, as it can take time for an outbreak across various states or counties to be detected. However, in some cases, detailed ecological studies can determine the exact route of food contamination from wildlife. For example, Nipah virus, a bat-borne emerging encephalitic Paramyxovirus, is primarily transmitted through contaminated date palm sap in Bangladesh. With annual outbreaks in people and very high fatality

rates (>80 %), this is a pathogen of special concern (Luby et al. 2006, 2009). Recent serological and pathogen discovery studies have shown that *Pteropus giganteus*, a large fruit bat, is likely the primary reservoir for this virus (Epstein et al. 2008). Further, using techniques of wildlife surveillance and infrared camera traps, the exact mechanism of transmission was determined. Bats were observed feeding from date palm sap collecting pots at night and currently specific interventions that do not entail bat eradication are being developed to prevent this transmission (Nahar et al. 2010; Khan et al. 2011).

4.2 Bushmeat and Healthy Communities

Wild animals provide a substantial portion of our food globally, with nearly half of all seafood coming from wild sources. In some regions of the world, wild meat from terrestrial animals represents a primary source of protein on which people are dependent. The volume of wild meat ("bushmeat") harvested from Central Africa alone totals more than 1 billion kg per year (Wilkie and Carpenter 1999). This volume of meat, almost all of which is processed and distributed to consumers with few if any modern hygiene practices, provides a constant opportunity for human exposure to both rare and common foodborne pathogens (Karesh et al. 2005; Smith et al. 2012). Modeling has been used to indicate direct linkages between health and bushmeat consumption. Golden et al. (2011) used generalized linear mixed-model regression to suggest that if bushmeat were removed from the diet of children in Madagascar, hemoglobin concentration would decrease by 0.7 g/dL leading to a likely increase in anemic children of nearly 30 %. The overconsumption of wildlife resources may soon lead to the loss of bushmeat protein to diets. Fa et al. (2003) predict that the percentage of dietary protein consumed through bushmeat is unsustainable and will decrease from an estimated 55 % in 2000 to 23 % by 2050 in the Congo Basin. This prediction is based on increasing wildlife extraction to production ratios that will ultimately lead to a decline in wildlife abundance. Without the availability of bushmeat or the redistribution of global food sources, food insecurity in this region is likely to increase. This link between bushmeat hunting and food insecurity has been supported by the results of a study, which found the alleviation of food security concerns of villagers in Zambia by improving domestic animal production over 2 years led hunters to turn in 12,000 snares and 76 firearms, saving an estimated 1,500 wild animals (Lewis and Jackson 2005).

4.3 Transmission to Domestic Animals

Wildlife can be reservoirs of important diseases of domestic animals, some of which were originally diseases of livestock and are now maintained in wildlife

populations despite eradication of the disease in domestic animals. Disease-induced morbidity and mortality in domestic animals as well as economic sanctions associated with the presence of certain diseases can adversely affect the supply of food animals.

Certain wildlife diseases can cause morbidity and mortality in domestic animals that are accidental or dead-end hosts. One such example is malignant catarrhal fever, caused by *Alcelaphine herpesvirus* 1 of wildebeest (*Connochaetes taurinus*), which can cause acute mortality in cattle (Russell et al. 2009). While its significance is limited to regions endemic for wildebeest (or zoos housing them), outbreaks of the virus can cause significant losses and hardships for local herders in Africa. Some diseases have larger economic ramifications, such as foot-and-mouth disease (FMD). Though the virus affects all species with cloven hooves (order: Artiodactyla), there are specific strains that are more likely to circulate in different geographic locations and possibly primary reservoir species (e.g., cattle or African buffalo, *Syncerus caffer*) (Klein 2009). While the virus is not highly fatal to the animals, trade restrictions to prevent the introduction of the virus in FMD-free regions has led to it becoming an economically important virus. It is estimated that during the 2001 FMD outbreak in the UK, losses to agricultural industry and the food supply chain amounted to £3.1 billion (Thompson et al. 2002). Outbreak response led to the destruction of 4 million animals (Thompson et al. 2002). It is likely that the virus was imported into the country from cattle in virus endemic regions (Samuel and Knowles 2001).

Some diseases of concern have their origins in domestic animals, but have now been established into wildlife populations where they can then be retransmitted back to domestic animals (Daszak et al. 2001). In the US, *Brucella abortus* is generally believed to be introduced to the continent by cattle (Meagher and Meyer 1994). After a successful eradication campaign, all 50 states were declared free of Brucellosis in domestic cattle herds in 2008; however, the maintenance of the bacteria in herds of elk and bison in the Greater Yellowstone Area has allowed the pathogen to persist and continue to cause outbreaks. The debate over how to eradicate brucellosis from the country is ongoing. Management methods that have been discussed include: test and cull, depopulation, and prohibiting winter feeding sites for elk as well as vaccination (Olsen 2010). A similar story follows the introduction of bovine tuberculosis (*Mycobacterium bovis*) into wildlife hosts (see Box 1).

One Health includes considering pathogens originating from domestic animals that can severely affect wildlife. Rinderpest virus was introduced into Africa during the early 1900s. The virus swept across the continent killing susceptible cattle and wild artiodactyls en masse. It has been reported that over 5.3 million cattle died in southern Africa and up to 90 % of the African buffalo population was decimated (Plowright 1982). Fortunately, rinderpest was not able to be maintained in large wildlife populations without the presence of cattle (Plowright 1982). It is believed that the massive loss of multiple species of grazers (buffalo, wildebeest etc.) actually led to a change in the ecosystem of the region that is still in effect today, although as these species are recovering, the ecosystem is likely reverting to

that which was believed to have been prior to the outbreak (Holdo et al. 2009). Rinderpest is now the second virus that has been eradicated through the use of vaccinations, after smallpox virus (Yamanouchi 2012).

Box 1. Bovine Tuberculosis: A Persistent Linkage between Wildlife and Domestic Animals

Wildlife reservoirs of domestic animal diseases can make it exceedingly difficult or even impossible to eradicate economically important pathogens. Often, diseases that originated in domestic animals persist in wildlife at such low prevalences that they are not detected in the wildlife until the disease is controlled or eliminated in domestic animals. In the US, a program to eliminate bovine tuberculosis (*Mycobacterium bovis*; bTB) was initiated in 1917. By 1990, every state had been declared to be free of bTB (Knust et al. 2011), when a case of bTB was reported in a white-tailed deer (*Odocoileus virginianus*; WTD) in Michigan. The outbreak was confirmed after 19 of 354 hunter-killed deer tested positive for bTB (Schmitt et al. 1997). Genetic analyses have confirmed that this strain of bTB has been circulating in the WTD population at a low prevalence (O'Brien et al. 2011).

Efforts by the Michigan Department of Agriculture and Michigan Department of Natural Resources (MDNR) initially focused on depopulation of WTD in the 5-county affected area and a ban on feeding or baiting deer during winter. While they have been successful in decreasing the prevalence by 60 %, low levels of bTB (0.2 % prevalence) continue to circulate in the WTD and occasionally spillover into cattle, leading to depopulation of the cattle herd (O'Brien et al. 2011). The circulation of bTB in wildlife has a high economic cost to agriculture in the region as Michigan now has a split-state tuberculosis accreditation (the Upper Peninsula of Michigan is still considered tuberculosis free, while the rest of the state is divided between Accredited Free, Modified Accredited Advanced, and Modified Accredited, depending on the distance from the nidus of bTB. It is estimated that bTB and the accreditation change cost Michigan's agriculture industry US$52 million from 1999 to 2003 and US$156 million from 1999 to 2008 (Thiel 2001). Eradication of bTB in the WTD population has been prevented partially due to the lack of public support for continued lethal population control. Hunters contribute US$507 million to Michigan's economy and with other sympathetic electorate, who desire to view deer in their yards, have significant political clout (O'Brien et al. 2011). Political pressure to decrease the level of lethal control has lead the MDNR to look to developing new vaccine-related technologies. While no such vaccine has yet been developed, pressure continues to mount as WTD in Minnesota were found to have bTB (most likely a cattle strain) following outbreaks in cattle in 2005 (Knust et al. 2011).

Several other wildlife species are known to be reservoirs of bovine TB in countries beyond the US, making it very difficult to eradicate globally.

Examples of bTB reservoirs include badgers (*Meles meles*) in Britain, buffalo (*Syncerus caffer*) in southern Africa, and brushtail possums (*Trichosurus vulpecula*) in New Zealand (O'Brien et al. 2011). Bovine tuberculosis demonstrates the difficulty of sustainable control of a zoonotic and economically costly disease. The challenges of either eradication or control in wildlife also highlight the cost-effectiveness of prevention, i.e., investment in efforts to prevent domestic animal diseases from becoming established in wildlife populations would be more cost-effective and more less effort than trying to remove a pathogen from wildlife populations.

5 Linkages with Human Livelihoods

Many of the most biologically diverse regions coincide with human populations living at the highest poverty levels. As people raise themselves out of poverty, they can provide their families with better medical care, leading to better health. One proposed method of community development for improving livelihoods and health is the sustainable use and conservation of wildlife. An important component of ensuring sustainable use of wildlife is engaging all of the relevant stakeholders, especially the people living around the conservation areas whose livelihoods can be directly impacted by wildlife. People living in areas with free-ranging wildlife are frequently in conflict with wildlife, e.g., crop raiding. The sustainable use of wildlife can lead the community to accept the risks of coexisting with wildlife to support conservation and the health of the natural ecosystem.

5.1 Ecotourism

Ecotourism has been defined by many different groups, here we will use the same definition as Stronza and Pêgas (2008)—nature tourism that intentionally seeks to deliver net positive contributions to environmental conservation and sustainable development for local communities. This definition links conservation directly with the health and development of the local communities. This concept aims to harness resources from the ever-growing tourism industry (Walpole and Thouless 2005). For example, in Kenya wildlife tourism grossed nearly US$1.2 billion in tourism-related industries in 2011, with 2.7 million visitors to parks and game reserves (KNBS 2012). That amount of earnings contributes significantly to the national economy. However, despite the significant earnings from wildlife-based tourism and safari hunting, the equitable distribution of the funds is important in achieving the sustainability of wildlife resources. The success of ecotourism can be evaluated by measuring local economic benefits and participation as well as conservation indicators. There are many factors that may contribute to the success or failure of ecotourism, including: the presence of a flagship species, the

biodiversity index and ease of viewing wildlife, the popularity of a particular location, the attitudes and current livelihood of the local communities, the perceived risk of wildlife to the community (e.g., crop raiding, disease, safety, or competition with, or consumption of domestic animals), and the perceived cost of living near the protected area (e.g., loss of access to cultivable or grazing land, watering holes, and inability to hunt) (Walpole and Thouless 2005). A recent analysis of perceived cost from villages around Kibale National Park, Uganda suggested a distinct geographical variation in households with perceived loss compared to those with perceived benefit. Households within 0.5 km of the park boundary perceived the highest losses, while benefits were perceived up to 15 km from the boundary (Mackenzie 2012).

Salafsky et al. (2001) worked with local communities to establish and support 37 business operations and evaluate them with financial, social, and conservation indicators. They found that community participation in an operation was significantly linked to conservation success, even if the focus of the operation itself was not involved in conservation, such as the example from Zambia discussed earlier where snares were turned in. Interestingly, few operations were able to cover their costs after 3 years and those that did required strong management systems to remain financially viable (Salafsky et al. 2001). In particular, creating successful community-based ecotourism programs can be very difficult given the competition and the high cost associated with start-ups in resource poor areas. It can take several years before such operations are able to cover their costs and it is not always clear that benefits for human health will trickle down from these operations (Kiss 2004; Walpole and Thouless 2005).

Few projects have successfully linked wildlife conservation directly to health care, although there are a few examples of large-scale initiatives seeking to do so. In the Qomolangma National Nature Preserve in Tibet, a collaboration among the villages, government, and various NGOs led to the training of local villagers to protect the nature preserve with the benefits being improved access to basic health care. Several individuals from local villages were educated in: preventative health care, distribution of medicines, environmental protection, ecotourism, poverty reduction, and income generation. These trainees provide services and education to the villagers. The success of the program was measured by a doubling of the estimated wildlife populations in the preserve, a decrease in logging by two-thirds, a decrease in the incidence of diarrheal diseases, and a reduction of infant mortality by 50 % (Melnyk 2001; Taylor-Ide and Taylor 2002).

5.2 Ecotourism Linked Anthropozoonoses

Rarely mentioned in One Health publications, discussions, or meetings is the topic of anthropozoonoses—diseases transmitted from humans to animals. Much of the original literature on this subject area comes from studies with nonhuman primates, especially the great apes. Butynski (2001) provides an extensive review of

anthropozoonotic risks to great apes, including measles, herpesviruses, poliovirus, *Mycobacterium tuberculosis*, *Sarcoptes scabeii*, and a number of intestinal parasites. One survey found that 15 % of 633 tourists visiting Sepilok Orangutan Rehabilitation Centre in Sabah, Malaysia reported having one or more symptoms of an infectious disease while they were visiting the center (Muehlenbein et al. 2010).

It has long been recognized that human tuberculosis (*M. tuberculosis*) can infect nonhuman primates. Standard practices for captive nonhuman primates include routine testing of both the nonhuman primates and people who have contact with them (e.g., zoo keepers). Interestingly, there is genetic evidence that suggests *M. tuberculosis* is significantly older than strains found in domestic livestock (*M. bovis*). It has been hypothesized that *M. bovis* evolved from an existing human pathogen or a common ancestor (Brosch et al. 2002). This is consistent with evidence of human tuberculosis preceding the 10 to15,000-year-old domestication of animals (Gutierrez et al. 2005). Excluding anthropozoonotic diseases from One Health discussions alters the discourse to a narrow anthropocentric view of the world. The prevention of transmission of human diseases and improved human health can provide simple and cost-effective methods to protect wildlife from anthropozoonotic diseases.

6 Understanding the Linkages

The linkages discussed above clearly indicate that wildlife health is intricately tied to the health of people, domestic animals, and the environment. Despite these linkages and their key role as reservoirs of human EIDs, global efforts for wildlife health surveillance are lacking and underfunded. Wildlife health surveillance can be used to better understand the pool of pathogens that may spillover into people or domestic animals; it can also be used to track the spread of wildlife diseases through populations. This surveillance can be used to investigate the ecology of the pathogen and hosts, which in turn can facilitate the prevention and control of important diseases.

6.1 Targeting Surveillance for EIDs

Frequently, responses to emerging disease outbreaks are reactive and costly (Childs and Gordon 2009). Surveillance based on disease-specific control programs has successfully mobilized financial resources and delivered short-term results against disease-specific objectives (Oliveira-Cruz et al. 2003). However, some have criticized this approach for focusing exclusively on a single disease and failing to reduce the risk of most pandemics (Oliveira-Cruz et al. 2003; Travis et al. 2004). Further, pathogen-specific surveillance often lacks sustainability and cannot be scaled-up, as benefits and outcomes are generally limited to the target

area and funding cycle (Oliveira-Cruz et al. 2003). To better target wildlife surveillance, there are several factors that need to be considered including geographic risk of emergence, the host species of the greatest concern for zoonotic spillover, and transmission pathways.

The initial work to identify geographic "EID hotspots" found that countries with high biodiversity and human density are at the greatest risk for outbreaks (Jones et al. 2008). Most of these hotspots are located within developing countries, which often lack the infrastructure to conduct wildlife surveillance, either active or passive, and the ability to conduct diagnostic assays for rare or new diseases. One example of a multinational effort is the USAID PREDICT project (see Box 2), which is based on initiating wildlife surveillance and investigating viral diversity in wildlife in these geographic hotspots.

As zoonotic disease surveillance in wildlife clearly represents a great challenge (i.e., there are 5,000+ mammal species globally), predictive modeling and known patterns in host range can be used to focus the effort on the species and pathogens that pose the greatest risk of zoonotic emergence. New tools may make it possible to predict general patterns of host range in unsampled hosts, given known patterns from the past 100 years of the published literature, knowledge of a species ecological and life-history traits, and some measure of surveillance or sampling bias from both a host and disease perspective. Initial reviews of the literature were largely descriptive and grouped host species at higher taxonomic levels (e.g., ungulates, carnivores, rodents, and nonmammals) (Cleaveland et al. 2001; Woolhouse and Gowtage-Sequeria 2005; Woolhouse and Gaunt 2007). More recent studies have tested patterns of pathogen–host range in a more mechanistic way, by explicitly including information on phylogenetic relatedness, although these studies are usually limited to a single host group or pathogen, e.g., bats and rabies (Streicker et al. 2010); primates (Davies and Pedersen 2008); and fish ectoparasites (Krasnov et al. 2010; Poulin 2010). Similar approaches are currently being used to look at patterns of zoonotic disease emergence for all known mammal viruses and to test mechanistic drivers of cross-species viral emergence (Bogich et al. 2012).

Another useful way to focus surveillance efforts, speed up early detection, and reduce the risk of cross-species transmission is to target transmission pathways at specific human–animal interfaces. A key advantage of this approach is that surveillance efforts and control measures for one route of transmission should also mitigate a number of infectious diseases sharing the same transmission pathway. A multipathogen approach targeting disease transmission routes would be a useful way to target pathogen surveillance and control. It may also effectively focus prevention efforts, achieve early detection, and reduce additional risk of transmission.

Box 2. The USAID PREDICT Project: Establishing a Global Wildlife Surveillance Network

The PREDICT project is part of the US Agency for International Development's Emerging Pandemic Threats Program. This project is developing a global wildlife virus surveillance system in 22 countries that are in geographic hotspots (Jones et al. 2008) in the Amazon Basin, Mexico, Southeast Asia, and China, the Gangetic Plain, and the Congo Basin. This active surveillance system is aimed at understanding the importance of various human–wildlife interfaces. Based on phylogenetic modeling, rodents, bats, and nonhuman primates were selected as target taxa due to their higher likelihood of harboring zoonotic pathogens (Olival et al., unpublished data). Specifically, the project is targeting bushmeat sold in markets, wildlife that is collected by hunters, and wildlife living in proximity and/or conflict with people. PREDICT is also investigating how changes in land use (using a landscape development index) can affect biodiversity and viral diversity of wildlife across a gradient of urban areas, rural areas with forest fragmentation, and in areas of pristine forest. This project works within each country's infrastructure to build surveillance and diagnostic capacity. Viral discovery is conducted using degenerative primers to target viral families of zoonotic importance, which is then confirmed through genetic sequencing. In addition, deep sequencing methods are being used to discover new viruses. This diagnostic method maximizes the likelihood of discovering viruses, instead of targeting specific pathogens that may not be present.

The PREDICT project is standardizing surveillance methods across the globe to target potentially zoonotic viruses before they spillover. It is an example of combining high-level modeling with on-the-ground field data to target a surveillance system to efficiently detect potential pandemic viral threats.

6.2 The Importance of Host and Pathogen Ecology to Prevent Zoonotic Diseases

Understanding wildlife diseases necessitates a multidisciplinary team, including epidemiologists, ecologists, and medical professionals. The ecology of the reservoir hosts as well as other competent species can be used to target disease management and mitigation (See Box 3). The importance of this is clear when considering pathogens such as Ebola virus, where we have only recently discovered the probable reservoir (Leroy et al. 2005), yet often cannot trace the transmission events from bats to nonhuman primates and/or people. Further, new surveillance is finding evidence for Ebola-like viruses in natural mammal reservoirs (e.g., bats and primates) well outside of their previously known range in Africa (Nidom et al. 2012; Olival et al. unpublished data). These recent findings point to a more urgent

need to implement general, not pathogen-host specific, strategies to prevent zoonotic disease spillover from wildlife, i.e., by targeting transmission pathways or specific groups of hosts as were mentioned above.

Highly pathogenic avian influenza A/H5N1 is a good example of the importance of understanding the ecology and epidemiology of a zoonotic disease in wildlife. This strain of avian influenza was first diagnosed in people in 1997 and in subsequent outbreaks has had an observed case fatality rate up to 84 % (Kandun et al. 2008), although seroprevalence data indicate that it may be as low as 14–33 % (Li et al. 2008). When A/H5N1 spread into Europe and Africa in 2005 there was an immediate reaction and assumption that it was transported by migrating birds, despite the lack of data at that time. The role of wild birds in the transmission and maintenance of A/H5N1 remains controversial.

Outbreaks of A/H5N1 in wild bird populations have occurred in isolation of poultry outbreaks and caused severe morbidity and mortality in some species. More than 1,500 birds at Qinghai Lake in China died during an outbreak, 90 % of which were bar-headed geese (*Ansar indicus*) (Chen et al. 2005). Similar outbreaks occurred in Mongolia and Europe, indicating that there is occasional long-distance transmission by migratory birds (Alexander 2007). The effectiveness of long-distance transmission varies by species, as some species are severely affected by A/H5N1 and others may be nonclinical shedders (based on studies in domestic mallards) (Sturm-Ramirez et al. 2005). Modeling by Kilpatrick et al. (2006) suggests that the spread of A/H5N1 may be a combination of the trade of poultry, the commercial trade in wild birds and transmission through migratory birds. Their model suggests that the spread throughout Asia was primarily due to poultry trade, and the spread in Africa was partly due to poultry trade and partly due to migrating birds and the spread in Europe was most likely through migrating birds. However, transmission by migratory birds appears to be rare, as proposed by Gilbert et al. (2010), who suggest that wild birds stopping over in areas at high risk for poultry strains of A/H5N1 may occasionally transmit the virus via migration. A lack of sufficient information on the frequency or likelihood of spread through migratory birds indicates that further surveillance of A/H5N1 should be conducted to better understand the transmission dynamics.

Without further ecological and epidemiological studies on the dynamics of A/H5N1, wild birds may have continued to be blamed for the maintenance of A/H5N1. It is known that waterfowl can be a mixing vessel for various subtypes of avian influenza (Hatchette et al. 2004), and it is rational to assume that they are the reservoir for A/H5N1. However, the seroprevalence of the H5 subtype is low in apparently healthy wild water bird populations (Kang et al. 2010). Analyses of epidemics of A/H5N1 in Thailand found a strong association with the presence of free-grazing domestic ducks (Gilbert et al. 2006). Additional analyses by Gilbert et al. (2010) suggest that the presence of domestic ducks is the main factor associated with risk of A/H5N1 in South Asia, while human population and chicken density were also associated. Recent modeling suggests that moderately sized flocks of poultry could maintain transmission of A/H5N1, whereas isolated small flocks or large commercial flocks are unlikely to maintain the virus (Hosseini et al.,

unpublished data). Thus, ecological studies of A/H5N1 in both wild and domestic birds will continue to be important in understanding the maintenance of this virus.

Box 3. Vulpine Rabies: The Importance of Understanding Ecology for Control of Rabies in Europe

Vulpine rabies was first introduced to Poland in 1939 and has since radiated out through Eastern and Western Europe (Anderson et al. 1981). Passive surveillance of wildlife throughout Europe found that red foxes (*Vulpes vulpes*) represented 75 % of all wildlife diagnosed with rabies (WHO 1981). Attempts to control the fox population through culling did not succeed at preventing the spread of rabies, which expanded at an annual rate of 30–60 km. Several papers in the early 1980s illustrate the need for approaches and models that combined research on the viral pathogenesis, fox ecology, mapping of the development of epidemics, and importantly, the contact rate between foxes (Anderson et al. 1981; Macdonald and Bacon 1982). The social structure and density of foxes in some urban areas (five foxes per kilometer) would require a culling rate of 80–100 % to have a high probability of eliminating rabies (Smith and Wilkinson 2003). Culling adult foxes leaves empty territories that are quickly filled by dispersing yearlings and other young foxes. Additionally, cub production is density dependent; thus, if culling were to decrease the population, more susceptibles would be introduced into the system as the reproductive rate of foxes would increase (Macdonald and Bacon 1982). Vaccination has been demonstrated to be effective in parts of Europe and has two major advantages over culling: (1) immunity decreases the likelihood of contact between two susceptible foxes and (2) the reproductive rate remains stable, preventing the surge of susceptibles that follows a decrease in fox density (Macdonald and Bacon 1982).

For point-source infections, such as what would happen if rabies was introduced into Britain, culling is more likely to be successful than in areas where rabies is endemic, especially as control efficacy may vary according to season (Smith and Wilkinson 2003). The current control method for Britain is to cull foxes within 19 km of the point source followed by a ring of vaccine bait to prevent escape (Smith 1995).

The ecological and epidemiological theory behind the development of control strategies for rabies in foxes can be transferred to other similar systems. In developing countries, the domestic dog remains the primary rabies reservoir. Research in India has shown that trap, vaccinate (with or without sterilization), and release programs have led to a decreased number of rabies cases in humans, and may have led to a decrease in the stray dog population as well (Reece and Chawla 2006). Understanding the ecology of rabies in foxes and other carnivores has lead to a significant decrease in human rabies cases.

6.3 Management of Wildlife Diseases

Wildlife are elusive, and have different ownership and custodian status among states and countries, and are often perceived in a variety of ways (emotional, religious, cultural, or utilitarian, etc.) by the general public; all of which necessitates new methods of disease control that consider the whole ecosystem including human interactions. Artois et al. (2011) recently wrote a review of methods for controlling disease in wildlife and the risks associated with these methods. The primary goals of control are to limit the number of susceptibles or to treat/eliminate infected individuals to limit infectious period. Lethal control and vaccination are the primary methods available to limit the number of susceptibles. Lethal control, or culling, has frequently been shown to be very difficult to maintain in large populations of wildlife with high reproductive or immigration rates and is increasingly considered socially unacceptable (Caughley and Sinclair 1994). Further, culling is generally not a viable option when dealing with outbreaks in rare or endangered species, and the act of culling itself actually increases the human–wildlife contact interface and potential transmission of zoonoses. Vaccination is increasingly being considered as a control option and is predicted to be the most efficient method to control hosts with relatively low reproductive rates. However, the production of a vaccine that is efficacious, stable in the environment, and easily deliverable (frequently orally) makes vaccination a difficult control method (Artois et al. 2011). In addition, most effective wildlife vaccines (e.g. for rabies) are modified live vaccines that have the potential to harm nontarget species. Another possible control method is fencing or other physical barriers to prevent direct contact. This is being recommended to farmers in Michigan and Minnesota as a method to prevent bTB transmission from WTD sharing feed or entering cattle lots (Palmer et al. 2004). Low-tech bamboo skirts are also being used to keep bats out of date palm sap harvest areas to prevent the transmission of Nipah virus (Nahar et al. 2010). However, fences and barriers can sometimes interrupt nontarget species as well as the local ecosystem, e.g., in southern Africa where fences prevent the migration of large herbivores, such as elephants (Loarie et al. 2009). Innovative methods of wildlife disease management will continue to be needed, especially as diseases emerge in difficult to manage species such as WNS in bats.

7 Conclusion

One Health links the health of humans with that of domestic and wild animals and the environment. In this chapter, we have explored various linkages that connect wildlife health to human and domestic animal health. Wildlife are linked to people through the risk of pathogen spillover, food security and safety, changes in the environment, and a human dependence on wildlife for livelihoods. Each of these linkages can have positive and negative effects; e.g., human and wildlife

transportation can increase the risk of spreading an emerging disease in either population; zoonoses may be balanced by the effects of anthrpozoonoses (though little research has been done to determine this); wildlife are a vital protein or income source for some human populations and can be responsible for food contamination or income loss for others.

A better understanding of the role of wildlife and a more robust surveillance system to investigate this will be critical to the One Health field in the future. Targeted wildlife surveillance, by coupling active and passive surveillance with predictive models, can be an important tool in understanding and preventing EIDs in people and in animals. This surveillance data and data from other ecological studies can be used to inform management of diseases in both wildlife and domestic animals. The linkages between people and wildlife are clearly an important part of One Health and there is a growing need to understand them.

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