

HUMAN BEHAVIORAL RISK FACTORS FOR ZOOONOTIC DISEASE TRANSMISSION IN LAIKIPIA COUNTY, KENYA

by

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Human behavioral risk factors for zoonotic disease transmission in Laikipia County,  
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## LIST OF ABBREVIATIONS

ASAL .....	Arid or Semi-Arid Land
CCHFV .....	Crimean-Congo Hemorrhagic Fever Virus
CDC .....	Centers for Disease Control
CHV .....	Community Health Volunteer
EID .....	Emerging Infectious Disease
EPT .....	Emerging Pandemic Threats
MERS .....	Middle East Respiratory Syndrome
RVF .....	Rift Valley Fever
SCBI .....	Smithsonian Conservation Biology Institute
USAID .....	United States Agency for International Development
WHO .....	World Health Organization

## **ABSTRACT**

### **HUMAN BEHAVIORAL RISK FACTORS FOR ZOOONOTIC DISEASE TRANSMISSION IN LAIKIPIA COUNTY, KENYA**

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Emerging infectious diseases (EIDs) are a significant threat to global security and human wellbeing. A majority of EIDs affecting humans are zoonotic, or originating from animals. Human risk of exposure to zoonotic pathogens is dependent on a variety of ecological and human behavioral factors, such as vector distribution and human-animal interaction. Mitigating the threat of EID spread is dependent on understanding the multifaceted drivers of disease and identifying potential outbreaks before they occur. The PREDICT project is a global effort to conduct surveillance and mitigation efforts in regions at high risk of disease emergence. Laikipia County, Kenya was selected as a PREDICT area of focus due to high rates of interaction between wildlife, humans, and livestock, which increases risk of disease spillover. Questionnaires were distributed among five communities within Laikipia. These surveys asked participants a series of questions about demographics, sanitation practices, and human-animal interactions. The objective of this thesis research was to analyze the survey data and identify trends in

behaviors that may increase pathogen exposure risk. Data analysis was conducted in R with Chi-squared tests and LASSO regression. Each community was characterized by one of three different land use strategies. Results revealed that communities with the same land use system express similar reports of high-risk behavior. Even so, variation was observed on an individual community basis. These results highlight the need to understand human behaviors and disease dynamics on a fine scale. Data from the PREDICT project will be used to develop intervention strategies, which must address specific behaviors within a local context. This study represents a growing body of research that aims to implement interdisciplinary studies to detect potential pandemic threats. Further research should combine quantitative and qualitative research to conduct holistic assessments of disease risk in order to develop relevant, tailored intervention strategies.

## **CHAPTER 1: ZOOONOTIC DISEASE: THREATS, HUMAN RISK, AND MITIGATION**

Emerging infectious diseases (EIDs), as defined by the Centers for Disease Control, are diseases "...whose incidence in humans have increased in the past two decades or threatens to increase in the near future" (CDC, 2018). Although this working definition has been developed in recent years, EIDs have long been recognized as a severe threat to human health. Disease events have entered into historical and cultural narratives, altering the way in which people view their relationship to the world around them. Disease outbreaks, from the Black Death of the middle ages to the Ebola outbreak of 2014, are historical events as much as they are pandemic events. Not only do these outbreak events result in massive loss of life, but they can cripple social and economic structures long after the outbreak has been controlled. The Ebola outbreak of 2014 is a prime example of a recent event that originated from wildlife and reached a pandemic level due to socio-cultural factors (Jacobsen et al., 2016). A single human-bat interaction is suspected as the initial spillover pathway, with subsequent infections spreading from person to person via contact with contaminated bodily fluids. Zaire Ebola, the strain of the 2014 outbreak, is most virulent in body fluids that have shed immediately following death. West African burial practices often involve close contact with the recently deceased, including washing and burying bodies (Sharareh et al., 2016). The disease-specific ecology of Ebola worked in tandem with deeply ingrained local customs to

facilitate the rapid emergence of the outbreak (Jacobsen et al., 2016). By the time Ebola was contained, Guinea, Liberia, and Sierra Leone had suffered over 28,000 infections and 11,000 deaths (Viboud et al., 2018). Intangible impacts, such as mental strain on survivors and loss of community cohesion, are no less impactful, albeit more difficult to account for. Despite the devastating impacts, the actual number of fatalities from of this outbreak was far less than was projected in predictive models. International aid, community education, and behavioral modification resulted in curbing the spread of the disease toward the end of the outbreak in 2016 (Viboud et al., 2018). In the modern day, in-situ surveillance and modeling of EID spread provides new insights as to the true effects of these diseases on the global community. EID emergence is dependent upon a complex system of interactions between humans, animals, and the environment. The Ebola outbreak demonstrates the complex interplay of human-animal interaction, human behavioral risk, and behavioral modification in disease spillover and spread. An estimated 60% of EIDs affecting humans originate from animals, making zoonotic disease a primary global health concern (Jones et al., 2008). Human-animal interactions within environmental contexts are therefore fundamental in driving disease emergence. Though not all EIDs are as recognizable as Ebola, they are all subject to the interplay of these factors. Understanding the driving forces of EID emergence is essential to implementing mitigation strategies to minimize the likelihood of disease spread. (Jacobsen et al., 2016).

The term “emerging infectious disease” refers to the identification of diseases that were previously unrecognized. The phrase most commonly applies to diseases that are

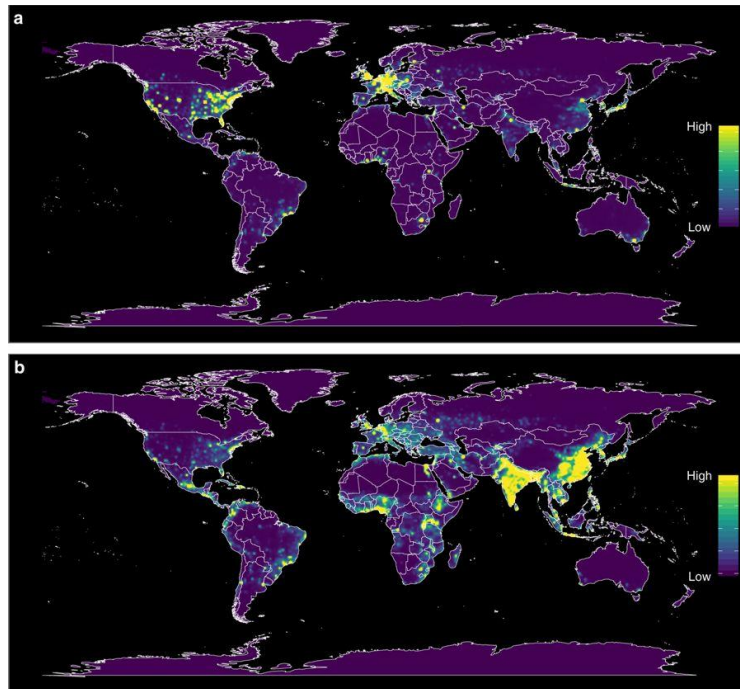
recently detected in novel populations, although it may also apply to pathogens that are suspected to have recently evolved (Institute of Medicine, 1992). “Disease risk,” in the context of human risk of EID spillover, is a multifaceted term. Risk can be described in terms of the probability of human contact with a pathogen, in addition to the probability that human contact with pathogens will ultimately result in the development of a disease (Han, Kramer, & Drake, 2016). This thesis will focus on specifically on risk in terms of human contact with pathogens; the pathogens referenced in this work are widely known to manifest as a disease within human populations. Therefore, assessing risk at first exposure is a justifiable “first defense”, and a starting point for determining the likelihood of an outbreak event.

Disease “hotspots” are regions of high pathogen presence where humans are at elevated risk of developing a disease. Factors such as poor sanitation, poverty, contact with animals, and lacking access to medical care can all increase exposure risk. Risk of human exposure to pathogens is dependent upon the diversity of pathogens and the density of hosts and vectors that propagate infectious agents. Human behaviors that facilitate contact with pathogens also serve as risk factors (Salerno et al., 2017). “Hosts” are defined as organisms that harbor a pathogen. “Vectors” are organisms, generally arthropods (i.e., ticks, insects), that transmit an infectious agent between hosts (Wilson et al., 2017). In a recent meta-analysis of global disease hotspots, Allen et al. (2017) suggest that risk of exposure to zoonoses is correlated to forested areas with high mammalian species richness that are undergoing alterations in land use (Allen et al., 2017). Tropical regions of Southeast Asia, Africa, and South America have the greatest land area

considered to be hotspots. These regions have high human population densities, rates of land use change, and human-animal interaction rates that facilitate zoonosis spillover (Allen et al., 2017). A majority of recent EIDs that spread globally (SARS, Ebola, Avian influenza) have emerged from these hotspot regions, making these areas a priority for disease surveillance and mitigation efforts (Rweyemamu et al., 2013; Drexler, Corman, & Drosten, 2014). However, all inhabited continents contain regions of hotspot EID potential (Fig. 1). Although mammalian diversity and tropical regions are often associated with EID risk, other studies disagree that this is a generalizable principle (Allen et al., 2017). More information is needed to further narrow the global regions at greatest risk for disease emergence, but the cost of EID emergence is most clearly observed in developing nations. Characterized by higher population densities, increased dependence on animals, and lower capacities for pathogen surveillance and health care, developing nations are disproportionately affected by emerging zoonoses (Rweyemamu et al., 2013). Tropical regions are therefore especially vulnerable to EID emergence due to resource limitations, elevated rates of human-animal contact, and high species richness of pathogens and hosts; however, these interactions are nuanced and depend on local context (Jones et al., 2008). Communities located in global disease hotspots are often less resilient due to exacerbated ecological pressures compounded with resource limitations (Dzingirai et al., 2017). For example, sub-saharan Africa is experiencing impacts of climate change to a greater degree than most of the world. Climate is becoming increasingly more arid, limiting access to water and other resources. Mosquito ranges are shifting as a result of changing temperatures, altering the distribution of malaria, dengue



fever, and other vector-borne diseases. Compounded with existing poverty and scarce medical resources, communities are increasingly susceptible to the impacts of diseases. Disease hotspots are not clearly delineated and may shift depending on environmental conditions (Allen et al., 2017). In addition, identifying these regions is difficult due to the uneven distribution of globally collected data. Allen et al. (2017) provide an estimate for hotspot areas based on risk of exposure, while accounting for reporting bias (Fig. 1). Even so, locations of high risk for disease emergence are subject to a variety of interconnected factors, implying the potential expansion of hotspot areas in the future.



**Figure 1** Global Hotspots for predicted EID emergence (Allen et al., 2017). A) Predicted emergence of new EID events, by report. B) Predicted emergence of new EID events, corrected for reporting bias.

Human behavioral and environmental factors both hold significant influence over disease transmission dynamics. Vaccination practices, food safety, sanitation, and interaction with animals can all facilitate disease transmission. Combined effects of environmental and behavioral drivers can affect the distribution and density of animal vectors, with implications for transmission to humans. Disease risk is exacerbated by pathogen diversity and ecological pressures resulting from climate change, such as severe weather patterns and increased temperatures (Morse et al., 2012; Jones et al., 2008). In addition, EIDs spread by a variety of mechanisms, ranging from direct to indirect contact with infectious agents. Since a majority of EIDs affecting humans originate from animals, human-animal interactions serve as a significant factor influencing spillover risk (Jones, 2008). Such emerging threats require a global framework of detection and prevention. Effective mitigation of disease threat must take in to account environmental health, biodiversity, climate change, and human wellbeing (Barnes et al., 2017; Gebreyes et al., 2014).

EIDs are widely recognized as a global public health and security threat. In 1992, the United States Institute of Medicine released a report describing EIDs as a global health concern. This report was prompted by “emergence” of newly identified diseases, such as HIV/AIDS, as well as “re-emergence” or “resurgence” of diseases with known outbreak potential, such as tuberculosis (Institute of Medicine, 1992). Beginning in the 20<sup>th</sup> century, rapid development of global travel has drastically increased the potential for pathogen spread outside of local origins. Social and behavioral factors intersect with the use of these technologies. This is reflected in the recurring outbreaks of meningitis

among Muslim travelers to Mecca for during the annual Hajj, or mass pilgrimage, to the sacred city (Institute of Medicine, 2003). Not only is disease spread from human-to-human contact, but also through international commerce of live animals, food, and timber products. Between 1995 and 2000, four separate outbreaks of cyclosporiasis, a food-borne illness, occurred in the United States. Each outbreak was associated to contaminated raspberries imported from Guatemala (Institute of Medicine, 2003). Livestock trade has also led to pandemics that affect animal communities, including illnesses like Middle East Respiratory Syndrome, which is transmitted to humans from camels (Gikonyo et al., 2018). Commerce, social behaviors, and technology altogether influence the risk of disease emergence by stretching the boundaries of localized pathogens.

EID emergence threatens not only public health, but biodiversity and conservation. Pathogens carried by invasive species and livestock can deplete native populations that lack resistance. Brucellosis, a disease that causes abortions in ungulates and febrile illness in humans, has a global distribution and is suspected to negatively affect populations of livestock and wildlife (Muendo et al., 2010). In a study comparing brucellosis seroprevalence and population health in African buffalo, Gorsich et al. (2015) observed a positive association between *Brucella* exposure and mortality, though there was no association with fecundity. Rates of infection varied geographically, indicating that individuals with lower resource availability are more susceptible to brucellosis exposure. High densities of other grazers, including cattle, can decrease the availability of graze land. Though more research must be conducted to investigate causal relationships,

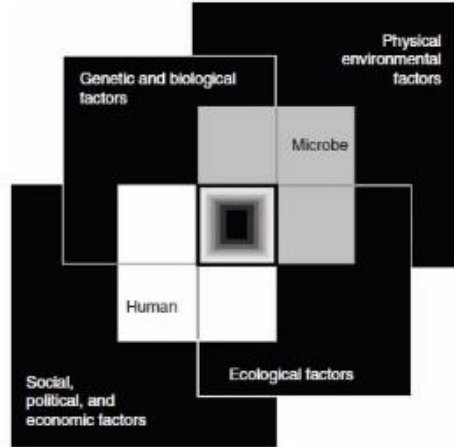
*Brucella* infection overall was “negatively associated with survival...” (Gorsich et al., 2015). Numerous other studies demonstrate that brucella can transmit between wild and domestic ungulates via land use overlap, and humans can contact the pathogen by consuming products from infected animals (Bett et al., 2017; Muendo et al., 2012). Human introduction of livestock species therefore can affect wildlife exposure to brucella by perpetuating the spread of the pathogen and decreasing resource availability, which may heighten wildlife vulnerability to disease effects (Gorsich et al., 2015; Rajeev et al., 2017).

In recent years, EID research focus has shifted from reactionary-based measures to proactive mitigation strategies. A core principle of this paradigm is the “One Health” approach, which seeks to understand the interconnectedness of human, animal, and environmental health. Accounting for all factors influencing health outcomes must include assessment of these forces within localized contexts. Disease transmission routes, climate change, and economic factors all play a role in resilience to emerging pandemic threats (Atlas & Maloy, 2014). The 2014 Ebola outbreak demonstrates these concepts, as it originated from animals and was amplified by human behaviors. Curbing infection rates depended on relevant community interventions that targeted behavioral risk factors in culturally relevant ways (Sharareh et al., 2016). Capacities should be developed on multiple strata, from global to local, in order to develop an understanding of local needs while contributing to the broader effort of pandemic preparedness. Several international partners, such as the World Health Organization and EcoHealth Alliance uphold the concepts of One Health, actively supporting an interdisciplinary approach to EID

research (PREDICT, 2017). Early, *in-situ* disease detection, capacity building in vulnerable communities, and behavioral risk assessments are a few of the primary aims of One Health organizations in mitigating human exposure to pathogens of pandemic potential and bolstering response capacities (Gebreyes et al., 2014).

### **Drivers of EID Transmission**

Factors influencing EID transmission to humans are diverse and interconnected. Ecological and anthropogenic pressures drive disease emergence by determining vector and host presence, species distributions, and modes of human contact with pathogen sources. Humans, though manipulating conditions for disease emergence, also are subject to risk from naturally occurring conditions. For example, intensive livestock management has led to spillover of diseases by increasing host densities and facilitating direct contact with pathogens. At the same time, disease emergence among humans is also affected by physical environmental factors, such as altitude and topography (Woodford, 2009). Furthermore, human susceptibility to disease varies on an individual level as a result of genetic variation. Fig. 2 depicts the complexity of EID emergence. Infection in humans depends upon the central intersection of human contact with pathogens. However, this interaction is nested within other factors, from human behavior and biology to environmental and ecological interactions (Institute of Medicine, 2003). EID emergence results from interacting conditions, which must all be accounted for when determining human risk of pathogen exposure.



**Figure 2** The Convergence Model (Institute of Medicine, 2003, p. 5). The center of the box represents the risk of infectious disease emergence. Human contact with disease-causing pathogens is a function of the surrounding factors affecting their development.

## Ecological Factors

Ecological influences on EID emergence include vector and host presence, land use, and climate, among other variables. With such a complex interface of variables affecting disease risk, understanding regional distributions of pathogens is an important starting point for assessing further shifts in emergence. Some diseases, such as toxoplasmosis, are known to have a global distribution. This parasitic infection can spread from animals to humans through many pathways, such as consumption of undercooked meat or contact with cat feces (Ogendi et al., 2013). Other pathogens are associated with a geographical region, with case reports fluctuating based on environmental conditions. Lassa Fever Virus is endemic to West Africa and can be transmitted from rodents to humans via contact with droppings. Reports of human cases

tend to be highest in dry seasons, when multimammate rats, the reservoir species for Lassa fever, migrate out of crop fields and in to human dwellings, thus increasing potential for human contact with infected droppings (Dzingirai et al., 2017). In both cases, humans interaction with the environment affects potential of exposure to pathogens.

Disease reservoirs, or organisms that serve as the initial host of a pathogen, transmit infectious agents to other susceptible organisms (Guerra et al., 2016). Pathogens can be spread directly between vertebrates via direct physical contact or indirect contact (i.e., contamination of shared land, water sources), or through an arthropod vector. The study of disease ecology seeks to determine the processes and cycles that allow specific pathogens to propagate within an environment. Vector-host interactions are a foundational component of disease cycles. Pathogen presence is directly related to the density, abundance, and interaction of its associated hosts and vectors (Johnson et al., 2015). Complex webs of vectors and hosts create cycles of disease transmission that are endemic in an environment. These interactions may vary naturally based on temporal or spatial variation in host presence. For example, seasonal migration of songbirds worldwide affects patterns of Lyme disease and West Nile Virus (Altizer, Barter, & Han, 2011). Modes of transmission also vary based on disease and host species. Some pathogens, such as the toxoplasma parasite, can be transmitted through direct contact with contaminated body fluids of an infected individual (Ogendi et al., 2013). Other diseases, such as malaria, require a vector to spread the disease to other individuals. Rift Valley Fever Virus is an example of a pathogen that can be spread via direct contact with

contaminated body fluids of ungulates, or via transmission by a mosquito vector (Anyangu et al., 2010). Transmission mechanisms are determined by the ecological niche of the pathogen, which is in turn influenced by environmental conditions.

Anthropogenic impacts on natural systems alter species distributions, land structure, and animal interactions that influence disease prevalence and spread. One of the most obvious influences is the introduction of domesticated animals. Additional species, such as cattle, sheep, and fowl, create a separate pool of potential hosts in addition to those occurring naturally within an ecosystem (Caron et al., 2015). Domestic animals, whether used for food or work, maintain a close relationship with human populations, yet may also share common resources with wildlife. Livestock serve as amplifiers of disease, as well as points of contact for human-disease interaction. As such, livestock often link disease pathways from wildlife to humans (Caron et al., 2015). Livestock played an important role in the emergence of Nipah virus, a novel zoonosis discovered in Malaysia in 1999 (Looi & Chua, 2007). Fruit bats are the natural reservoir of this encephalitic virus. Spillover of the disease occurred when pigs consumed the partially eaten fruit that bats dropped on farm land. The virus was propagated within the pigs, which was then passed on to humans during slaughter and consumption of the infected meat. The disease was initially misdiagnosed as Japanese Encephalitis, which precluded effective mitigation efforts early in the outbreak. Nipah infection spread throughout Malaysia and Singapore via the sale of infected pigs. As a result, 265 patients developed acute encephalitis, with 105 fatal cases (Looi & Chua, 2007). This case demonstrates the emergence of a pathogen that was previously unrecognized, facilitated



by shifting relationships among humans and animals. The pig farms at the epicenter of the Nipah outbreak are primary examples of a human-wildlife-livestock interface in relation to modes of disease transmission.

Livestock movement also displaces native species, further altering naturally occurring disease transmission cycles. Density of wild herbivores varies in relation to livestock densities in African savannahs. Graze routes of pastoralists and livestock in Kenya have been shown to alter movement patterns of native herbivores. Humans tend to move domestic animals near water sources, which depletes forage for wildlife surrounding important resources, especially in arid climates. (Ogutu et al., 2014). Ogutu et al (2014) observed that the resulting wildlife densities vary by species. Some, such as zebra, express a wider distribution when forage is limited; other species, such as eland, compress in these conditions. Species that are more tolerant may be more likely to co-exist and interact with livestock, affecting the types of diseases that may be transmitted (Ogutu et al., 2014).

Land alteration for human development, agricultural, or livestock rearing purposes is also a significant driver of disease emergence (Wiethoelter et al., 2015). Expansion of human communities often involves encroachment on wildlife habitat, resulting in overlap of human-wildlife land use and shifts in species composition. Tolerance of human modified environments varies from species to species. Many rodent species, for example, have evolved with human populations and thrive in urban and rural environments where human activity provides food and shelter. Rodents are commonly implicated with diseases such as plague, which is more likely to spread with higher

human population densities (Atlas & Maloy, 2014). Deforestation and habitat fragmentation are also drivers of disease risk. This land alteration is often associated with increased rodent populations. In North America, Lyme disease may exist in higher densities in deforested areas. Rodent species that host the tick vectors are tolerant of fragmented habitats; the decline in other vertebrate species that prey on the rodent hosts therefore results in population increases of both the mice and ticks (Allan, Keesing, & Ostfeld, 2003). Habitat disturbance eliminates many species while allowing others to fill the vacated niche, which influences pathogen presence and risk of contact.

Agricultural development also affects species distribution, which in turn impacts host-vector interactions. Irrigated lands, for example, are more likely to house large populations of mosquitoes, increasing prevalence of mosquito-borne illness when compared to drylands (Bett et al., 2017). Human exposure to pathogens is heightened when vector and host densities are high (Olive et al., 2016). However, host presence is affected by temperature, rainfall, and season, among numerous other ecological factors. These environmental conditions, in turn, are affected by anthropogenic activities. As a result of climate change, rainfall patterns and temperatures are shifting to the point of altering species distributions. Ultimately, human behavior is a primary driver that affects host ecology and transmission of disease from animal hosts to humans. Land use and livestock presence alter disease cycles by providing new hosts, changing distributions of wildlife, and introducing a new interface for human-animal interaction. Though humans adapt to environmental conditions, anthropogenic activity across the globe is affecting environmental systems even to the point of shifting climatic cycles. This is evident from

the emergence of West Nile Virus (WNV) in the United States (Paz, 2015). WNV, a mosquito-borne disease, is endemic to tropical regions of Africa, Southeast Asia, and Australia. The virus was introduced in to north America in 1999, although the mode of transmission remains unknown. In addition to causing over 1,300 human fatalities in North American from 1999-2010, wildlife were also drastically affected (Kilpatrick, 2011). Millions of birds died as a result of WNV infection, with population declines of up to 50% for some North American species. Land use is associated with prevalence of WNV, as reports of infection are higher in humid, warm regions conducive for mosquito breeding. Warming trends in Europe and North America are expected to facilitate maintenance of WNV in ecological systems as ranges of mosquito vectors increase. Further expansion of WNV and other diseases should be anticipated as climate change continues to influence climactic patterns and vector distributions (Paz, 2015).

### **Anthropogenic Factors**

In addition to anthropogenic change on an ecological scale, pathogen exposure risk is a result of community and individual-level behaviors. Food and water safety practices, for example, may result in direct or indirect pathogen exposure. Human consumption of infected meat and milk is a well-cited example of direct pathogen exposure from the original host organism. Diseases such as Rift Valley Fever and Nipah Virus can be contracted by humans who consume livestock products from infected animals (Ng'ang'a et al., 2016; Looi & Chua, 2007). Occupational exposure is also a significant hazard. Slaughterhouse workers, butchers, and hunters are at especially high risk of exposure to zoonotic pathogens due to high rates of contact with bodily fluids.

Personal protective equipment (PPE) can reduce this risk, though it is seldom implemented or improperly used in many contexts (Cook et al., 2017). Occupations that require consistent interaction with livestock can also be a risk factor for transmission. Pastoralists and ranchers are likely to share space and water resources with animals. Presence of livestock waste increases risk of disease caused by fecal contamination. Cryptosporidiosis, salmonella, and other diarrheal diseases can lead to serious health effects, especially in developing nations (Conan et al., 2017). In addition, some disease-causing agents, such as *Brucella* bacteria, may remain virulent in food or water sources that have been utilized by an infected animal. Resource sharing between humans and animals is therefore a risk factor for certain diseases, even without direct human-animal contact (Germeraad et al., 2016). Humans who engage in activities that increase rates of direct or indirect pathogen exposure are at heightened risk of exposure to zoonotic pathogens.

Bushmeat consumption and production facilitates the spillover of diseases from wildlife. Emergence of HIV, monkeypox, and Marburg filoviruses in humans is associated with bushmeat collection. Not only can consuming meat introduce zoonotic pathogens, but the process of capturing and slaughtering exposes humans to bodily fluids. Individuals may be bitten or scratched in the process, further facilitating pathogen transmission (Friant, Paige, & Goldberg, 2015). Bats, primates, and ungulates are hunted throughout Africa, Asia, and South America. Poorer communities may rely more heavily on bushmeat, though this is dependent on resource availability and may vary with context (Brashares et al., 2011). Understanding human dependence on bushmeat as a

food source, as well as cultural practices surrounding wild game, is essential to understanding drivers of disease spillover.

Sociopolitical factors also affect human behaviors related to disease risk. Lacking infrastructure reduces access to medical care, including vaccines and other preventative measures. Conflict and poverty intersect to create environmental and societal conditions that increase vulnerability to EID emergence. Disease is rampant in refugee camps where people and animals live in dense populations with poor sanitation and lack of healthcare access (McGready et al., 2010). Food-borne and vector-borne diseases are of primary health concern in these situations. Studies of refugee camps along the Thai-Burmese border in the 1980's revealed that vector-borne zoonoses were a leading cause of death in pregnant women, demonstrating how physiological and social stressors increase risk (McGready et al., 2010). Human risk of pathogen exposure is at the nexus of biological, environmental, societal, and ecological factors. Understanding risk depends on analyzing interactions of all of these factors in a localized context (Institute of Medicine, 2003).

Interactions of these features may either exacerbate risk or serve as protective factors against EID spread. For example, a study of pathogen presence in Eastern Kenya by Bett et al. (2017) suggests that irrigation of dry lands may limit livestock densities and human-livestock interaction, serving as a protective factor against spread of certain bacterial zoonoses. However, irrigation expands breeding habitat for mosquitoes, therefore presenting an increased risk for West Nile Virus and Dengue Fever Virus (Bett et al., 2017). Vaccination is an example of a protective factor that is implemented on the individual level. Humans who receive vaccinations reduce risk of developing a disease.

In addition, vaccinating domestic animals also reduces the risk of spillover from animal to human populations. Other protective behaviors include wearing personal protective equipment (PPE) when handling livestock, slaughtering, or cleaning up after animals (Abdi et al., 2015). Protective behaviors can alter behavioral patterns to reduce risk of contact and reduce the risk of a disease manifesting in the event that contact is made with a pathogen.

### **One Health as an approach to EID analysis**

Traditional EID research approaches determine risk of disease emergence based on a particular pathogen. However, pathogen risk is associated with multiple factors, such as comorbidities from other diseases. For example, HIV/AIDS patients are at significantly greater risk of infection from other pathogens due to their compromised immune system (Ogbuagu & Bruce, 2018). Diseases interact with each other, in addition to the myriad other factors influencing emergence. A holistic approach to global health must therefore include consideration of environmental factors, human behavior, and wildlife interactions, among other variables that influence health outcomes. These principles form the basis of the One Health paradigm (Figure 3), which strives to conceptualize health by accounting for the various forces that influence health within localized contexts. Disease transmission routes, climate change, and economic factors all play a role in health capacities and resilience to emerging pandemic threats (Schwind et al., 2017).



Figure 3: One Health Model (Schwind et al, 2017). One Health surveillance accounts for the interaction between humans, animals, and the environment in assessing health outcomes.

Traditional disease management involves primarily reactionary measures, such as quarantine and vaccine development after outbreaks occur. However, resources are best spent in surveillance and early detection prior to pandemic events (Allen et al., 2017). Outbreaks, following onset, require massive amounts of money and energy to mitigate. At the point of implementing control measures, mortalities and morbidities have already taken a toll on local wellbeing and economy (Allen et al., 2017). Zoonotic diseases pose a continually growing threat to public health and economic stability, particularly in resource-poor communities. The One Health approach implements proactive disease surveillance, in contrast to reactionary methods of disease containment. Detecting diseases in wildlife and livestock populations prior to spillover in human communities

can aid in reducing risk of emergence. In addition, understanding human perceptions related to disease risk can elucidate behavioral risk factors. Because pathogen exposure risk depends on localized culture and ecological interactions, surveillance must be tailored to individual communities (Atlas & Maloy, 2014)

As our world becomes increasingly interconnected, the risk of disease emergence elevates. Pathogens that have been geographically isolated are now expanding due to air travel, human expansion, and trade of goods. Numerous pathogens have the capacity to cause pandemics that threaten global health and economic stability (Allen et al., 2017). Early detection of these pathogens can reduce the risk of human contact and propagation of these diseases. Proper surveillance requires researchers to understand the human, animal, and ecological components that affect pathogen exposure and the subsequent spread of disease (Gebreyes et al., 2014). The One Health paradigm provides a framework for assessing various components that affect health outcomes. Each of these interacting pieces are instrumental in assessing disease emergence and spillover (Gebreyes et al., 2014).



## **CHAPTER 2: *PREDICT-KENYA*: DISEASE SURVEILLANCE IN A HUMAN-WILDLIFE-LIVESTOCK INTERFACE**

In 2009, the United States Agency for International Development (USAID) established the Emerging Pandemic Threats (EPT) program to combat the growing threat of EIDs (Schwind et al., 2014). This program aims to minimize zoonotic disease spillover by supporting EID surveillance and response efforts with a focus on developing nations (Emerging Pandemic Threats, 2016). Pathogen surveillance in the EPT program includes identifying pathogen presence in wildlife, livestock, and humans in order to assess risk of spillover. Qualitative methods, such as focus group discussions and semi-structured interviews with community members, are used to assess attitudes and perceptions relevant to disease spread. An interdisciplinary program by design, EPT seeks input from professionals spanning human and animal health sectors to facilitate early detection of environmental pathogens. EPT researchers partner with national governments and health agencies to develop research protocols and communicate information relevant to disease control to at-risk communities (Emerging Pandemic Threats, 2016). Enacting preventative measures depends on identifying pathogens, understanding modes of transmission, and communicating information to stakeholders (Schwind et al., 2014). The EPT program is composed of four components. *PREDICT* focuses on identifying zoonoses “in the human-wildlife-livestock interface” (Emerging Pandemic Threats, 2016). *PREVENT* identifies risks of disease transmission and develops strategies for

mitigating risk of emergence. IDENTIFY aims to develop capacities for laboratories across the globe to diagnose pathogens. RESPOND provides global workforce training, especially relating to response capacities (Emerging Pandemic Threats, 2016).

PREDICT, the focus of this thesis, was initiated to enhance in-situ disease surveillance in low-capacity regions with the goal of identifying potential EID threats prior to reaching pandemic status. The program enacts targeted disease surveillance in hotspot locations such as East Africa and Southeast Asia (Schwind et al. 2014).

PREDICT is rooted in a One Health paradigm, incorporating livestock and wildlife surveys, human behavior analysis, and environmental surveillance into localized disease risk assessments. PREDICT acknowledges the inextricable link between human and environmental health and holds human behavior as a primary factor influencing disease spread. Global partners include USAID, The University of California-Davis, EcoHealth Alliance, and the Smithsonian Institution, among others (Emerging Pandemic Threats, 2016).

PREDICT is currently in its second iteration (USAID PREDICT-2), which has further developed a focus on identifying animal reservoirs and modes of disease spillover to humans, and strengthening intervention mechanisms (PREDICT, 2017). Results from analyses are used to develop interventions, such as community engagement and education programs, aimed at informing best practices for disease prevention. Global researchers partner with local institutions and leaders to communicate results to community members to enhance comprehension and acceptance of official recommendations (PREDICT, 2017). Determining pandemic potential relies on an accurate and regional assessment of

pathogen presence and transmission modes. Following through with community-specific communication is integral to local acceptance and implementation of protective behaviors, which is crucial in mitigating risk of pathogen exposure.

### **PREDICT-Kenya**

East Africa is a region of high disease endemicity and low surveillance and mitigation capacities. Rift Valley Fever, anthrax, and hemorrhagic viruses are a few priority diseases of pandemic potential (Munyua et al., 2016). Lacking resources leads to drastic consequences for human health and economic viability in the event of an outbreak (Rweyemamu et al., 2012). In 2017, Kenya was a designated PREDICT-2 country of focus due to the high rates of human-animal interaction that parallel a well-documented presence of zoonotic diseases. Researchers collected biological samples from humans and wildlife within Kenya in order to examine the presence of antibodies that indicate exposure to pathogens (PREDICT, 2017). Discovering common pathogens shared among these groups can elucidate transmission linkages and reveal diseases that pose a threat to human and animal populations. Researchers also utilized behavioral questionnaires to determine if individuals engaged in high-risk behaviors that could result in pathogen exposure. Biological, environmental, and human behavioral mechanisms of disease spread are all incorporated into assessment of exposure risk.

In addition to identifying potential outbreaks, PREDICT aims to develop in-country capacities to survey for and mitigate emerging threats. This includes local-level community engagement and education (PREDICT, 2017). Local research partners

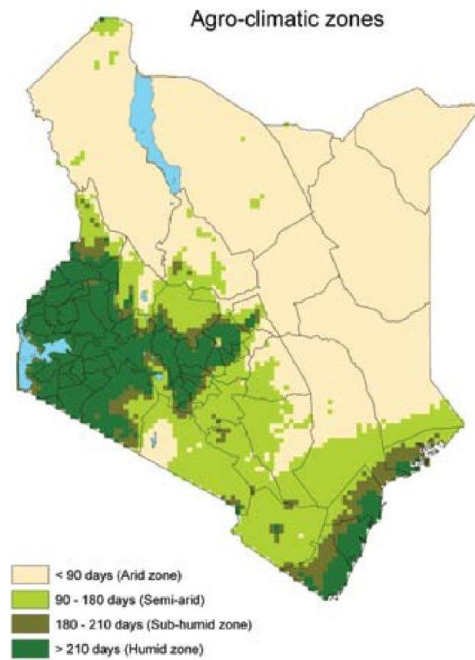
coordinate public outreach programs that inform at-risk individuals of EID risk and modes of containment. Though education programs have previously been implemented in high-risk communities, information gaps hinder effective disease mitigation efforts. A study by Conan et al. (2017) revealed that public education programs in Kenya encourage improved human sanitation practices, such as hand washing after contact with human waste. However, these programs often fail to include information on waste management and sanitation practices for livestock. Children in areas with sanitation intervention programs were still at greater risk of diarrheal disease if they reported interaction with animals or animal feces (Conan et al., 2017). Intervention programs must include best practices for human and animal sanitation, in addition to basic education on environmental health. Global and local leadership structures partner within Kenya to develop programs that communicate multifaceted disease risk to communities that are most affected by EID emergence (PREDICT, 2017).

## **Ecology**

### *Climate*

The ecological structure of Kenya, from coastal tropics to the arid east and central regions, are fundamental to interactions of humans, animals, and pathogens. Climate is therefore a component of EID transmission dynamics. Rainfall and temperature are primary factors that affect distributions of vegetation, animals, and human land use systems (Obiero & Onyando, 2013). Both of these climatic conditions are affected by variations in Kenya's topography and influences of the Indian Ocean in the east, and Lake Victoria in the west. Proximity to water periodically cools temperatures on the coast

and in the lake basin, while altitude results in cooler temperatures in the northwest. Average rainfall varies regionally, from 200mm/year to 1200 mm/year (Obiero & Onyando, 2013). Wet and dry seasons alternate annually, but this pattern is not uniform across the country. Figure 4 shows a map of Kenya's climate as measured by the average Length of agricultural Growing Period (LGPs) per year, in days. Nearly 90% of Kenyan land is categorized as arid or semi-arid land (ASALs), which contain approximately 30% of the nation's population (Odhiambo et al., 2013). ASALs compose most of the eastern and northern regions, which receive less than 500 mm of annual rainfall. Humid regions that receive reliable rainfall above 750 mm per year are located in coastal, central, and western districts (Obiero & Onyando, 2013; Herrero et al., 2010). Southern Kenya is a tropical climate with high rainfall and high temperatures, though differences in relief also cause variation within the region. The Great Rift Valley is a geographical region that extends from the arid northwest through the central sub-humid zone (Herrero et al., 2010). This feature exerts significant influence on the local climate, as altitude gradients cause variation in temperature and rainfall. Even so, the Rift Valley is largely composed of ASALs. These landscapes influence distribution of disease vectors, wildlife distributions, and human land use which interact to create variation in EID exposure risk (Obiero & Onyando, 2013).



**Figure 4:** Herrero et al., 2010. Agro-climatic zones of Kenya, as determined by average annual Length of Growing Period (LGP) for agriculture.

### ***Species Interaction and Vector Distribution***

Disease presence is closely linked to ecological regions within Kenya, largely due to the environmental pressures that drive distributions of host and vector species.

Arboviruses, or viruses that are transmitted by arthropod vectors, are a central cause of EID risk. In Kenya, the primary arthropods of vector potential are ticks, fleas, and sand flies. When manifested in humans, arbovirus symptoms may range from mild febrile illness to hemorrhagic fever (Lutomiah et al., 2013). A mosquito sampling study by Lutomiah et al (2013) compared the distributions of arbovirus mosquito vectors among

different regions in Kenya. As could be expected, regions with high reports of human RVF cases also had high densities of the mosquito species known to transmit RVF. Tropical regions of western Kenya contained some of the highest densities of these vectors. In addition, high vector densities were also reported in arid northeastern Kenya (Lutomiah et al., 2013). Studies further suggest that human irrigation of drylands has facilitated mosquito adaptation to dryland regions (Lutomiah et al., 2013; Bett et al., 2017). High risk areas are delineated along ecological boundaries with environmental conditions conducive to mosquito breeding. Even so, high vector density did not coincide with human case reports in every region. Some areas had low report rates of human arbovirus infection, yet contained high densities of arbovirus vectors. The researchers suggest that vector presence works in tandem with other factors, such as human movement and animal presence, to affect arbovirus spread (Lutomiah et al., 2013). Ecology of vector distributions is a significant contributing factor to pathogen exposure risk, but it does not explain all cases of human arbovirus infections.

Vector borne diseases with mammalian reservoirs are also distributed along ecological gradients (Guerra et al., 2016). Semiarid to tropical regions hold high densities of rodent reservoirs that host mite and tick vectors (Guerra et al., 2016; Oguge et al., 2009). Tropical regions may hold higher species richness and density of both rodents and associated ectoparasites (e.g., ticks, fleas). Oguge et al (2009) conducted a small mammal trapping survey in tropical and arid regions of Kenya. Two species of ectoparasite were discovered in mammals from semi-arid savannah habitat, while fifteen were found on mammals from humid regions. Rates of infestation were significantly higher in mammals

from moist climates when compared to dry. Higher mammal densities likely lead to greater rates of ectoparasite spread among individuals, which also explains the higher counts of parasites on individual mammals in tropical habitats. Vectors on small mammals are known to carry diseases such as plague, typhus, and cat scratch disease throughout east Africa (Oguge et al., 2009). These host-parasite relationships play an important role in maintaining the life cycles of these diseases, as delineated by habitats conducive to both the host and vector species (Guerra et al., 2016). Humans that interact with animals in these settings are therefore more likely to be exposed to arthropod vectors that harbor disease.

Globally, disease risk is commonly assessed at a national level, while risk variation at the local level is often neglected (Frings et al., 2018). Using data from the most recent Kenyan population census in 2009, Frings et al. (2018) compiled a map that shows clusters of early mortality, as measured by years of life lost (YLLs) among individuals as compared to average life expectancy. Clusters of high YLLs were located around Lake Victoria (Western), Turkana County (Northwest), and in territories between the Ethiopian and Somali borders (Northeast). Higher densities of people per dwelling and association with certain ethnic groups were correlated to higher proportions of early mortality. Human density in households is a risk factor for communicable diseases, such as tuberculosis or respiratory diseases. Association with an ethnic group may be a covariate of environmental risks, as many ethnic groups are geographically clustered. However, ethnic ties could indicate shared behaviors that influence patterns of disease emergence (Frings et al., 2018). These regions are also associated with high HIV/AIDS



rates, increasing the risk of comorbidities with other diseases (Frings et al., 2018). Regions with higher YLL values are also known to be regions of malaria endemicity. Distribution of vectors, therefore, may be a factor associated with clustering of YLLs. Additional research is needed to further assess linkages between EID emergence and spatial grouping of early mortality. In general, this study represents a dynamic approach in determining factors associated with early mortality, though disentangling the various components associated with regions of high YLL values proves a continuing challenge. Despite these uncertainties, assessing regional trends in mortality is a potential starting point for identifying factors associated with EID trends (Frings et al., 2018).

Wildlife interactions and distributions also propagate pathogen life cycles. An estimated 72 % of all diseases affecting humans and livestock originate from wildlife (Jones et al., 2008). Due to ecological pressures on host species, disease ranges tend to be geographically restricted when carried by larger wildlife reservoirs (Woodford et al., 2009). RVF is an example of a zoonosis that is maintained in wildlife populations, with potential for transmission to livestock and humans. RVFV antibodies have been identified in numerous Kenyan wild ungulates, including buffalo, black rhino, and impala, with significantly higher rates recorded during the RVF outbreak of 2006-2007. This event began in Kenya and spread to five other East African countries, causing abortions in millions of livestock and several hundred human fatalities. Using samples collected between 2000 and 2009, Britch et al. (2013) compared spatial data of RVF seroprevalence in wild ungulates and domestic camels. They determined that seroprevalence of RVF was significantly higher in wildlife during the 2006-2007

outbreak and decreased again in 2008 in the “post-epizootic” period. Waterbuck, buffalo, and domestic camels expressed significant seropositivity during the outbreak. Though transmission mechanisms for this period are unclear, wildlife may have played a role in maintaining this disease in the wild and facilitating the outbreak. All of these species are associated with habitat along the edge of woodlands and grasslands, revealing a potential environmental risk factor for RVF exposure (Britch et al., 2013). The 2006 outbreak first began in northeastern and coastal regions and is attributed to an increase in mosquito populations following flooding from abnormally heavy rains (Munyua et al., 2010). Though more research should be conducted to determine the specific risk factors involved in transmission, this study suggests a correlation between habitat, climate, and wildlife exposure to RVF (Britch et al., 2013).

On a national scale, Kenya has experienced significant declines in wildlife populations since the 1970s (Ogutu et al., 2016). Wildlife populations declined by an average of 68% from 1977-2016 among all regions in Kenya. This decline is not uniform among regions or species affected. Warthog, oryx, impala, and Grevy’s zebra are among the species that experienced the greatest declines in this timeframe. Concurrent to wildlife declines, livestock populations are increasing exponentially in Kenya. Populations of sheep and goats, camels, and donkeys increased by 76%, 13%, and 7%, respectively, from 1977-2016. As of 2016, livestock biomass was approximately 8 times that of wildlife from (Ogutu et al., 2016). Numerous studies suggest that wildlife densities decrease with increasing livestock populations as a result of competition for food and grazing resources, although this is a debated concept with nuanced and species-

specific interactions (Young et al., 2005; Kimuyu et al., 2016). As resource use overlaps, livestock are increasingly likely to contact pathogens originating in wildlife hosts (Rajeev et al., 2017). Livestock and wildlife can serve as host species, allowing several zoonotic pathogens to be sustained in the environment despite decreasing wildlife densities. Livestock may then transmit these pathogens to humans via physical contact or consumption of infected animal products. Livestock therefore serve as a linking factor of diseases between wildlife and humans, as they interact with both communities (Caron et al., 2015). Though livestock introduce pathogens into human communities, other factors, such as land use, livestock management, and human behavior influence the modes of human contact with pathogens.

### **Land Use**

Human alteration of natural landscapes influences risk of exposure to pathogens for humans, wildlife, and livestock. Ecological influences on vector distribution greatly affect the range and spread of diseases. Anthropogenic activity has the capacity to influence distributions of disease-carrying agents, thereby affecting human and animal interactions with pathogens (Lindblade et al., 2001). Food production is a primary mechanism by which humans shape and interact with their environment; in Kenya, livestock production is a predominant strategy that relates to culture and adaptation to arid environments (Odhiambo, 2013). Three primary land use structures are commonly utilized in Kenya: pastoralism, commercial ranching, and wildlife conservancies (Gikonyo et al., 2018; Kinnaird & O'Brien, 2012). Seventy percent of ASAL land in Kenya is utilized by pastoralists, making livestock production one of the most important

economic activities in the nation (Odhiambo, 2013). Pastoralism is a traditionally held and collectively practiced arrangement in which livestock keepers move herds depending on seasonal conditions and resource availability (Lengoiboni et al., 2010). Commercial ranches are owned by individuals for production of dense herds, which vary in size from large to small-holder ranches. Animal products are primarily sold, rather than kept for subsistence. Wildlife conservancies are government owned areas that are designed to protect wildlife, while permitting some livestock production activities. Conservancies may also incorporate ecotourism activities into wildlife management systems (Lengoiboni et al., 2010). These regimes are not mutually exclusive, as pastoralists often graze livestock on unfenced conservancy land with higher wildlife population densities (Georgiadis et al., 2012). In addition, pastoralists may employ a mixed commercial/subsistence ranching system or integrate agriculture (Browne et al., 2017). Irrigation of ASALs has increased capacity for agriculture, though this is highly variable depending on regional infrastructure (Hodbod et al., 2019). Land alteration influences local ecosystems, with potential to expand the range of vector species. In addition, animal production strategies influence the dynamic of wildlife-livestock interaction and associated pathogen transmission. This in turn affects pathogen exposure risk in humans who interact with livestock and wildlife (Nyariki, Mwang'ombe, & Thompson, 2009). Assessing variation in human-animal interactions within the context of land use systems is a crucial component of informing disease risk assessment.

In ASAL regions, irrigation for agriculture is a significant driver of land change. Regions of East Africa that were once considered malaria-free zones due to

impermissible climate are now experiencing outbreaks of malaria (Lindblade et al., 2001). Among numerous factors, including climate change and human population increase, land modification is a primary driver of disease expansion. In southwestern Kenya, pastoralists of the semi-arid Mara region are shifting from nomadic pastoralism to incorporating more sedentary pastoralism and agriculture (Nyariki, Mwang'ombe, & Thompson, 2009). Concurrent with enhanced irrigation, human reports of vector-borne diseases such as malaria have increased in this region (Hodbod et al., 2019). A comparative land use study in Kenya assessed that humans and livestock in irrigated lands were significantly more likely to express seropositivity for mosquito-borne diseases, such as malaria and West Nile Virus, than in dry graze lands. In comparison, humans and animals in dry rangeland were more likely to be exposed to bacterial diseases, such as brucellosis, which are spread via contact with contaminated graze land or water sources (Bett et al., 2017). Irrigating land does not necessarily increase risk of pathogen exposure in every situation, but human influence on water systems can expand or restrict ranges of certain vectors depending on the species ecology. It is important to note that most dryland areas do not implement irrigation extensively. Though some communities are able to supplement pastoralism with agriculture, infrastructure does not support this as a viable alternative throughout the majority of ASALs in Kenya (Mutambara, Darkoh, & Atlhopheng, 2016). Irrigation provides significant benefits by enhancing stability of water resources for livestock and crops, particularly as drought frequency increases (Opiyo et al., 2015). In terms of EID research, irrigation can be regarded as a human adaptation to arid environments that affects vector distributions.

Future research should study shifting irrigation patterns, while assessing regional risk for human interaction with potential disease vectors (Hodobod et al., 2019). Water resource use is an important component of land use in terms of EID dynamics.

Shifts in livestock management practices often occur as a result of human adaptation to challenging conditions. Throughout the horn of Africa, rainfall in the last decade has totaled 50-75% below the normal accumulation. Drought frequency has increased from once a decade in the 1970's to once every three years in the 1990s (Opiyo et al., 2015). Turkana county in Northwest Kenya has experienced the most severe droughts in the last 10 years since 1950 (Opiyo et al., 2015). Trends in pastoralism, the primary economic activity in this region, have been adjusted in response to climactic variation. This includes diversification of occupation and livestock species, as well as increasing livestock movement (Bett et al., 2009; Opiyo et al., 2015). Herder preference is shifting toward incorporating more camels and goats than in previous years due to their increased drought tolerance when compared to cattle. Herders also drive livestock across greater distances in order to access sufficient water and graze land. Pastoralists interviewed by Opiyo et al. (2015) described increased incidence of disease outbreak among livestock in drought years, though no specific diseases were identified. However, this shift in herd composition has implications for disease risk, as pathogen presence varies based on livestock species. Camels, for example, are a reservoir species for Middle East Respiratory Syndrome (MERS) (Mackay & Arden, 2015). Though little is known about this virus, it is believed to be transmitted to humans via consumption of infected camel meat and milk. Though no human cases have been reported in Kenya, increased

density of camel herds and human-camel interaction have been linked to human MERS outbreaks in the Arabian Peninsula and North Africa (Mackay & Arden, 2015). In this instance, climate patterns, human culture, and livestock preference are driving a changing human-animal interface of disease risk. Drier climates are shifting herder preference to species with varied disease reservoir potential. Human risk of exposure is then dependent on interactions with these animals. Pastoralist shift of livestock preference is an adaptive strategy that carries implications for disease risk.

Disease transmission dynamics among commercial ranching communities are distinct from those of traditional pastoralist communities. Ranches tend to have higher wildlife densities than pastoralist areas due to their closer proximity to wildlife conservancies. Ranches often integrate wildlife-centered ecotourism activities into their economic structure (Rajeev et al., 2017). Higher wildlife densities may result in increased disease transmission between domestic and wild species, particularly among ungulates. Ranches and wildlife conservancies may or may not be contained in fencing; unfenced areas generally have higher rates of resource overlap between livestock and wildlife (Kinnaird & O'Brien, 2012). In Laikipia County, which is primarily unfenced, Rajeev et al. (2017) found that cattle in ranching systems were significantly more likely to express seropositivity for *Leptospira* when compared to cattle in pastoralist systems, indicating heightened spillover of pathogens from wildlife. However, the researchers did not detect significant variation in *Brucella* exposure among land use types (Rajeev et al., 2017). Both of these diseases are transmissible to humans via direct contact with livestock. Land use type is likely a significant driver of exposure to pathogens, though this risk is

dependent on disease, herd densities, and environmental conditions (Rajeev et al., 2017). Ranching systems that are situated near wildlife-dense areas can facilitate disease transmission between wildlife and livestock, though this is dependent on specific management systems, such as fencing and herd densities. Transmission risk is also disease-specific.

### **Human Behavior and Pathogen Exposure**

In addition to anthropogenic modification of natural environments, human exposure risk is also affected by specific behaviors expressed among Kenyan communities that facilitate contact with pathogens. Cultural practices, sanitation capacities, and knowledge of disease dynamics all determine direct and indirect transmission pathways. Vector-borne diseases can be mitigated by minimizing contact with the vector, though capacities are often limited by regional infrastructure and funding. A study of *Plasmodium* infection in malaria-endemic regions of western and coastal Kenya revealed behavioral trends in exposure. Use of mosquito nets that were treated with insecticide was associated with lower rates of infection among school-aged boys in high-risk areas (Gitonga et al., 2012). Using treated nets is therefore suggested to be a protective factor against malaria. However, many communities cannot afford mosquito nets, or are unaware of their proper use. Lack of funding and access to nets and treatments is a significant risk factor for malaria-prone communities in Kenya (Wang'ombe & Mwabu, 1993). In addition to lacking materials, inadequate knowledge of preventative measures may serve as a risk factor in disease transmission. Mosquito nets



are significantly more effective when treated with insect deterring chemicals, but many communities are not aware of proper standards for net treatment. Even if communities choose to take protective measures, lacking community education can still put individuals at risk of exposure to pathogens (Kinung'hi et al., 2010). Community engagement and education is therefore a practical mitigation strategy in regions within Kenya where malaria risk is understood, but lacking resources is still an obstacle to effective use (Wang'ombe & Mwabu, 1993).

Human interactions with wildlife and livestock are a strong determining factor for pathogen exposure risk. In livestock rearing communities, individuals regularly contact animal bodily fluids (Thumbi et al., 2015). Poor waste management practices lead to contamination of food and water with animal fecal material, leading to a variety of diarrheal diseases. These infections are globally a leading cause of mortality in children under the age of five, including Kenya (Conan et al., 2017). This is of particular concern in peri-urban communities, where livestock are raised in dense herds and roam through settlement compounds. A study by Barnes et al. (2018) revealed that peri-urban communities in Kisumu, Kenya express poor sanitation practices, despite previous public education campaigns. Manure is utilized to fertilize crops and may be left in mounds throughout the community. In these situations, cross-contamination occurs through failure to properly wash vegetables, or failure to wash hands after handling animal waste (Barnes et al., 2018). A majority of households in this study had drinking water that was contaminated with fecal matter. Families with animals in the household compound were significantly more likely to have contaminated drinking water. Previously implemented

community education programs tend to focus on sanitation in regard to human waste. Individuals are still at high risk of diarrheal diseases if they maintain human waste sanitation practices, but neglect livestock sanitation (Conan et al., 2017). Effective and holistic engagement should equally emphasize the importance of safe practices in all aspects of sanitation (Barnes et al., 2018).

Rift Valley Fever, Brucellosis, Q Fever, and numerous other zoonoses can be transmitted from animals to humans via consumption of infected meat, milk, or blood (Gwida et al., 2012; Murithi et al., 2011). Cultural structures, as a factor of animal management strategies, exert a strong influence on this exposure risk. Pastoralist groups, such as the Maasai, rely primarily on meat and milk for subsistence (Nyariki, Mwang'ombe, & Thompson, 2009). Risk of contracting a disease from infected livestock increases when animal products compose a majority of the diet (Bett et al., 2017). These risks are elevated when there is significant sharing of water and grazing resources between wildlife and livestock (Caron et al., 2015; Rajeev et al., 2017). Rajeev et al. (2017) found that cattle on private ranches were more likely to express seropositivity for leptospirosis when compared to cattle on group ranches within Laikipia County, Kenya. Private ranches express lower livestock densities, but higher wildlife populations when compared to group ranches. Land use and wildlife interactions may facilitate pathogen exposure to livestock and humans (Rajeev et al., 2017). However, subsistence use of animal products reduces the risk of disease spread. Commercial sale of animal products is associated with increased risk, as infected animals travel beyond their geographical boundaries and may introduce pathogens when integrated into new herds (Gikonyo et al.,

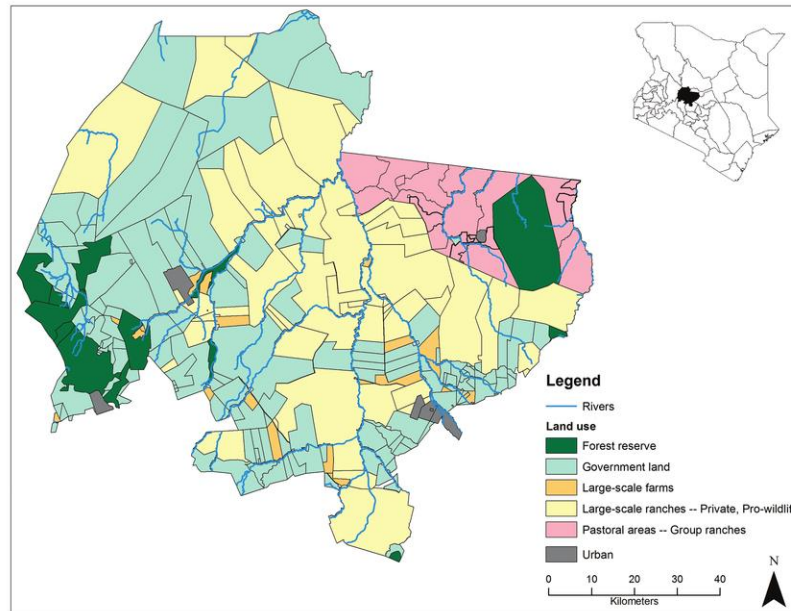
2018). Trade routes are often difficult to trace and extend the geographical range of pathogens outside of their origin site. A study by Gikonyo et al. (2018) assessed risk factors for MERS amplification and spread within Kenya. In addition to livestock densities, presence of camel trade routes and markets is a significant factor in increasing risk of MERS spread. Markets and animal trade routes are therefore identified as regional hotspots of pathogen spillover. At-risk individuals may not understand the association between animal illness and human illness. Even if humans are concerned about livestock disease, they may not be able to recognize symptoms in animals (Gikonyo et al., 2018). MERS may produce mild symptoms in animals that are difficult to detect, though human cases are more severe (Mackay & Arden, 2015). Increasing awareness of zoonosis spread depends on training for identifying livestock illness and associating human health with animal health. These challenges must be overcome in order to promote safe practices in handling and trading livestock.

### **Laikipia County as a Study Site**

Laikipia County, located in the Rift Valley region of Kenya, spans 9,666km<sup>2</sup> between latitude 0°53' N, 0°16'S and longitude 36°11', 37°23'E. The climate, while semi-arid, is prone to seasonal flooding. Annual rainfall varies within the county, from 900 mm/yr along the southern equatorial border to 400 mm/yr along the northern boundary (Deem et al., 2015). The county is subdivided into three districts: Laikipia North, East, and West. The total population of the county is 466,419 (49.8% Male, 50.2% Female) (Health policy Project, 2015). Laikipia is predominantly composed of Maasai, Samburu, Turkana, Pokot, and European-descended ethnic groups, all of which rely heavily on

animal production. Livestock keepers from all ethnic backgrounds historically depend on cattle, sheep, and goats (Gadd, M., 2005). An aerial survey of Laikipia County in 2016 estimated livestock populations of 546,153 sheep and goats, 249,510 cattle, and 6,936 camels (Smith et al., 2016).

Laikipia County was selected as the area of focus for PREDICT-Kenya. This region demonstrates an extensive and well-documented human-wildlife-livestock interface, even in the context of nationally high rates of human-animal interaction. Laikipia is largely dependent upon livestock production and contains a mixture of traditional pastoralism, commercial ranching, and mixed pastoralism/ranching systems within wildlife conservancies (Gikonyo et al., 2018). In addition, Laikipia houses several unfenced wildlife conservancies. Figure 5 depicts regional land use within the county. This mosaic of land use creates a dynamic interface of human-wildlife-livestock interaction. Regions of the county with high wildlife densities also hold livestock, with potential for pathogen exchange among animals.



**Figure 5:** (Sundaresen & Riginos, 2010) Land Use map of Laikipia County, Kenya

Laikipia is one of only two counties in Kenya whose wildlife population has increased in recent decades, despite the national decline. This is attributed to successful interventions from privately owned wildlife conservancies and economic benefits from tourism. Though this is a success for conservation, increasing animal density brings competition and risk of zoonotic disease transmission. The growth in wildlife is exceeded by exponential increases in livestock populations (Smith et al., 2016). From a county-wide survey by Smith et al. (2016), the ratio of livestock mammals to wildlife mammals is 12:1 individuals, or 3:1 in terms of biomass. From 2012-2016, cattle numbers increased by an estimated 66%, while sheep and goats have increased by 44%. Camels have increased by 67% in these four years. Since 1985, camel populations have risen exponentially, from 742 individuals to 6,936 individuals county-wide in 2016. This

increase of 835% is by far the greatest change in any livestock species in the county in the past 30 years (Smith et al., 2016). Livestock numbers are projected to increase due to growing demand for animal products throughout Kenya (Food and Agriculture 2017). Interaction between livestock and wildlife varies depending on land use systems implemented by local communities. Pastoral regions in Laikipia tend to hold greater densities of livestock and lower densities of wildlife. Commercial ranching communities, on the other hand, hold lower densities of livestock and incorporate ecotourism activities in to their economy. Several group ranches are located near wildlife conservancies. Wildlife conservancies in Laikipia hold higher wildlife densities than pastoral areas (Rajeev et al., 2017). In some parts of Laikipia, wildlife to livestock ratios are 14 times higher on ranches than on pastoral lands (Georgiadis et al., 2007). Laikipia County is an ideal site for examining disease risk due to the matrix of land use and animal interactions that prevail over relatively short geographical distances.

A dynamic human-wildlife-livestock interface, varied land use change, and historical presence of zoonotic disease emergence makes Laikipia county a point of interest in EID research. Rift Valley Fever, leishmaniasis, and brucellosis have all posed public health threats in the past and continue to be diseases of concern (ProMED, 2018). Disease surveillance in Laikipia is essential for determining the pandemic potential of endemic diseases, as well as identifying any novel EIDs. Previous studies can be used to pinpoint potential risks of emerging threats. Laikipia has been identified as a region of high disease risk in camel trade, largely due to the rapid increase in camel populations (Gikonyo et al., 2018). Animal production, as well as the animal market and value chain,

are known to be points of spillover risk due to high rates of animal interaction and dispersal. Assessing risk in these areas should be a surveillance priority.

Human perceptions of environmental variation provide key insight for assessing the future of disease risk in Laikipia County. In a qualitative study by Ogalleh et al. (2012), residents of Laikipia county described that the climate has become less hospitable over time, with heavier rains or droughts at abnormal times and heightened temperatures overall. These observations are corroborated by data collected from the nearby Laikipia Air Base station, indicating weather patterns that differ from historical trends. Farmers associated the changing climate with increased disease prevalence in animals. They also indicated a correlation between livestock die-offs and increased herd densities, likely due to disease spread (Ogalleh et al., 2012). Human and livestock populations have increased in recent decades, intensifying competition for graze land and water. Competition is exacerbated by climate change, as higher temperatures and abnormal rainfall are compounding resource scarcity (Bond, 2014). Increased competition is likely to drive heightened resource use overlap of water and graze land between livestock and wildlife, creating further opportunities for pathogen transmission. These changes are affecting social stability in addition to disease dynamics. Participants in Laikipia focus group discussions identified water resources as a primary source of conflict among local pastoralists (Bond, 2014). Land use, water availability, and animal population densities affect pathogen prevalence in livestock and wildlife species, with implications for human health. Conflict in central Kenya is rooted in several other interconnected factors, such as civil unrest, poverty, HIV/AIDS and livestock theft. Climate change serves as a catalyst

that increases the severity of these issues by further limiting access to necessary resources (Bond, 2014). These destabilizing factors, in tandem with lacking disease mitigation resources, result in a feedback cycle that increases vulnerability to EID threats. Though EID emergence is a primary concern, disease risk is rooted in these other factors that still need to be assessed holistically in order to understand all of the interconnected effects.

### **Zoonoses**

Though several zoonoses are found within Kenya, some are designated as "priority diseases" due to severity of illness in humans and potential for spread (Munyua et al., 2016). Rift Valley Fever Virus (RVFV), a mosquito-borne pathogen, was first characterized in Kenya's Great Rift Valley in 1931. Outbreaks occur more frequently in Kenya than any other country where the illness has been reported (Baba et al., 2016; Murithi et al., 2010). RVF causes mass abortions in livestock, and can induce acute febrile illness symptoms in humans, potentially leading to encephalitis and hemorrhage (Murithi et al., 2010). Humans can contract the disease from livestock via contact with contaminated bodily fluids or consumption of infected meat. Though livestock outbreaks do not always carry over to humans, several outbreaks have caused human fatalities. A 2006 outbreak affected 5 countries in East Africa: in Kenya alone, 684 cases were reported, with 155 deaths (Anyamba et al., 2009). A study by Lwande et al. (2015) showed that RVF antibodies were present in wildlife even years after the most recent RVF outbreak, indicating that the disease expresses "long-term persistence" in animal populations. Demographic studies reveal trends in behavioral exposure risk. Focus group



discussions in Baringo County, Kenya revealed that most participants were aware of RVFV transmission modes, such as consuming infected meat or milk. However, males were significantly more likely to express these behaviors, indicating heightened disease risk (Mutua et al., 2017). RVFV infection rates in humans have been on the rise since 1996, likely due to anthropogenic factors, such as increased irrigation, deforestation, and fertilizer use that increases contact with mosquito vectors and animal hosts (Baba et al., 2016). Human behavioral factors, from food safety practices to land use, increase the outbreak potential of RVFV.

Brucellosis, an infectious disease caused by *Brucella* bacteria, is one of the most common zoonoses worldwide (Germeraad, 2016). Brucellosis is transmissible between ungulate wildlife and livestock via indirect contact, such as shared use of water and grazing resources (Bett et al., 2017). Increasing animal populations yield heightened inter-species interactions, increasing risk of *Brucella* exposure. Humans contract the disease almost exclusively from ruminant hosts via direct contact, such as consumption of raw milk or undercooked meat. Infected animals express clinical symptoms of abortion, "...infertility, and decreased milk production" (Germeraad et al., 2016). Human cases are suspected to be underreported or misdiagnosed, as symptoms are often indistinguishable from other fever-inducing illnesses (Muendo et al., 2012). Serological surveys in Kenya have revealed significant seroprevalence of *Brucella* in camel and cattle herds, but symptom expression varies by species (Muendo et al., 2012; Gwida et al., 2012). Cattle tend to show classic symptoms, while camels express few clinical signs, often impeding diagnosis (Gwida et al., 2012). Further studies are needed to elucidate

trends in livestock-human transmission. Brucellosis is a priority disease of concern due to its ubiquitous presence in Kenya, and the common practices that facilitate its spread.

Livestock type may also affect humans' ability to distinguish symptoms and subsequent risk of infection (Gwida et al., 2012).

Middle East Respiratory Syndrome (MERS), though no human cases have yet been reported in Kenya, is a growing EID of concern due to shifting livestock management practices. The first human MERS outbreak occurred in Jordan in 2012 and has since spread throughout the Middle East and East Africa (Mackay & Arden, 2015). Serological studies indicate camels as the natural host of the disease, which can spread to humans via close contact (Mackay & Arden, 2015; Gikonyo et al., 2018). Though camels express symptoms consistent with mild respiratory illness, human cases are more severe, albeit much less common. MERS in humans begins as a lower respiratory tract infection with fever and impeded breathing, which may lead to organ failure and death in 20-40% of cases (Mackay & Arden, 2015). Deem et al (2015) conducted an analysis of archived camel biological samples collected in Laikipia county from 1992-2013. An average of 29.5% of camels tested positive for MERS antibodies throughout these years. Though camel densities have been historically low in Kenya, pastoralist preference is shifting towards camels due to their heightened resilience during water and food shortages. Localized impacts of climate change have reduced water presence and increased resource constraints on herders, heavily influencing the shift in livestock makeup (Browne et al., 2017). Herders surveyed by Browne et al. (2017) cited camel resilience in the face of an increasingly dry climate as the primary rationale for this transition. Camel-dense

pastures, markets, and trade routes are therefore potential hotspots for MERS outbreak. Researchers are unsure as to why a human outbreak has not been reported in Kenya, and additional research is needed to understand MERS transmission patterns (Gikonyo et al., 2018). MERS has high pandemic potential due to its documented presence in camels, and environmental conditions that influence human pastoral preference for the natural reservoir (Gikonyo et al., 2018).

Numerous other diseases of concern to Kenya have resulted in massive loss of human and animal life throughout the African continent. Marburg is a hemorrhagic filovirus related to Ebola that has been detected in Kenya, Uganda, Democratic Republic of Congo, and Angola (Zehender et al., 2016). An outbreak along the Kenya-Uganda border of 2017 prompted international response efforts emphasizing community education. Though all three confirmed cases resulted in fatality, the disease was prevented from spreading any further. The first suspected case in this outbreak was a herdsman who reported hunting near caves that house fruit bats, which may be the reservoir for Marburg. Human-bat contact is likely a spillover route for Marburg. Ongoing surveillance of Marburg can facilitate early detection and implementation of containment measures to prevent future outbreaks (Marburg Virus, 2017). Crimean-Congo Hemorrhagic Fever Virus (CCHFV) is a widely distributed disease that has been detected in Africa, Asia, Europe, and the Middle East. This virus has been detected in small mammals and domestic mammals, with ticks serving as the vector. CCHFV emergence in humans has been linked to livestock trade, climate change, and land modification. Vector control is an important step in containment, along with surveillance

and education of transmission mechanisms (Burt, Goedhals, & Mathengtheng, 2014). Some viruses of concern have not yet been detected in Kenya, but surveillance is still recommended to facilitate early detection and mitigation in the event of disease spread. Lassa fever, a hemorrhagic virus, is endemic to West Africa and is transmitted by ticks (Dzingirai et al., 2017). The natural rodent host species, *Mastomys natalensis*, is distributed throughout east, west, and central Africa, indicating potential for transmission across regional boundaries. The World Health Organization has identified Lassa as a virus of epidemic potential and recommends extensive and ongoing surveillance (Richmond & Baglolle, 2003; The Lancet, 2018). Though Lassa has not yet been identified in Kenya, monitoring wildlife and human viral loads is essential for assessing spillover risk (Dzingirai et al., 2017).

## **Objectives**

The complex human-wildlife-livestock interface in Laikipia County, Kenya leads to a heightened risk of zoonotic disease spillover. Human behaviors, such as livestock management and food safety practices, affect public health risks. Identifying high-risk behaviors and perceptions related to human-animal interactions will elucidate potential mechanisms of disease transmission within vulnerable populations. Significant variation of land use strategies within Laikipia County leads to potential for variability in disease risk. This study aimed to assess variation in risk, including human behaviors and animal interactions, among study communities that implement different land management schemes. The study will also determine whether reports of high-risk behaviors correlate

to increased prevalence of illnesses reported among the participants. Creating a holistic assessment of risk must incorporate complexities of disease ecology and human behavioral drivers. These data will inform best practices for localized intervention measures that can be targeted to effectively minimize risk of disease exposure on a local level.

## **Conclusion**

Surveillance, ecological research, and community engagement are central tenants of the One Health approach as applied by the PREDICT project (PREDICT, 2017). Regional climatic factors determine range and distribution of disease vectors, which are further influenced by human activity. In Kenya, irrigation, livestock propagation, and wildlife-livestock contact all contribute to pathogen maintenance and expansion in natural systems. This increases risk of human exposure to pathogens when compounded with human-animal interactions and poor sanitation practices. Collecting environmental and human behavioral data is necessary to understand pathogen dynamics in context. These data must then be analyzed to assess risk factors relevant to communities, with the goal of implementing relevant mitigation efforts. Community members and leaders are also critical in gaining community acceptance and applying best practices for public health management.

## CHAPTER 3: *PREDICT*-KENYA STUDY RESULTS

### Methodology: *PREDICT*-Kenya

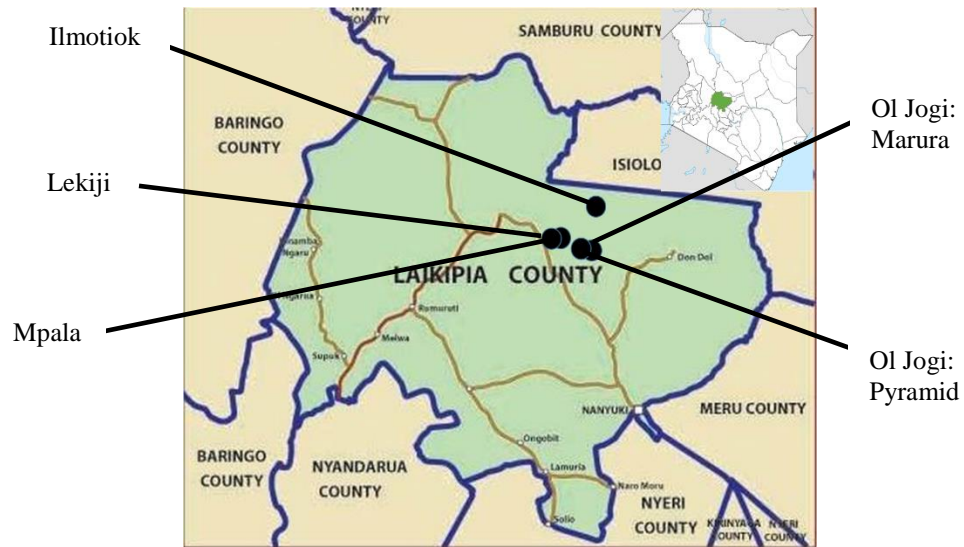
#### **PREDICT- Kenya Overview**

The global *PREDICT* project follows research protocols established by USAID and the University of California-Davis. In alignment with goals to identify risk factors for emerging pandemic threats, *PREDICT*-Kenya researchers distributed human behavioral questionnaires to community members of Laikipia County (*PREDICT*, 2017). Materials for Institutional Review Board (IRB) approval were compiled by the University of California, Davis which approved both survey distribution and data analysis. Prior to accessing human behavioral data, I completed CITI human subjects research training, accessed through the Smithsonian Institution. While conducting data analysis, I did not have access to personally identifiable information, and no key exists to connect participant ID numbers with names or other identifiable information.

#### **Sampling Methodology**

Questionnaires were administered in two rounds in 2016, with one round in both wet and dry seasons. Five communities were surveyed: Ilmotiok, Lekiji, Mpala, Ol Jogi-Marua, and Ol Jogi-Pyramid. Figure 6 shows the distribution of these communities. Human behavioral data was collected with *PREDICT* universal questionnaires, which

were utilized in all 29 PREDICT focus countries. In each community, PREDICT researchers conducted a human behavioral survey individually with participants. Prior to survey distribution, a community mobilizer met with residents of each township to inform residents of the date, location, and purpose of the survey, inviting all to participate. Survey questions and answers were read aloud in the participant's preferred language. Some questions allowed only "yes or no" responses, while other questions permitted free responses from participants. The general survey distributed to all participants contained 57 questions examining demographics, human-animal interactions, sanitation, and disease perception among respondents. Additional module surveys were distributed based on responses from the general questionnaire. Participants who identified animal production as their primary occupation completed an additional survey with 30 questions pertaining to animal management, sanitation practices, and diseases affecting livestock. Surveys developed for occupations in resource extraction, wildlife restaurants, and health care were available, but were not applicable to any of the participants, and are therefore not included in the analysis.



**Figure 6:** Map of Laikipia County, with communities where human behavioral data was collected

## Data Analysis

### *Human Behavioral Questionnaires*

Quantitative analysis of the behavioral questionnaire responses was conducted in R (R Core Team, 2013). All questions relating to animal interaction, sanitation practices, and demographics were included in analysis. Chi square analysis was conducted with the EpiTools package to determine associations between reported behaviors and demographic features of the sample population (Aragon, 2017). The goal of this analysis was to assess variables that correlated to reports of high-risk behaviors. Examples of high-risk behaviors include eating raw meat and not treating drinking water. Reported high-risk behaviors serve as indicators for risk of pathogen exposure. Analysis of reported behaviors was conducted first for the entire sample population overall. The data was then



subdivided by community, gender, and age group, and the analysis was repeated. This enabled the comparison of response variables by various demographic features.

A question on the general survey asked participants if they had experienced an “unusual illness” in the past year. The “yes/no” response of participant's self-reported illness was used as an outcome variable indicating illness. Chi-square analysis was conducted to determine factors significantly associated with reports of individual illness in the past year. LASSO regression was then conducted using the glmnet package to determine significant interactions of multiple response variables in relation to the outcome variable of reported illness (Friedman, Hastie, & Tibshirani, 2010).

### ***Community Engagement Observational Data***

Following data analysis, a community engagement trip was held in each of the communities to discuss risk of disease spread. Each community was represented by a Community Health Volunteer (CHV): a local in the community who served as a liaison between their village and the PREDICT researchers. CHVs and researchers jointly engaged the communities in discussions of health-related issues, such as food safety and risk of human-wildlife interactions. I joined a group of graduate students from various universities in Nairobi and conducted an observational assessment of community practices and conditions that relate to One Health and PREDICT goals. Engagement programs were held in all communities except Mpala due to logistical constraints; therefore, observations in this community were less detailed than in the others. During each visit, the team explained the concept of One Health, and showed a video to the

communities detailing the causes of the 2014 Ebola outbreak (Elisco & Barrat, 2016). This opened up community discussion of drivers of disease spread, which was facilitated by community health volunteers associated with each locality. The discussion was also facilitated by PREDICT staff who had initially distributed behavioral questionnaires among the communities. The objective of my participation in this trip was to gather observational data contextualize the quantitative data gathered from the questionnaire assessment. In addition, I gathered information about health care accessibility in each location by observation and talking with PREDICT staff. Quantitative results will be analyzed while considering these observations.

## **RESULTS**

### **General Questionnaire**

#### ***Behaviors and Exposure Risk***

A total of 327 participants responded to the General questionnaire among the five study locations. Overall, 194 respondents were female (59%), and 132 were male (41%). Gender of one participant was listed as “other”; this data was excluded from all tests that involved gender, but responses were included in all other analyses. The distribution of respondents by township is as follows: Ilmotiok (n = 102), Lekiji (n = 103), Mpala (n = 53), Ol Jogi Marura (n = 51), and Ol Jogi Pyramid (n = 18). Median ages were 30, 28, 30, 29, and 34.5, respectively for each community. Among all participants, 284 were adults ( $\geq$  age 18) and 43 were children ( $<$  age 18). Differentiating between “Child” and “Adult” at age 18 is consistent with local perceptions of age of adulthood. Participants reported a

variety of primary occupations, which were categorized as Animal Production (n = 119), Migrant Laborer (n = 52) Student (n = 41), House Work (n = 24), and Crop Production (n = 9). The remaining 82 participants reported other primary occupations, such as sales, construction, and teaching, that did not fit in to a listed category.

Each township sampled was classified based on the primary land use system. Ilmotiok and Lekiji are primarily categorized as group pastoralist communities. Mpala is characterized by a private commercial ranching structure. Ol Jogi-Marura and Ol Jogi-Pyramid are communities located within a wildlife conservancy that contain commercial ranches. It is important to distinguish the Ol Jogi communities from Mpala, as these communities also implement tourism as an economic activity. In addition, the Ol Jogi communities are funded by the privately-owned group ranch. Medical services and housing are provided for the residents in Ol Jogi, who are mostly employees working on the conservancy. In addition, the Ol Jogi sites may have different livestock-wildlife interaction rates due to their location within a conservancy.

Analysis of behavioral variation reported by township indicates prevalence of behaviors among land use systems. Behaviors related to food and water consumption and animal interaction practices varied significantly based on land use type. Three primary questions related to water safety, as shown in Table 1. A majority of participants from pastoralist communities (Ilmotiok and Lekiji) did not treat drinking water, while being highly likely to obtain water from an uncovered source, such as a river or dam, and also share a drinking water source with animals. Humans, livestock, and wildlife utilize the same water resources in pastoralist communities. During the dry season, pastoralist

communities dug in the river bed to reach ground water. Wildlife also utilized the river bed, as evidenced by the presence of dung from elephants and ungulates. Livestock were also reported to use the river bed for watering. In addition, Ilmotiok residents were likely to report eating sick animals (98%), collecting animals found dead to eat (95%) or sell (94%), and eating raw or undercooked meat in the past year (98%). Reports of these high-risk behaviors were scarce or nonexistent in wildlife conservancy communities. One exception to this is the drinking water habits reported in Ol Jogi-Marura. A relatively high percentage of participants share a drinking water source with animals, but a majority (86%) do not treat drinking water.

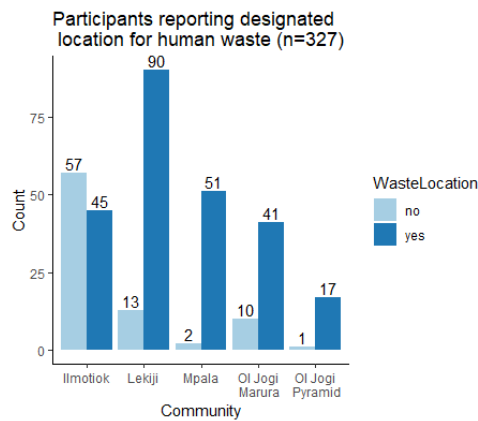
Mpala is the only location that relies mainly on commercial ranching as a land use strategy. Most high-risk behaviors are less frequently reported in Mpala when compared to pastoralist communities, but more frequently reported than in the wildlife conservancy communities. However, significant differences in reported behaviors vary by location of comparison. Ilmotiok is significantly more likely to report certain high-risk behaviors when compared to Lekiji (Eating raw meat, collecting dead animals to sell:  $p < 0.0001$ ). For some activities, such as eating raw meat, there was no significant difference in the reported behavior between Mpala and Lekiji ( $p=0.5$ ); however, reports of raw meat consumption were significantly lower in Mpala when compared to Ilmotiok ( $p < 0.0001$ ). Similar trends are observed for the behaviors of eating sick animals and collecting dead animals to sell. These data indicate that behavior prevalence, though delineated by land use strategies, still varies on a community level.

**Table 1:** Variation in response frequency of reported behaviors, based on location

	<i>Number of respondents per site (%)</i>				
	Pastoralist		Commercial Ranching	Commercial Ranching/Wildlife Conservancy	
	Ilmotiok ( <i>n</i> = 102)	Lekiji ( <i>n</i> = 103)	Mpala ( <i>n</i> = 53)	Oi Jogi Marura ( <i>n</i> = 51)	Oi Jogi-Pyramid ( <i>n</i> = 18)
Water from uncovered source	101 (99)	100 (97)	5 (9)	0 (0)	3 (17)
Drinking water untreated	83 (81)	57 (55)	22 (42)	44 (86)	11 (61)
Drinking water source used by animals	92 (90)	103 (100)	12 (23)	22 (43)	2 (11)
Eaten raw/undercooked meat in past year	100 (98)	51 (49)	30 (57)	3 (6)	1 (6)
Eaten Sick animal in past year	100 (98)	57 (55)	24 (45)	1 (2)	0 (0)
Found dead animal, collected to eat or share in past year	97 (95)	52 (50)	16 (30)	5 (10)	0 (0)
Found dead animal, collected to sell in past year	96 (94)	13 (13)	6 (11)	1 (2)	0 (0)

Sanitation risk factors are most prevalent in pastoralist communities. Livestock freely roamed through communities and were penned near household compounds. Animal feces covered the ground surrounding dwellings. In addition, the survey

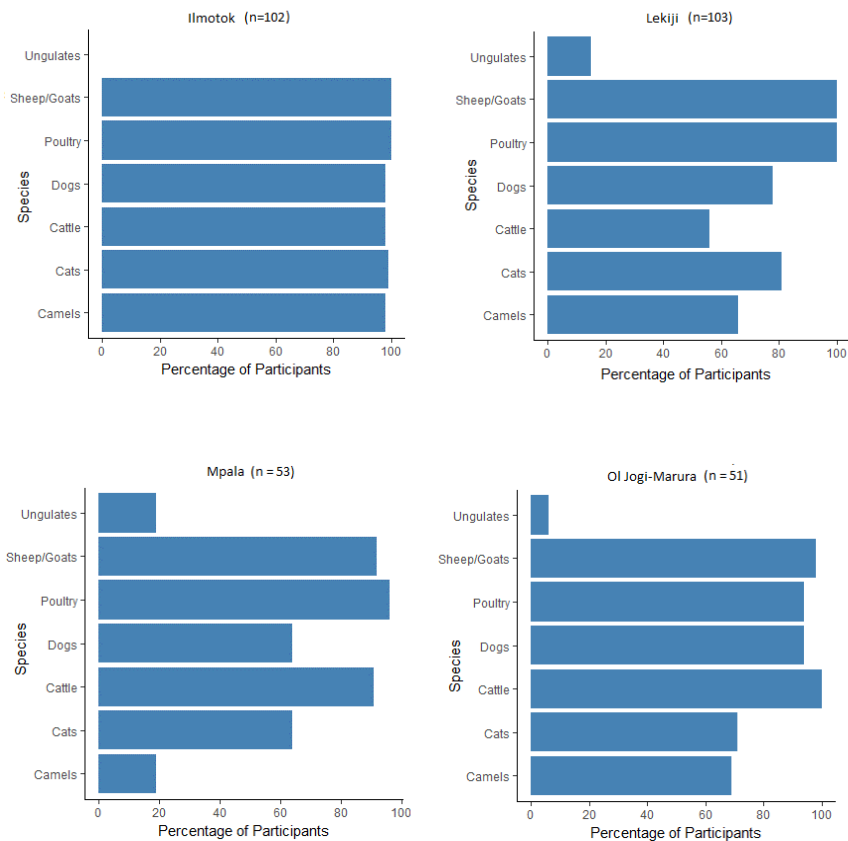
responses indicate a lack of proper waste disposal in pastoral communities. Ilmotiok was significantly less likely to report a designated location for human waste when compared to all other communities ( $p < 0.001$ , Figure 7). Chickens in pastoralist and wildlife conservancy communities freely entered and left human dwellings, and chicken waste was present in areas surrounding households.

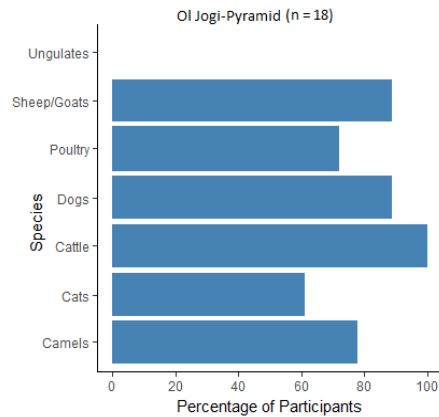


**Figure 7:** Participants reporting presence of a designated location for human waste, by community.

Reports of species-specific interactions also varied significantly among sites (Figure 8). In every community except Lekiji, >90% of participants reported interactions with cattle in the past year. Mpala was the only site in which a majority of participants did not interact with camels. Nearly all Ilmotiok respondents (98%) reported camel interactions. All communities had high rates of interaction with sheep and goats (>90%). Over 90% of participants in all communities except Ol Jogi-Pyramid reported interactions with poultry. Ungulate interactions were reported in Lekiji (15%), Mpala

(19%), and Ol Jogi Marura (6%). Only 2 participants in Lekiji and 2 participants in Ol Jogi Marura reported interactions with carnivores. Local customs regarding animal management contextualize these interaction reports. Goats are kept within household areas in Lekiji and Ilmotiok, but are not present in either Ol Jogi site. Cattle roam freely in Lekiji and Ilmotiok, but are not present in either Ol Jogi site. Cattle roam freely in Lekiji and Ilmotiok, but graze outside of the Ol Jogi communities. Though no accurate wildlife population estimates were obtained, the livestock roam throughout the areas that wildlife are known to inhabit. Opportunity for resource use overlap between livestock and wildlife, especially grazing ungulates, is a concern for pathogen transmission.





**Figure 8:** Percentage of Respondents Reported Interaction with Animal Taxa, by community

Participants were asked whether they had experienced an “unusual illness” in the past year, with a series of symptoms to select from. The “yes or no” response indicating presence or absence of an illness was tested as an outcome variable against all behavioral and demographic variables via Chi-Square analysis. The seven variables reported in Table 2 represent the variables significantly associated with participant’s self-reported illness experienced in the past year from the overall data set. Each behavior references a question with a “yes or no” response. Overall, 72 people (22%) reported an illness in the past year. The data was then subdivided by township, and the same analysis was repeated for each community. Ilmotiok, Lekiji, and Ol Jogi-Marura were the only locations where any behavioral variables significantly correlated to reports of illness. Each of these locations revealed a significant association between illness of household members and self-reported illness. There is no significant difference in frequency of illness reported based on location ( $p = 0.1$ ).



**Table 2:** Behavioral variables significantly associated with outcome variable “Participants self-reporting illness in the past year” (Survey Questionnaire #30). Each behavior shown represents a bivariate response.

	P-value	Risk Ratio	CI
<b>Overall (n=327)</b>			
Not treating drinking water	0.014	1.93	1.14-3.24
No designated waste location	0.005	1.87	1.25-2.80
Primary Occupation: Migrant Laborer	0.01	1.90	1.23-2.92
Ill Household member in past year	< 0.0001	6.24	4.50-8.66
Found dead animal; collected to sell in past year	0.026	1.63	1.09-2.44
Scratched/bitten by animal in past year	0.016	1.72	1.12-02.63
Camel Interactions in past year	0.002	2.44	1.34-4.44
<b>Ilmotiok (n=102)</b>			
Primary Occupation: Migrant laborer	0.029	2.18	1.23-3.87
Ill household member in past year	< 0.0001	4.67	2.82-7.72
<b>Lekiji (n=103)</b>			
Ill household member in past year	<0.0001*	4.87	4.87-17.63
Scratched/bitten by animal in past year	0.0043	3.3	1.56-6.96
<b>OI Jogi-Marura (n=51)</b>			
No designated waste location	0.007*	4.1	1.67-10.04
Ill household member in past year	0.002*	5.36	2.48-11.56

\*Fisher’s Test

LASSO regression was performed on 30 behavioral variables from the data set, with self-reported illness as an outcome variable. The regression returned groupings of variables that are associated with participants' reports of illness. Output variables reported in Table 3 were the nonzero coefficients reported. Reporting a designated location for human waste was indicated as a protective factor, and was negatively correlated to reported illness (OR 0.85). Illness reported in another household member in the past year was a risk factor positively associated with illness presence (OR 17.16). Odds ratios are approaching 1 for the other variables, indicating a weaker association to reports of illness. Having an ill household member and reporting a location for human waste disposal are the variables most strongly associated with reported illness from this model.

Table 3: Nonzero Coefficients from LASSO regression  
Variables associated with participant Illness reported in past year.

Variable	Coefficient	Odds Ratio
Ill Household Member	2.84	17.16
Treating Drinking Water	-0.01	0.99
Designated Location Present for Human Waste	-0.16	0.85
Camel Interaction	0.05	1.04

Livestock populations varied among communities. Ilmotiok has an estimated 10,000 sheep and goats, along with 4,000 cattle. In Lekiji, an estimated 6-7,000

sheep/goats and 400 cattle are held within the community. Mpala has an estimated 400 cattle, 2,000 sheep, and 90 camels. An estimated 1,000 sheep are present between both Ol Jogi sites. Wildlife estimates could not be accurately estimated between sites, but wildlife population densities are generally greater within and around the Ol Jogi wildlife conservancy. This is consistent with previous studies in Laikipia County, which report significantly greater wildlife densities in conservancy areas compared to non-conservancy areas (Georgiadis et al., 2007).

### ***Knowledge and Attitudes***

Of 34 people who experienced an illness and also had an ill household member in the past year, only 9 (26%) listed contact with sick people as a possible cause of illness (Table 4). When asked if worried about disease outbreaks among animals at local markets, 225 responded “yes” (69%). The questionnaire asks if there are risks associated with slaughtering or butchering if the participant has an open wound; only 44 (13%) overall made an association to risk of disease infection. Respondents most frequently reported that the behavior was risky, but did not know what the risks were (n=131, 40%). In addition, 94 (29%) reported “no” or “don’t know” regarding this risk. Participants also responded that this behavior could “make them sick” or “poison them,” with some participants reporting multiple responses. There was no significant difference in self-reported illness among participants who acknowledged a risk, versus participants who did not ( $p = 1$ ).

**Table 4:** Responses to questions regarding knowledge and perceptions, categorized by township and land use system.

		Total	Pastoralist		Commercial Ranching	Commercial Ranching/Wildlife Conservancy	
			Ilmotiok (n = 102)	Lekiji (n = 103)	Mpala (n = 53)	Ol Jogi-Maura (n = 51)	Ol Jogi-Pyramid (n = 18)
Worried about disease outbreak among livestock in markets?	Yes	225 (69%)	56 (55%)	89 (86%)	51 (96%)	21 (41%)	8 (44%)
	No	102 (31%)	46 (45%)	14 (14%)	2 (4%)	30 (59%)	10 (56%)
Are there any risks to slaughtering/butchering when you have an open wound?	Yes	233 (71%)	69 (68%)	82 (80%)	47 (89%)	27 (53%)	8 (44%)
	No	38 (12%)	19 (18%)	5 (5%)	4 (7%)	8 (16%)	2 (12%)
	Don't Know	56 (17%)	14 (14%)	16 (15%)	2 (4%)	16 (31%)	8 (44%)

### **Animal Production Module**

The 112 participants who reported “Animal Production” as their primary occupation were also administered a separate survey with questions relating to animal management practices. Table 5 shows the variation in responses by community. Ilmotiok and Ol Jogi Marura were the most likely to have bushmeat available on site, despite the fact that few in each community reported hunting wild game. There was no significant association between seeking veterinary care and experiencing outbreaks among livestock. Pastoralists in Ol Jogi-Marura and Mpala were the most likely to have sought veterinary care, while Ilmotiok pastoralists were least likely. Also, 15% of pastoralists in Ilmotiok reported an outbreak in animals during the past year, yet only 5% said animals were quarantined or destroyed. Only one participant who reported a livestock outbreak also

reported contact with a wild ungulate, and no participants who reported outbreaks had interactions with carnivores. This may suggest limited interactions between livestock and wildlife, which is useful for analysis of disease transmission mechanisms among animals.

**Table 5:** Responses to questions from the Animal Production Questionnaire (distributed only to participants who listed “Animal Production” as their primary occupation).

Animal Production Module (n = 112)			Pastoralist		Commercial Ranching	Commercial Ranching/Wildlife Conservancy
		Total	Ilmotiok (n = 65)	Lekiji (n = 18)	Mpala (n = 10)	Ol Jogi-Maura (n = 19)
Bushmeat available on Site?	Yes	76	51 (78%)	9 (50%)	1 (10%)	15 (79%)
	No	36	14 (22%)	9 (50%)	9 (90%)	4 (21%)
Outbreak among livestock in past year?	Yes	15	10 (15%)	3 (17%)	2 (20%)	0 (0%)
	No	97	55 (85%)	15 (83%)	8 (80%)	19 (100%)
Have livestock received veterinary care in the past year?	Yes	48	14 (22%)	8 (44%)	10 (100%)	16 (84%)
	No	64	51 (78%)	10 (56%)	0 (0%)	3 (16%)
Have animals been quarantined or destroyed in the past year because of disease?	Yes	6	3 (5%)	2 (11%)	1 (10%)	0 (0%)
	No	106	62 (95%)	16 (89%)	9 (90%)	19 (100%)

## **Community Engagement and Health Care Access**

Health care access is a significant driver of disease vulnerability. Access is highly variable among sites, and is determined by distance from the community, transportation, cost, and services provided. A private dispensary is located in Mpala township, which has a variety of medicines, vaccinations, family planning services, with a clinician on staff. However, the cost of treatment makes these services inaccessible to many community members. This is the closest clinic to Lekiji, which is seven kilometers away. Lekiji residents must access a vehicle in order to reach the clinic. A mobile clinic is available periodically to transport patients between Lekiji and Mpala, but this service is not always available. In the event that a patient is severely ill, they will be referred to Nanyuki hospital, which is an hour drive south. Ilmotiok, on the other hand, has a dispensary in the center of the group ranch that offers free preventative services, including vaccination and health screenings. However, no curative services are available. In addition, it is the only facility available within the 4,000 hectare group ranch. Households are distributed throughout the ranch, and access depends on proximity to the dispensary. Ol Jogi Marura has a clinic within the community, which is just a few hundred meters from the residences. The dispensary offers both preventative and curative services with a clinician on staff. Services are free of charge, and provided by the ranch management. This is the closest facility available to Ol Jogi Pyramid. Services are likewise free, but participants must arrange their own transit to reach Marura. Like Lekiji and Mpala, severe cases are referred to Nanyuki hospital. Nanyuki hospital has vehicles that can reach communities

and transport patients, but this service is not consistently available. There are no emergency services available to respond to these communities. Health education is also lacking. Public health groups may visit the communities once a year, but their focus is limited to family planning. Health care accessibility, community education, and community ownership of health outcomes are important and nuanced factors influencing risk of disease exposure in each community.

**Table 6:** Factors affecting health care accessibility by community

	Nearest Facility	Transportation	Cost
Ilmotiok	Ilmotiok (0-7 km)	1 facility, 4,000 ha ranch; few motorized vehicles	Free
Lekiji	Mpala (7 km)	Mobile clinic, not consistently available	Paid
Mpala	Mpala (0 km)	Unknown	Paid
Ol Jogi: Marura	Ol Jogi: Marura (0 km)	Walking Distance	Free
Ol Jogi: Pyramid	Ol Jogi: Marura (10 km)	Some motorized vehicles available	Free

## **CHAPTER FOUR: *PREDICT*-KENYA AND PERSPECTIVES FOR FUTURE EID EMERGENCE**

### **Overview**

Emerging infectious diseases are a growing concern of the modern world. Despite advancements in disease mitigation, such as vaccination and in-situ surveillance, ecological and behavioral factors continually drive disease spread. Global travel, human decision-making, and deeply rooted cultural practices all influence outbreak risk. Diseases affecting humans are most likely to originate with animals, making zoonoses of particular concern (Jones et al., 2008). This study, as a component of the global PREDICT project, represents a growing body of research that aims to assess behaviors, perceptions, and interactions that influence risk of disease spillover within complex human-wildlife-livestock interfaces (PREDICT, 2017). Factors affecting exposure risk must be identified at a community level in order to effectively implement mitigation efforts. Laikipia County contains high densities of wildlife that share land with livestock-dependent human communities, heightening opportunities for disease spillover. The objective of this study was to compare behaviors among land use systems in order to assess risk of human exposure to zoonotic pathogens. After identifying trends in behavior, a community engagement trip was held to discuss disease risk with locals, collaborating with community health volunteers to communicate findings.



The human behavioral questionnaire was designed to assess risk factors for disease spillover, including sanitation, food safety practices, human-animal interactions, and wildlife-livestock interactions. Collectively, these factors can be analyzed to assess relative exposure risk among communities of different land use types. Wildlife-livestock interactions indicate potential for disease transmission, especially between animals in within a taxa. Wild and domestic ungulates share common pathogens, such as brucellosis and Rift Valley Fever, which can then transmit to humans via consumption of animal products (Evans et al., 2008). Likewise, spread of avian influenza is a concern among poultry and wild birds. Further assessing human-livestock interactions therefore indicates the likelihood that livestock will serve as a “bridge” species in transferring pathogens to humans (Caron et al., 2015). Practices such as eating raw meat or eating sick animals put humans at greater risk of contacting pathogens of both livestock and wildlife origins (Bett et al., 2017). The results indicate that land use strategy is associated with variation in reports of high-risk behaviors. Distinct variation in reported behaviors was observed among communities, despite the relatively small geographical spread of the study (< 200 km<sup>2</sup>). Pastoralist communities exhibited the greatest frequency of reported high-risk behaviors overall, followed by the Commercial Ranching community. Wildlife Conservancy areas expressed the least frequent reports of high-risk behaviors. Little research has been done to date on the relationship between land use practices and human behavioral risk for disease spillover (Rajeev et al., 2017). This research provides evidence that land use that should be assessed to a greater degree in further studies when determining exposure risk in global disease hotspots.

## **Risk Assessment by Land Use System**

### **Pastoralist**

The two sites that employ a pastoralist management system (Lekiji and Ilmotiok) were most likely to report a series of high-risk behaviors that are known to increase likelihood of disease spillover. Interaction with live animals is a primary factor of exposure risk. Livestock populations are highest in these communities, and livestock freely wander through human settlements. Survey results do not reveal definitive information on human-livestock interaction frequency, but these communities expressed consistently high rates of interaction with all livestock species. Ilmotiok residents reported the highest rates of interaction with all domestic animal species, but Lekiji residents were least likely to report interactions with cattle. This is not necessarily significant for exposure risk, as sheep and goats are the primary source of livestock in both communities. Sheep, goats, and poultry were observed living in close proximity to humans throughout both pastoralist communities. Goats wandered freely around human dwellings, and droppings were observed throughout the communities. Efforts were made to improve sanitation, as Ilmotiok households heaped a majority of goat dung outside of their compounds. However, goat dung still covered the ground of many household areas. Contact with animal waste may increase risk of food and water contamination. Other sanitation issues, including a lack of human waste locations in Ilmotiok, implicates heightened risk of fecal contamination in drinking water. LASSO regression also revealed that having a designated location for human waste was associated with lower likelihood of illness reports among participants. Improper management of both human

and animal waste increases the risk of food and water contamination via runoff into waterways. A study by Conan et al. (2015) revealed that presence of animal waste and increased number of livestock in household compounds correlated to infection of diarrheal diseases among children in Western Kenya. This likely results from contaminants leaching into drinking water sources, or failure to wash hands after contacting waste. In order to serve as a protective factor, sanitation measures must be applied to both human and animal waste (Barnes et al., 2018). Human practices regarding sanitation are a prominent feature of pathogen exposure risk in pastoralist communities and must be addressed in future interventions.

In addition to human-animal interactions, other human behaviors lead to increased risk of disease transmission. Based on survey results, participants in pastoralist settings were least likely to treat water, while utilizing open water sources that are also used by animals. Poor waste management and failure to treat drinking water represents a clear risk of contamination and contraction of cholera, hepatitis, and other diarrheal diseases (Barnes et al., 2018). Report frequencies of other behaviors, such as eating raw or undercooked meat, and consuming animals found dead were significantly in pastoralist communities than in other land use systems. Furthermore, collecting animals found dead was significantly associated with self-reported illness in the chi square analysis of the general questionnaire. These behaviors can result in direct exposure to pathogens such as RVF, MERS, and Marburg virus (Anyangu et al., 2010; Gikonyo et al., 2018). Pastoralist communities are assessed to be at highest risk of pathogen exposure based upon data

from surveys that indicate high-risk behaviors in regard to food, water, and sanitation practices.

According to the Animal Production survey, livestock in pastoral communities were least likely to receive veterinary care. This precludes the identification and quarantine or destruction of sick animals. Combined with the common practice of consuming sick animals, these reported data provide evidence of high risk of zoonosis transmission from infected animals to humans. Consumption of animals during an outbreak is a high-risk behavior that must be addressed in future interventions. Contact with infected bodily fluids or consumption of products from ill animals have facilitated outbreaks of Rift Valley Fever in Kenya (Anyangu et al., 2010). In addition, a study by DePuy et al (2014) found high seroprevalence of Q Fever in sheep, goats, and camels in Laikipia County, which could spread to humans by contact with infected animals. In pastoralist communities, lacking veterinary care precludes disease detection and reveals a clear risk of human pathogen exposure.

Though interactions between domestic and wild animals are difficult to assess from the survey data, livestock roam freely throughout these pastoral areas. Wildlife and livestock are therefore likely to share water and graze resources, which are limited in these semi-arid regions. This resource overlap permits the indirect spread of diseases such as brucellosis and leptospirosis (Rajeev et al., 2017; Bett et al., 2017). In addition, vector-borne diseases, such as Rift Valley Fever, are known to perpetuate within both wild and domestic species (Baba et al., 2016). Little information was gathered regarding

inter-species interactions in these specific locations. However, previous research indicates that wildlife-livestock land overlap can perpetuate cycles of disease endemicity within a region, providing viruses an opportunity to propagate among diverse animal hosts. Close proximity of these animals may provide viruses such as RVF with a means of amplification (Baba et al., 2016). This, combined with close human-animal interaction, increases risk of spillover into human populations. Human-wildlife-livestock contact is readily observable with birds in both communities. Wild birds and chickens shared the same land, and chickens freely entered human dwellings. This could provide a direct transmission link for avian influenza, among other diseases (Caron et al., 2015).

In addition, the Animal Production module revealed that bushmeat is widely available at pastoralist sites, especially in Ilmotiok. Bushmeat can carry a wide variety of diseases, but is highly variable depending on species. Bats are a reservoir of Marburg virus, while ungulates may carry brucellosis or leishmaniasis (Zehender et al., 2016). Further assessment of risk should identify specific animals consumed in each region.

Despite the high report frequencies, behavioral variation is evident between the pastoralist locations. The vast majority of Ilmotiok respondents reported all high-risk behaviors, while Lekiji residents were significantly less likely to report eating raw meat and collecting dead animals to eat or sell. Though pastoralist communities exhibited an overall trend of high-risk behaviors, community-specific variation is still evident. Other factors are likely working to create nuanced differences in reported behaviors that were not covered in the scope of this survey. Cultural variation, land features, or animal distributions could influence these reported behaviors. Additional qualitative research

should be conducted to assess regional differences in community behaviors within similar land use categories.

### **Commercial Ranching**

Mpala is the only study location that relies mainly on commercial ranching as a land use strategy. This site was not available for observation during the community engagement trip, so evidence supporting this is derived solely from the behavioral questionnaires. Most high-risk behaviors are less frequently reported in Mpala when compared to pastoralist communities, but more frequently reported than in the wildlife conservancy communities. When considering questions related to food consumption (collecting dead animals, eating raw meat), response frequencies of Mpala are similar to those of Lekiji. However, Mpala expresses more protective factors related to water safety when compared to Lekiji. In addition, Mpala was most likely to report veterinary care, a significant protective factor. Though Mpala had the lowest reports of bush meat availability, the fact that it was reported at all within this small community indicates that the risk may be greater than is suggested in this survey. Proximity to other communities is an additional factor that may affect expressed behaviors, as Mpala and Lekiji are only seven kilometers apart. These data further demonstrate the variability of practices even within short distances. Associations in behavior between Mpala and Lekiji require additional research into community-level factors in order to understand the variation. Mpala is the only community in this study that exhibits commercial ranching as its primary land use system, which impedes comparison with other locations.

Human-livestock interaction was high for cattle, poultry, and sheep/goats. However, Mpala residents reported the lowest camel interaction rates. Species-specific interactions can determine disease risk. Camel interaction is a risk factor for MERS transmission. Though an outbreak has never been detected in Kenya, lower interaction with camels may serve as a protective factor. In light of rising camel populations in Laikipia, however, this dynamic has the potential to change. Mpala is near other communities, such as Lekiji, that have reported high rates of human-camel interactions. Laikipia County is also known to be a trade route for camels (Gikonyo et al., 2018). Assessing species-specific disease transmission routes relies on analyzing animal movement, climate change, and pastoralist preference as related to human-animal interaction. MERS risk in Mpala may be lowered due to contact patterns with camels, but these interactions occur within the scope of a rapidly changing county. Disease emergence must be continually monitored and addressed within the context of other related factors.

### **Wildlife Conservancy**

Participants from the Commercial Ranching/Wildlife Conservancy communities (Ol Jogi Marura and Pyramid) reported high rates of livestock interactions, however, this interaction is nuanced. Livestock roamed within the conservancy, but outside of the fenced communities. No ungulates or dung were observed within the community, indicating a reduced risk of fecal contamination of food and water sources. Similar to pastoralist communities, domestic fowl roamed freely in and out of human dwellings,

increasing potential for transfer of avian influenza, or other bird-borne diseases. Wild birds were also prevalent in each site, sharing land with the free ranging chickens. Interaction between wild birds, chickens, and humans was readily observable in household areas within each community observed. These observations enhance survey data, which indicates high rates of interaction with both birds and poultry. Based on the Animal Production questionnaire, livestock were highly likely to have received veterinary care, which supports overall health of the animals and reduces human risk of pathogen contact. However, risks of human-livestock interaction are compounded by livestock-wildlife interaction. Ungulates in the wildlife conservancy communities were free to roam through areas utilized by wildlife. This could lead to transmission of diseases such as brucellosis and leptospira from sharing of food and water resources between wild and domestic ungulates. In a study of disease prevalence among land use types in Laikipia County, Rajeev et al. (2017) found that *Leptospira*, a bacterial infection, was significantly higher in cattle within wildlife conservancy areas than in pastoralist areas. *Leptospira* can be transmitted via indirect means, such as contact with contaminated water or grazing resources. Wildlife populations are considerably denser in conservation areas of Laikipia County, indicating that wildlife-livestock interaction may facilitate transmission of this infection (Mureithi et al., 2019; Rajeev et al., 2014). The wildlife conservancy communities, though livestock populations are lower, may be at greater risk of wildlife-livestock disease transmission.

Despite the potential for livestock-wildlife disease spillover, Conservancy communities expresses relatively low frequency of behaviors that elevate risk of direct



pathogen exposure (i.e., consuming raw meat, eating sick animals). This serves as a protective factor against food-borne diseases that depend upon direct human contact. However, the question of bushmeat from the Animal Production questionnaire suggests another risk factor for exposure. Ol Jogi Marura was the most likely to report a presence of bushmeat available on site. This is another means of potential wildlife disease spillover that is difficult to assess from the data provided. Knowing that it is available, however, is important to better understanding local disease dynamics. Participants were also unlikely to treat drinking water, and likely to report sharing a drinking water source with livestock. Though direct contact may be a lesser concern in Ol Jogi, zoonosis transmission via contaminated drinking water is a risk factor for these communities. Water safety practices are more difficult to differentiate based on land use systems for this study. Ol Jogi-Marura expresses high risk behaviors in terms of water safety, though Ol Jogi-Pyramid expresses low risk. These sites utilize similar land use systems and are also in close proximity. Additional research of livestock watering practices may elucidate variation among the Ol Jogi sites. Overall, livestock-wildlife interaction is a potential risk factor for zoonosis spillover in Conservancy communities, but proper food safety practices are a significant protective factor. In areas where livestock-wildlife land use overlap is difficult to avoid, behavioral preventative strategies can be a practical defense against zoonosis spillover. However, these practices must also integrate safe drinking water practices while reducing bush meat consumption in order to provide greater protection.

### **Health Care Accessibility**

Access to health care is a significant driver of vulnerability to EIDs. Preventative and curative services available determine population susceptibility and severity of outbreak events. Higher vaccination rates result in greater collective immunity, and readily available treatments reduce rates of mortality and morbidity (Rwyemamu et al., 2012; Thumbi et al., 2015). Ol Jogi Marura has the greatest access to health care. Services are free and easily within walking distance of the community. One dispensary serves about 700 people including Marura and Pyramid. Mpala likewise has readily available health care, though services are less accessible due to the cost. Ol Jogi Pyramid subsequently has middling access to health care. This community can freely utilize the Marura dispensary, though the distance makes services less readily accessible. Pastoralist communities have the least access to health care. The Ilmotiok dispensary provides free services that parallel those of the Ol Jogi Marura facility. However, there is only one dispensary to service all 5,000 inhabitants who are distributed among the 4,000 hectares of the group ranch. Vehicles are also scarce within the ranch, further restricting community-wide access. Lekiji has the least available access to health care. Mpala dispensary is not only seven kilometers away, but the cost of services is prohibitive for most residents. Transportation, though periodically available, is not consistent. All considered, pastoralist communities are at highest vulnerability to an outbreak event. Along with expressing the greatest degree of high-risk behaviors, Ilmotiok and Lekiji also have the least access to preventative and curative treatments.

### **Perceptions and Understandings**

Results from the general questionnaire indicate limited understandings of disease transmission mechanisms within the communities. The most significant risk factor associated with self-reported illness was having an ill person in the household. However, a minority of individuals who reported self-illness in addition to illness of a household member associated contact with sick people as a cause of illness. This could indicate a lack of understanding regarding human to human transmission, however, the data available do not inform whether or not the illnesses suffered were contagious. Depending on the illness, contact with sick people may or may not be an actual cause of disease. Multiple ill people in the same household could also be related to sharing the same contaminated food or water source, or contact with sick livestock. However, in the event of an unidentified illness, avoiding direct contact with ill people serves as a protective behavior reducing the likelihood of spread. Additional research into understandings of communicable disease spread should also be conducted to elucidate perceptions of disease risk in all communities.

Concern over disease in general varied among locations. Participants from wildlife conservancy communities were least likely to report concern over disease outbreak in markets. They were also least likely to associate risk with slaughtering or butchering with an open wound. While these results are interesting, there is little other data available to assess the reasons behind these perceptions. Even so, this information is useful when developing interventions. Community engagements should emphasize

blood-borne pathogens as a transmission mechanism, and train locals on safe practices when handling recently killed animals. Few questions on the survey assessed perceptions, precluding detailed assessment of local knowledge of disease risk. However, these details can be used to develop more in-depth questions on beliefs and local knowledge surrounding diseases.

### **Implications for Future Disease Emergence**

Human-animal interaction, poor sanitation, and unsafe food practices are known transmission routes for several zoonoses affecting humans in Laikipia county. Rift Valley Fever, Brucellosis, Q Fever, and numerous other febrile illnesses have been identified in this county, resulting in livestock losses and human fatalities. These EIDs may be transmitted from animal to human hosts via contact with contaminated meat or body fluids (Anyangu et al., 2010; Salerno et al., 2017). Higher reports of these activities may indicate greater risk of exposure to zoonotic pathogens via direct contact with animal products in pastoralist communities. Lower instances of these behaviors may serve as a protective factor against zoonosis spillover in communities that implement wildlife conservancy/ranching economic strategies.

In 2017, an unidentified tick-borne outbreak among ungulates in Laikipia County resulted in die-offs of buffalo, impala, and domestic cattle (ProMED-Mail, 2017). The following year, an RVF outbreak spread to nine different counties in Kenya. Laikipia, though no cases were reported, is situated in between Isiolo, Meru, and Baringo counties, which all reported RVF outbreaks. Though both of these incidents are of unknown origin, human migration patterns are cause for concern (ProMED-Mail, 2018). Pastoralists from

neighboring counties regularly come to Laikipia to graze. From 2016-2017, pastoralists illegally brought livestock to graze in conservancy land, resulting in local conflict (ProMED-Mail, 2017). This unrestricted movement presents a challenge for disease mitigation, as pathogens may spread with migrating livestock. Underlying these behaviors are complex conflicting beliefs of land ownership and access rights. Abnormally heavy rains and resulting increases in mosquito populations are suspected to have initiated the 2018 RVF outbreak (ProMED-Mail, 2018). Following amplification in ungulates, humans contracted the disease via mosquito bites or consumption of infected animal products. Livestock movement through wildlife-dense areas can facilitate endemism of RVF, brucellosis, leptospira, and other zoonoses. Human behaviors, in terms of sanitation and food consumption practices, can then lead to risk of transmission (Rajeev et al., 2017; Bett et al., 2017; Baba et al., 2016). Drivers surrounding these recent outbreaks present implications for risk assessment from this study. Conservancy communities therefore could have the greatest risk of overlap, but protective behaviors may reduce risk of spillover. Pastoral communities, with high livestock densities sharing land combined with high-risk behaviors, increases risk of pathogen exposure.

In general, close contact with animals is a key feature of pastoralist societies, and animal products constitute the majority of the diet. Higher proportions of animal product consumption, especially if products are undercooked or unpasteurized, increases risk of exposure to zoonoses (Bett et al., 2017). Livestock interaction with wildlife further exacerbates this risk, exposing domestic animals to a wider range of diseases, or allowing disease cycles to perpetuate between wild and domestic communities (Jones et al., 2017).

Meanwhile, communities with mixed economic strategies do not depend solely on livestock for sustenance. Supplementing economic systems with tourism or agriculture may limit human dependence, and therefore high-risk interactions, with livestock. Though domestic animals are still an important feature in the ranching and wildlife conservancy communities from this study, less overall high-risk interaction was reported. Decreased rates of interaction may yield lower rates of exposure to diseases. Even so, this economic supplementation is not always feasible due to cultural or logistical constraints. Laikipia County has high elephant populations, which often destroy crops and discourage locals from agricultural activities (Smith et al., 2016; Gadd, 2005). In addition, low rainfall limits the growing season in these semi-arid regions (Herrero et al., 2010). Ecotourism has succeeded in diversifying local economies and facilitating development throughout Kenya (Mureithi et al., 2019). Many residents of the Ol Jogi communities are employed by the conservancy as security workers, laborers, and teachers; these opportunities are less accessible in pastoralist and commercial ranching areas. This diversification can limit livestock interactions, which may reduce threat of spillover. However, conservancies cannot serve as a model for diversification in every context. Successful ecotourism requires high startup capital and infrastructure that enables tourist access. Tourism sites must also be reasonably safe and contain features desirable for tourists (Mureithi et al., 2019). While this information is important in assessing local disease risk, it is difficult to implement as a solution for economic diversification in new settings, as culture and financial limitations impede successful implementation. If economic diversification is identified as a promising mode of reducing disease

transmission, local concerns must be addressed to build sustainable solutions (Gadd, 2005). This connection to economic sustainability further demonstrates the link between resource access and disease susceptibility.

This study provides insight for future disease surveillance efforts within high-risk human-wildlife-livestock interfaces in Kenya. Projections of climate change and population growth carry significant implications for disease dynamics within land use structures. With the Kenyan population expected to more than double between 2016 and 2050, livestock populations in rural areas are expected to rise exponentially to meet the growing food demand. In addition to a growing population, GDP is expected to rise. As is consistent with global trends, Kenyans with higher incomes tend to purchase more animal food products, indicating that the demand for meat and milk may rise at a greater rate than is expected solely from the population increase (Food and Agriculture, 2017). Intensification of livestock production will likely follow, which correlates to greater herd densities that increase risk of communicable livestock diseases (Liverani et al., 2013). Veterinary care, which is already lacking, may become even sparser as populations increase. In the event of an outbreak, disease containment measures may also become more difficult (Liverani et al., 2013). Greater livestock densities are also correlated to increased presence of food and water contamination in communities that lack proper waste disposal systems (Conan et al., 2017). Though an outbreak has never been detected in Kenya, interaction with camels may serve as a risk factor for MERS exposure. In light of rising camel populations in Laikipia due to increasingly arid climate, this dynamic has the potential to change. Laikipia County is known to be a trade route for camels (Gikonyo

et al., 2018). Assessing species-specific disease transmission routes relies on analyzing animal movement, climate change, and pastoralist preference as related to human-animal interaction.

Increases in livestock density may also result in greater overlap of wildlife-livestock resource use. Compounded with impacts from climate change, resource use may further overlap as suitable water and graze land become scarcer. Livestock expansion may result in increased disease transmission between wildlife and livestock populations (Gorsich et al., 2015). Throughout the Laikipia, pastoralists, commercial ranchers, and conservancies compete for land with variable livestock-wildlife interactions. The majority of wildlife in Laikipia are located within conservancies. Some regions report high rates of wildlife-livestock land use overlap (Gadd, 2005), while others report that wildlife densities decrease in the presence of livestock with resource partitioning expressed between wild and domestic animals (Georgiadis et al., 2007). Animal behavior is furthermore influenced by species composition and human land use strategies (Georgiadis et al., 2007; Riginos et al., 2012). These varied reports reveal the need for detailed research on animal interactions and land sharing within livestock management systems. Wildlife-livestock interactions may shift even further in the event of increased animal densities and resource scarcity, making it increasingly difficult to predict future resource use overlap. Therefore, changing environmental conditions and human interaction may yield increased risk of pathogen spillover if livestock and wildlife are driven to utilize the same resources. Results from this thesis research indicate that livestock and wildlife coexist near human communities, presenting the risk for inter-



species disease spread. Wildlife densities are greater in conservancy areas with lower livestock populations. This indicates increased risk of disease spillover from wildlife, but the potential for resource partitioning must be considered when assessing this risk (Georgiadis et al., 2007). Though there is still considerable research that needs to be done, these data reveal the opportunity for spillover when wildlife and livestock share land. Changing climactic conditions must be continually assessed in order to understand shifting disease dynamics among animal populations, within the context of human land use change. Additional research can elucidate how animal movement patterns and wildlife-livestock interactions affect spillover risk in conservancies and pastoral areas. Identifying emerging pandemic threats is a crucial step to mitigating disease spillover in the face of changing population dynamics.

### **Limitations and Recommendations**

PREDICT aims to assess risk of disease spillover in disease hotspot regions worldwide. A primary feature of this assessment is human behavioral questionnaires that ask participants to self-report behaviors that may increase risk of pathogen exposure, particularly relating to animal interactions. Questionnaires were distributed in 29 countries, which will be used to analyze trends in high-risk behaviors in the world's most prominent disease hotspots. However, some limitations preclude definitive assessment of these reported behaviors. As with any survey, reliability of the results depends on participant's accuracy in self-reported behaviors. Community Health Volunteers, who are trusted representatives within their communities, facilitated the research process and encouraged accurate reporting among locals. However, there is a chance that responses

were not accurately reported. For example, one question asks participants if they had hunted or trapped an animal in the past year. Hunting wild game is illegal in Laikipia County, and participants may be reluctant to report illegal behaviors, even if informed that their response would not be traceable. In addition, a follow-up question on the Animal Production module indicates that bushmeat is readily available on most sites. Though only eight participants reported hunting on the general module, there is a likelihood that more participants engage in this activity.

Certain questions on the questionnaire were ambiguously worded and difficult to extract meaning during analysis. For example, participants were asked if their drinking water source has been used by “animals”, without differentiating between wildlife and livestock. Observation from the community engagement trip suggested that all animals used the same water source in each community, however, this is not evident solely based on the survey. In addition, one question asks whether participants “cooked or handled meat, organs, or blood” from an animal. This covers a broad range of activity and does not provide additional information to the rest of the survey. Questions would benefit from being tailored to provide more context. Many questions permitted only a “yes/no” response. While this is useful for gaining a baseline of data for overall presence of behaviors, questions that assess drivers of behavior would enhance researcher understandings of these drivers. The survey contained only three questions about participant perceptions. When studying disease dynamics, assessing reasons for behavior is critical to understanding the risk underlying the behavior itself (Ng’ang’a et al., 2016). Overall, survey questions were not context-specific. This is useful for comparing

responses among study countries, but impedes detailed analysis at a local level. An additional questionnaire tailored to each study site would aid in assessing local drivers and perceptions of disease spread. For example, detailed questions about livestock management practices known to exist in Laikipia county would allow researchers to further analyze effects of land use on behavioral variation. The survey contained no questions about land use. The association between land use and human behavior dynamics was only discovered after discussing Laikipia-specific information with local PREDICT researchers. Collaborating with local experts in developing the questionnaires would allow researchers to further target relevant issues that drive disease dynamics. Future studies could incorporate an abbreviated global questionnaire and a site-specific questionnaire, which would provide detailed data both for global comparison and local risk assessment.

PREDICT aims to implement mixed-methods research by integrating quantitative and qualitative methods to better understand behavioral drivers and perceptions underlying disease dynamics. Qualitative methods, such as focus group discussions, were implemented in several focus countries. However, limitations with IRB approval and budget restrictions precluded qualitative assessment in Kenya. As a result, contextualized analysis of questionnaire responses is difficult to assess. Observational data gathered during the community engagement trip was helpful for framing the study sites and understanding some situational factors that influence relevant behaviors. However, I was not able to report on the full range of topics of interest due to lacking IRB approval. Several CHVs mentioned that they would like to better serve their communities by

accessing training programs on health education. Many did not have any formal training and learned about behavioral drivers of disease spread through interactions with PREDICT researchers. CHVs are a crucial element of this project. Without their local power and influence, communities would be much less likely to participate in the study and receive recommendations for disease mitigation. Lacking training for CHVs is a significant, yet addressable, limiting factor. Their local knowledge and community rapport is essential to this project, and their support facilitates the overall goal of encouraging communities to reduce risky behaviors and implement protective strategies. Diverting resources to provide training to these individuals would be an efficient means of informing a community via a trusted messenger. Providing training for one individual would result in localized and practical knowledge dissemination to an entire community. Developing regional capacities is a core goal of the PREDICT program, and supporting local health workers is the most direct and efficient means of engaging communities.

### **Conclusion**

Understanding disease exposure risk depends upon contextual and localized understandings of ecology, human behaviors, and animal distributions. To date, little research has been done on land use as a driver of zoonotic disease transmission and behavioral variation. This study, as part of the PREDICT project, revealed significant variation in high-risk behaviors as delineated by human land use strategies. Pastoralist communities expressed the greatest behavioral risk of direct contact with pathogens, while communities within a wildlife conservancy expressed the least risk. In addition,

communities with the highest risk behaviors also had the lowest overall access to health care. These trends are nuanced, as communities that were geographically closer also expressed similarities in reported behaviors. Geographic location and cultural features that were not assessed in this study likely influence these behaviors, with implications for disease risk. However, these results indicate an association between land use system and overall risk of pathogen exposure and vulnerability. Poverty is a significant underlying factor in these communities. Pastoralist communities in Laikipia County tend to be less wealthy than Conservancy communities, which receive funding from private owners. Poverty can be associated with health care access, as the Ol Jogi conservancy had access to free services provided by the ranch owners. Ilmotiok also received free services while Lekiji did not, though distance served as a significant limiting factor for health care in both contexts. Human behavioral variation, while linked to land use structures, is also influenced by poverty. This relationship is difficult to disentangle, as pastoralist communities in this study were the least wealthy. Climate change vulnerability is also a factor of land access and poverty, as disadvantaged communities in Kenya are most likely to be impacted by decreasing availability of water and graze resources (Opiyo et al., 2015). Human behaviors are also shifting in adaptation to this changing environment, as evidenced by increased herder preference for camels (Browne et al., 2017). These rapidly changing conditions make the future of disease emergence in Kenya difficult to predict. Further studies should assess the interaction of animal management practices, herd densities, and wildlife presence on disease risk.

Mitigation efforts of human behavioral risk factors should include basic education programs to affected communities. Many high-risk behaviors are avoidable, but communities often lack awareness of illness symptoms and self-protection. Efficient education programs should empower community health workers that already hold positions of power within their communities, while providing a greater understanding of disease risk. Providing targeted training for these key individuals can result in efficient dissemination of public health information. Partnering with locals to a greater degree enables community access and bolsters PREDICT goals of creating sustainable and culturally appropriate solutions to EID emergence.

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## **BIOGRAPHY**

Elizabeth Ashby received her Bachelor of Science in Biology from Christopher Newport University in 2013. She worked in various wildlife research positions before enrolling in a Master of Science at George Mason University in 2017, where her interests became focused on emerging infectious diseases. Her research in human behavioral drivers of zoonotic disease transmission blends her interest in human culture and human-animal interactions.