Global Scenario of Wild Animal Disease Prevalence and Transmission in One Health Perspective

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SUMMARY

Zoonotic diseases are accountable for more than 60% of total infections in humans that are associated with long-term interactions among animals and humans. Wild animals are considered as fundamental pathways underlying the pathogenesis of various zoonotic diseases. A plethora of research has revealed that most emerging infectious diseases are linked with various sorts of wild species including the wild bats that are well known for hosting viruses. However, the occurrences and prevalence of these infectious diseases are due to a wide range of anthropogenic activities. Different preventive indications as well as cross-sectoral collaboration can prevent the onset of these diseases. Nevertheless, various sorts of challenges including the lack of data are indispensable to address. Researchers have emphasized "one health approach" to combat these infectious diseases. This chapter has discussed a wide range of infectious diseases, underlying factors and primary challenges to combat these diseases.

INTRODUCTION

Zoonotic diseases which include about 60% of all known infectious diseases in humans, have been present throughout human history and are linked to both human interactions with animals and environmental factors. Researchers found that wild animals were the source of almost 70% of newly discovered zoonotic disease cases between 1940 and 2006 (Jones et al., 2008). Before the year 2000, the primary focus of research on wildlife diseases was to enhance the survival and well-being of zoo animals. There was a shortage of literature on diseases that affected free-living wildlife, except extensively targeted animals such as North American deer, or diseases that threatened cattle health, such as rinderpest and tuberculosis. Non-communicable illnesses, such as DDT poisoning in raptors, have long been acknowledged as significant causes of species reductions (Baker et al., 2022).

ZOONOTIC DISEASE EMERGENCE FROM WILDLIFE

Daszak et al. (2000) identified wildlife as the reservoir for several high-impact, newly emerging human illnesses. The concept that most emerging diseases start in animals and spread to human hosts as a result of various ecological, demographic, and socioeconomic changes was reaffirmed by these authors (Krause, 1992; Lederberg et al., 1992; Morse, 1995). The Ebola and Marburg viruses, HIV-1 and HIV-2, Sin Nombre virus, Nipah, Hendra and Menangle virus, West Nile virus, Borrelia burgdorferi, and other illnesses with animal origins were known to exist before 2000. Since then, further discoveries have been made on the patterns of zoonotic disease development, and more human illnesses, such as Middle East respiratory syndrome (MERS) and many subtypes of avian influenza, have been linked to animals. Numerous studies examining an inventory containing all documented human EIDs discovered that most have biological connections, with viral making up a sizable portion (Taylor et al., 2001; Woolhouse et al., 2001; Woolhouse et al., 2002; Woolhouse et al., 2005). After a rationalized form of this databank was examined further, it was found that the frequency of EIDs had grown (even after controlling for the increase in researchers) and that during the final forty years of the 20th century, a significant increase had occurred in the percentage of EIDs arising from animal hosts. (Jones et al., 2008).

Daszak et al. (2000) emphasized the rise in bat-origin viral EIDs in humans in the 1990s. Since then, research has demonstrated that bats act as carriers for an astounding variety of infectious agents, particularly well-known infections with significant mortality ratios, such as filoviruses, SARS-like

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coronaviruses, Nipah and Hendra paramyxoviruses, and maybe even MERS coronavirus. (Memish et al., 2013; Calisher et al., 2006). Because of this, a few authors have suggested that, in comparison to other mammalian groups, bats contain an excessive quantity of newly developing zoonoses (Dobson, 2005; Wang et al., 2006): a theory that has been validated by two independent assessments of datasets related to mammal viruses. (Luis et al., 2013; Olival et al., 2013). Understanding how bats host numerous infectious diseases that cause serious illnesses in humans and how bat-to-human spread occurs is necessary for controlling these and perhaps undiscovered ailments (Morse et al., 2012; Wood et al., 2012; Luis et al., 2013; Luis et al., 2015).

DRIVERS OF DISEASE EMERGENCE

Novel disease emergence is likely to have many causes, but one important one has been identified as the human-directed movement of pathogenic entities or vectors (frequently contaminated hosts) across geographic or ecological boundaries. "Pathogen pollution" is the term for this process, which significantly impacts plants (Anderson et al., 2004) and animal life (Cunningham et al., 2003). Several well-known animal EIDs, such as B. dendrobatidis and B. salamandrivorans, the two main sources of frog chytridiomycosis, have emerged as a result of the anthropogenic spread of infections (Fisher et al., 2009; Martel et al., 2014). Ancestral meiosis has produced an individual hybridized genesis for the global pandemic lineage of B. dendrobatidis, possibly through human-caused environmental merging of allopatric lineages (James et al., 2009; Farrer et al., 2011). However, further research suggests that this is just half of the tale. A large number of investigations show how this virulent lineage was originally spread over the world by frog trade and the emergence of exotic species with human aid (Gilbert et al., 2012; McKenzie & Peterson, 2012; Peel et al., 2012; Schloegel et al., 2012; Liu et al., 2013).

The concept of disease prevention as a community function has evolved in several recent publications. Although this theory is still up for debate and probably not applicable to all situations (Johnson & Thieltges, 2010), it contends that biological diversity limits the possibility of infectious agents spreading from wildlife to humans by reducing or preventing the effects of various infectious agents, such as pathogenic ones (Salkeld et al., 2013).

As demonstrated by the hantavirus (Suzan et al., 2009) and B. burgdorferi, the causal agent of Lyme disease (Ostfeld & Keesing, 2000; LoGiudice et al., 2003), the environment facility favours, and transmissible infections are much more prone to occur when biodiversity is reduced (typically by human actions). Furthermore, rather than a loss of biodiversity in and of itself, changes in species complements-again, generally the result of human impacts can affect infection dynamics and raise the threat of zoonotic diseases (Kilpatrick et al., 2006). However, we still don't fully understand how changes in ecosystems, the control of disease, and human health interact.

Policies to lower risk have not been implemented with much of an effort since the hazards that wildlife EIDs represent to human health and conservation were first brought to light, nearly 20 years ago. To stop the spread of several domestic animal illnesses that are important for the economy or public health, it is common practice to identify and stop the importation of affected hosts. Some nations even use this concept for international travel, conducting (often haphazard) monitoring for sick individuals entering at their borders, especially in the event of a pandemic (Cetron & Landwirth, 2005; Waterman et al., 2009).

Possibly aware of this, the USA banned the importation of salamanders in the first month of 2016 following the finding of B. salamandrivorans, most likely to protect local wildlife from this uncommon infection. Such preventive intervention was swiftly implemented after B. salamandrivorans was identified as a new and dangerous fungal infection that infects and kills salamanders in captivity as well as in the wild in Europe (Martel et al., 2014; Martel et al., 2013; Cunningham et al., 2015). To protect ecosystems from the transmission of illnesses by humans, it is hoped that this will open the door for other nations to implement trade limitations for other illnesses. There are ongoing challenges to discovering the animal source of infectious EIDs. Finding the background of freshly emerging human diseases is sometimes exceedingly expensive, long, logistically complex, and difficult. For instance, in the early 1980s, viruses resembling HIV/AIDS were found in non-human primates; nevertheless, it took nearly ten years of further research to identify the genuine progenitor viruses in chimpanzees (Gao et al., 1997).

Comparably, research on the sources of the Ebola and Marburg viruses has lasted for more than 30 years. On the other hand, conclusive confirmation of Marburg disease in bats is currently limited to specific regions, while suggestions that these viruses naturally occur in bats (Amman et al., 2012; Amman et al., 2015; Jones et al., 2015). Finding the potential reservoir host or host is simply the initial phase; understanding the ecology of the virus in its native host or hosts as well as interactions between humans and hosts is essential to decide which measures are necessary to prevent or limit future zoonotic transmission (Wood et al., 2012).

ENDEMIC ZOONOTIC DISEASES ORIGINATING FROM WILDLIFE

Over the last 20 years, EID events, even though very few people have been diagnosed with them, have been the subject of much investigation. Human society's intolerance to ambiguity, or, to put it another way, our dread of the unknown, is most likely the reason for the increased attention on EIDs. This might affect bizarre situations where people's dread of getting sick can have a bigger effect than the actual effects of the wide-ranging. For example, at the peak of the current Ebola virus pandemic in West Africa, it is thought that malaria killed more individuals than the several hundred casualties the virus directly caused because people avoided hospitals out of concern about contracting the illness (Plucinski et al., 2015). In fact, when one looks at the whole effect of infectious illnesses on the inhabitants, the most common (identified) affliction is linked to properly recognized, but often ignored (in the industrialized north) ailments like rickettsioses, brucellosis, and Rift Valley fever. Since scarcity is a key threat aspect for the majority of zoonoses, certain clusters are disproportionately affected by the burden of zoonotic infections. As a result, the global poor bear a heavy weight of this predicted burden (Halliday et al., 2015). Neglect of these diseases extends to historical and contemporary research neglect, analytical negligence [misperception of other ailments such as malaria (Jephcott et al., 2017)], and treatment neglect. The achievement of the Viable Expansion Aims set out by the United Nations would significantly lessen the burden of zoonotic disease and lead to greater health and a significant decrease in poverty.

ONE HEALTH INTERVENTIONS FOR WILDLIFE DISEASE MANAGEMENT

One Health interventions for wildlife disease management encompass a multifaceted approach aimed at mitigating the extent and impact of infections in wildlife populations while considering the interconnectedness of human, animal, and environmental health. The management of wildlife diseases can be made possible by considering surveillance and monitoring programs, habitat conservation and restoration, vaccination and disease control measures, and most importantly policy intervention and legislation (Erkyihun & Alemayehu, 2022).

Habitat conservation and restoration

Wildlife conservation and wildlife rehabilitation programs are aimed to protect and restore the habitats required for the health of wildlife and its ability to adapt. Conservation issues including habitat destruction through activities that include deforestation, urbanization, and pollution pose additional stress on wildlife and lead to the spread of diseases among the animals. Conserving substantial habitats, creating wildlife boulevards, and practicing desirable terrestrial stewardship keeps threats from destruction and fragmentation, and enables better health and well-being of wildlife populations (Aronson et al., 2020).

Vaccination and disease control measures

Vaccination and disease control measures entails the identification of appropriate measures to prevent or even treat particular wildlife diseases. These vaccination programs are used with the intention of vaccinating vulnerable population with effective doses of the specific pathogen or viruses which are then expected to lower disease prevalence within the identified wildlife population units. Furthermore, disease control measures may involve settings measures like quarantines, populace controlling measures and essential treatments in case of disease outbreaks so as to reduce the impact of these diseases on the wildlife. Such interventions are usually disease-specific and consider the habitats of the diseases in which the diseases emerge (Schreiner et al., 2020; Edward et al., 2021).

CHALLENGES AND OPPORTUNITIES

Challenges and opportunities in wildlife disease management present a complex landscape, requiring concerted efforts and innovative approaches to address emerging threats and capitalize on potential advancements.

Cross-sectoral collaboration challenges

A key weakness in the strategy for coping with diseases in wildlife consists in the lack of communication and cooperation between different fields belonging to the human-animal-environment system. Integration deficits inherent in silo approaches that characterize governance structures mean that there are disconnects in areas such as surveillance, response and resource mobilization. To overcome such obstacles, it is important to encourage collaboration between professionals from different field and improve the methods of sharing the information between them, as well as increased awareness about the connections between human, animal and environmental health. Such cross-referral encourages various players within the One Health concept to harness the different knowledge set and assets and come up with an array of sustainable approaches to wildlife disease control systems (Machalaba & Sleeman, 2022).

Data and surveillance gaps

The lack of coordinated, centralized, and up-to-date data constitutes a major challenge to the comprehensiveness of approaches that would enhance understanding the wildlife disease dynamics. Lack of surveillance contributes to poor identification and intervention of new diseases in distinct geographical areas and puts at risk the wildlife populations for disease outbreaks and spillovers. Also, other hindrances such as inadequate funding, insufficient technical competence, as well as difficulties in the organizational and logistical arrangements also compound the efforts of data collection, as well as surveillance. These gaps must be met by increased investment in effective surveillance programs supported by advanced approaches like remote sensing and genomics as well as by active collaboration with local communities and citizen scientists. Through increasing recall, organization and regularity of data acquisition and reporting, all stakeholders will be in a better position to make decisions concerning the reduction of wildlife disease hazards selectively (Carlson et al., 2021).

Opportunities for innovation and research

Nevertheless, there is much potential for growth and future advances in the appreciation of illness and invention of new technologies and experimental techniques to control and modulate those zoonotic diseases from the one health viewpoint. Notes, for instance, machine learning, modeling, or genomic data for effective and efficient identification of the novel germs, routes of spread, and outlooks of zoonotic diseases in animals. In addition, the synthesis collaborations allow for cross-over of knowledge and ideas, ideas in various fields including in developing vaccines, surveillance mechanisms, and disease control by considering ecosystem approaches. Thus, increasing the amount of funding for research and promoting the culture of innovation, the stakeholders can use scientific breakthroughs in the emergence of new threats and enhance the applicability of approaches to the prevention and control of wildlife diseases in the framework of the One Health concept (Buregyeya et al., 2020; Osterhaus et al., 2020).

CONCLUSION

We have identified key pillars of action, including robust surveillance and monitoring programs, habitat conservation efforts, targeted vaccination campaigns, and policy interventions. However, the path forward is not without its challenges, as highlighted by barriers to cross-sectoral collaboration, data gaps, and the ever-evolving nature of emerging threats. Therefore, a call to action is essential. It is incumbent upon stakeholders across sectors to strengthen partnerships, integrate wildlife health into global health agendas, and elevate public awareness and education efforts. By spending time in exploration, innovation, and capacity-building initiatives, we can improve our understanding of wildlife disease dynamics and develop effective interventions within the One Health framework. Through collective action and shared responsibility, we can pave the way toward a more resilient and sustainable future where the health of humans, animals, and ecosystems is safeguarded for generations to come.

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