Control of Potential Hazards of Zoonosis towards Threatened Wildlife Population

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Abstract

Zoonotic diseases are infectious illness that spread from non-human vertebrate to human and can also be transmitted from human to non-human vertebrate. These diseases are mainly caused by various viruses and parasites. Different type of diseases appeared as potential hazards for threatened wildlife species that cause visible decline in their population. Many mammals including the endangered Amur leopard species, are afflicted with CDV, a virus that damages epithelial tissue, causing a wide range of clinical problems. Mountain gorillas are susceptible to human pneumovirus from Pneumoviridae family, a respiratory infection transmitted from humans to mountain gorillas. Domestic dogs are a rabies reservior which is an infection with a genotype of single stranded RNA viruses from Rhabdoviridae family and rabies poses a threat to Ethiopian wolves, potentially leading to a rapid drop in their number. The threatening crayfish plague in freshwater crayfish imposes a significant impact on the individuals and it is infected by *Aphanomyces astaci* causing fatal symptoms. For endangered wildlife populations to be conserved, possible zoonotic threats must be controlled.

Keywords: Zoonosis, Infectious diseases, Wildlife, Pandemic, Pathogens, Chronic, Epidomology, Control

Cite this Article as: Manal R, Mariam L, Iftikhar MS, Asif M, Ilyas Z, Toor H, Saeed S, Hashir M and Jutt M, 2025. Control of potential hazards of zoonosis towards threatened wildlife population. In: Abbas RZ, Akhtar T and Jamil M (eds), Pathways of Infection: Zoonoses and Environmental Disease Transmission. Unique Scientific Publishers, Faisalabad, Pakistan, pp: 120-125. https://doi.org/10.47278/book.HH/2025.211

A Publication of
Unique Scientific
Publishers

Chapter No:
25-017

Received: 29-Feb-2025
Revised: 25-March-2025
Accepted: 12-Apr-2025

Introduction

The origin and spread of various infectious diseases are significantly influenced by humans, animals and the environment (Thompson & Kutz, 2019). While animals are majorly responsible for these infectious diseases. Undomesticated animals and uninhabited plant species that can survive in their natural habitat are referred to as wildlife, but the term has expanded to encompass any living things that naturally develop or exist in a region without human intervention (Usher, 1986). Over 60% of the newly discovered human infections are zoonotic with more than 70% of these viruses come from the wild animals according to the Asia Pacific strategy for emerging diseases, 2010 report (WHO, 2010).

An infection that naturally spreads from vertebrate animals to humans or the other way around is known as a zoonotic disease (Rahman et al., 2020). The amount and percentage of these diseases that emerge in wild animals in particular has grown significantly in the last several decades, even after taking into account increasing reports of novel emerging infectious diseases (Jones et al., 2008).

Mycobacterium leprae caused a pandemic disease called Leprosy. Leprosy epidemics have occurred in ancient Greece, India, and the Middle East since 23 AD (McLeod and Yates, 1981). *M. leprae* is the main cause of the chronic illness leprosy. This infection is most likely transmitted to humans by the armadillo species (da Silva et al., 2018).

Tuberculosis, caused by *Mycobacterium tuberculosis*, is a contagious illness that has posed a significant socioeconomic issue throughout history. The sickness was recognized. "King's evil" refers to France and England. In 1720, TB was identified as an infectious disease, leading to the development of effective treatment methods (Barberis et al., 2017). Elephants most likely spread *M. tuberclosis* to humans (Michalak et al., 1998).

The H1N1 virus caused almost 50 million fatalities globally during the 1918 Spanish influenza pandemic (Taubenberger and Morens, 2006). Swine influenza emerged in 2009 and expanded worldwide. Swine influenza viruses can spread sickness to people of all ages. In 2009, the World Health Organization proclaimed an H1N1 pandemic, and over 70 nations reported over 30,000 instances of illness (Rewar et al., 2015).

The avian influenza virus caused pandemics in 1957 and 1968. It was caused by an H5N1 contagion with avian origin (Peiris et al., 2007) identified an avian-derived H5N1 virus as the culprit. The Ebola viral disease (EVD) outbreak began in Africa in 1976 and resulted in Ebola hemorrhagic sickness. The fatality rate of EVD among individuals is about 50% (WHO, 2020a).

Zoonosis can be caused by the numerous disease pathogens including viruses, bacteria, fungi, and parasites (Taylor et al., 2001). These disease causing agents can be transferred from animals to humans through a variety of pathways such as ingestion, animal bites, penetration through damaged skin, carriers (such as insects) and animal-human contact (Gauthier, 2015; Rahman et al., 2020) . There are different examples of zoonotic diseases that are transmitted to the wildlife animals and cause threatened wildlife population such as CDV, Human metapneumovirus (HMPV) in gorilla, Rabies in Ethopian wolf and Crayfish plague in *Austropotamobius pallipes*, etc.

Impacts of Zoonosis on Wildlife

Zoonosis in wildlife play a crucial ecological role but it also poses severe health risks to people, animals, and threatened species. It is believed that 2/3 of newly developing or reappearing infectious diseases are thought to originate from wildlife (Mathews, 2009).

Lately it has been recognized that the survival of endangered wildlife can be seriously threatened by disease (Smith, 1982; May, 1988; Lyles & Dobson, 1993). This can happen directly, when losses outnumber births, or indirectly, through effects on survival, durability, and fertility rates, which reduce the population size to the point where stochastic reasons could lead it to go extinct.

Because pathogenic species might persist in other hosts while causing the unusual host to go extinct, generalist diseases with a wide host range are particularly harmful (Begon & Bowers, 1995).

The possibility of a zoonosis spreading from wildlife to another host population whether people, domestic animals, or an endangered wild species is constantly impacted by a number of critical factors, regardless of the specifics of a given relationship. Important considerations include the degree and type of contact between infected individuals or infectious particles in the environment, such as infected feces, the size or density of the infected host population, the vulnerability of the in-contact animal, and the severity of infection in reservoir hosts (Mathews, 2009).

CDV in Amur Leopard

The viral disease infected by single stranded RNA virus from the family Paramyxoviridae is called canine distemper. The sickness is very contagious by inhalation (Deem et al., 2000). It is a disease of global importance that affects both common and endangered animals, and it is the second most prevalent cause of infectious illness mortality in dogs. Additionally, it is the cause of fatal encephalitis and neurological disorders in wild, endangered Amur Leopards (Seimon et al., 2013).

There are three primary stages viz, the virus replicates in lymphoid tissue during the first phase, which happens soon after exposure and is characterized by acute pyrexia and lymphopenia (Meli, 2010).

The Amur leopard (*Panthera pardus orientalis*) is a subspecies of leopard found in the Primorye area of southern Russia and northern China (Jeong et al., 2024). Tiger sightings in the Russian Far East and China are uncommon due to their small population and solitary and reclusive character; sightings of sick tigers are even more uncommon. Since 2001, reports of severe brain illness in several wild tigers have surfaced, suggesting that the endangered species is beginning to suffer from the condition.Reverse transcription-PCR, in situ hybridization (ISH), immunohistochemistry (IHC), and histology were used to analyze samples from five impacted tigers that perished or were eradicated in 2001, 2004, or 2010.Based on the findings, it is possible that two tigers' neurologic disease was caused by a canine distemper virus (CDV) infection, while a third tiger had a confirmed infection. CDV killed about 1 percent of Amur tigers in 2010.

The fact that positive cases are dispersed across a vast geographic range indicates that CDV is widely present in tiger habitat. As human populations increase and move into natural settings, interspecies interactions are becoming increasingly frequent. Finding CDV reservoirs in animals and the strains of the virus that may infect and spread across wildlife, such as sympatric severely endangered Amur leopards and Amur tigers (*Panthera pardus orientalis*) (Seimon et al., 2013).

Control of domestic dog, Amur leopard low-coverage vaccination, and extension of habitat are the three management strategies aimed at reducing the impact of CDV on the Amur leopard population. As the number of animals vaccinated annually rose, the size, survival probability, and genetic diversity of the population after 100 years increased to differing degrees for low-coverage vaccination of Amur leopards as a direct method of reducing CDV (Wang et al., 2023).

In order to prevent Ethiopian wolves from going extinct because of the rabies virus, low-coverage vaccination—that is, immunizing a tiny portion of the population—has been shown to be beneficial (Haydon et al., 2006). By restricting interactions between domestic dogs and leopards or by vaccinating domestic dogs, the CDV mitigation technique aims to lower the transmission to leopards. Nowadays, domestic dogs regularly encroach on the habitat of Amur leopards (Seimon et al., 2013; Gilbert et al., 2020). The Amur leopard's habitat area has grown with the creation of the national park on the Chinese side. They have also contributed significantly to the decline in the number of Amur leopards and the CDV epidemic among them (Fahrig, 2001)

Human Metapneumovirus (HMPV) in Gorilla

Human metapneumovirus (HMPV or hMPV) is a negative-sense single stranded RNA virus from the family *Pneumoviridae* (Rima et al., 2017). The close genetic relationship between mountain gorillas and humans has raised worries about the possible interspecies transfer of pathogenic pathogens (Hastings et al., 1991; Köndgen et al., 2008).

Infectious are an additional hazard to mountain gorilla populations. Second only to trauma, infectious illnesses, primarily respiratory, account for 20% of unexpected deaths (Mudakikwa et al., 2001). The last 786 mountain gorillas (*Gorilla beringei beringei*) live in two parks in Rwanda, Uganda, and the Democratic Republic of the Congo. All three countries have robust ecotourism industries that allow visitors to see human-habituated mountain gorillas in their natural habitat. Mountain gorilla tourism helps to ensure the species' survival by generating much-needed cash and raising global awareness of the animals' critical situation in the wild. Tourism, however, creates a risk of illness transfer from people to gorillas (Palacios et al., 2011).

The Incidence and severity of respiratory illness epidemics among mountain gorillas in the Virunga Massif have lately increased. From May to August 2008, four groups of mountain gorillas accustomed to tourism in Rwanda had sequential respiratory outbreaks In 2009, two wild mountain gorillas died as a result of an HMPV-related respiratory illness epidemic in Rwanda. One of these groups, Hirwa, had its fifth outbreak from June 28 to August 6, 2009 (Palacios et al., 2011).

Mountain gorillas have frequently contracted harmful respiratory viruses, mostly HMPV, from humans. The average distance between mountain gorillas and tourists is 2.7 meters, which is closer than the minimum 7-meter suggested distance (Sandbrook & Semple, 2006).

The governments of Rwanda, Uganda, and Congo limit the number of visitors and their vicinity in order to reduce the risk of disease transmission (Palacios et al., 2011).

Furthermore, residents of the neighborhoods around the mountain gorilla parks self-report significant rates of symptoms including fever (56.1%) and coughing (72.1%) (Guerrera et al., 2003). However, visitors, researchers, and park staff are asked to avoid seeing the mountain gorillas if they are feeling unwell (Cranfield & Minnis, 2007).

It is generally advised that anyone who is around mountain gorillas wear a surgical-grade facemask (Gilardi et al., 2015).

Since it is nearly impossible to enforce visitation restrictions for individuals who do not shed human pathogens, it is also important to enforce the maintenance of a safe distance between humans and gorillas more strictly in order to help prevent contact with infected respiratory droplets from both symptomatic and asymptomatic individuals (Mazet et al., 2020).

Rabies in Ethiopian Wolf

Rabies are caused by infection with a genotype of single stranded RNA viruses of *Lyssavirus* genus and *Rhabdoviridae* family (Rupprecht et al., 1995). Many wildlife species serve as rabies virus maintenance hosts. The United States recorded over 5,500 instances of animal rabies in 2015, with animals accounting for 92% of these cases (Birhane et al., 2017). The interpretation of disease breakout reveals that carnivores tend to be more vulnerable (Woodroffe et al., 2004). Rabies has been emerged as a the most prevalent source of illness outburst in wild canids (Woodroffe et al., 2004).

Ethiopian wolves (13-20kg) may be found in just seven Afroalpine highlands in Ethiopia. The most extensive and significant wolf population is found in the Bale Highlands in south central Ethiopia, with up to 300 out of a global estimate of 500 (Marino, 2003). Rabies was determined as the most likely cause of this abrupt decrease in number of the wolf present in Bale Mountains of Ethopia which was thought to have declined from roughly 450 to 120-160 persons in the early 1990s (Laurenson et al., 1998).

To the north, in the Gaysay Valley, two carcasses were found, and to the south, in the Morebawa. During this time, Ethiopian wolves which were about ten in number showed clinical signs of rabies. Two bodies were recovered in the Morebawa and Gaysay Valley. Ten Ethiopian wolves were observed to exhibit clinical signs during this time, including hind limb ataxia, depression, acute loss of appetite, anxiety or unusual varying actions, rage, disappearance of human fear and death thirst.

About 77% of 53 known wolves died or disappeared in the Web Valley between 1991 and 1992 (Kissi et al., 1995). Furthermore, among 23 known wolves 52% perished or disappeared in the Sanetti Plateau between April and June 1990, rabies was their main cause (Sillero-Zubiri et al., 1996).

All available data implies that domestic dogs are the reservoirs for rabies in both the Bale Mountains and Ethiopia; genetic study revealed the virus as canid type, and no wildlife reservoirs have yet been detected in this nation. In Ethiopia, rabies is prevalent and still a public health concern (Tefera et al., 2002; Laurenson et al., 1997).

The strong genetic link between wild canids and domestic dogs, as well as the high rates of interaction in locations where wild canids and people live, make them especially vulnerable to generalist viruses spread by domestic dogs (Randall et al., 2004, Woodroffe et al., 2004).

To decrease the prevalence of illness, especially rabies, in the reservoir population, the EWCP has been administering parenteral vaccinations to dogs in and around the BMNP since 1996, with a greater effort from 1998 to the present. By lowering the number of vulnerable hosts for the disease and, consequently, the prevalence of rabies, the dog vaccination effort aims to lower the risk of transmission from dog to wolf. Approximately 30,000 immunizations have been administered in the BMNP and its environs thus far (Randall et al., 2004).

The control phase of the intervention involved the vaccination of sixty-nine wolves, 36 from the Morebawa subpopulation and 33 from the Sanetti subpopulation, between November 2003 and February 2004. Seven animals were tested from the Web Valley outbreak region two months after the final carcass was discovered, and eight more animals received vaccinations during the follow-up recapture phase (March–November 2004).

The overall vaccine coverage, which was initially focused on the packs closest to the illness front, was 37% of all persons in 16 packs in Morebawa and 48% of all individuals in 9 packs in Sanetti (Randall et al., 2006).

Prohibiting direct contact between Ethiopian wolves and domestic dogs might reduce the risk of infection, which could lead to a significant pandemic in the wolf population (Woodroffe et al., 2004).

Over time, Ethiopian wolves have adopted a multidisciplinary and flexible approach to illness care. The long-term population monitoring in the Bale Mountains and other wolf areas is crucial. Continuous population monitoring guarantees the timely detection of epidemics by the observation of clinical symptoms and/or the discovery of corpses, in addition to making it possible to gather comprehensive wolf demographic and geographic data (Randall et al., 2004, Woodroffe et al., 2004).

Crayfish Plague in *Austropotamobius pallipes*

Austropotamobius pallipes, often known as the white clawed crayfish is a freshwater crayfish specie indigenous to the Iberian Peninsula, and endemic to Southern and Western Europe (Martínez-Ríos et al., 2023). Over the past few decades, this species' variety of habitats, abundance, and dispersion have all significantly decreased. Consequently, *A. Pallipes* has been listed as a vulnerable species on the International Union for the Conservation of Nature and Natural Resources (Füreder et al., 2010).

Initially, the crayfish plague pathogen, *A. Astaci*, coevolved with freshwater crayfish species found in North America. As a result, crayfish species of North America typically serve as carriers of *A. astaci*, with the exception of a few cases where they are infected under specific conditions (Di Domenico et al., 2021).

However, the North American crayfish's migration to Europe was a major source of the *A. Astaci* disease, which was especially common in Europe as invaders (Casabella-Herrero et al., 2021).

The disease affects all freshwater crayfish species in Europe, but it primarily affects the white-clawed crayfish *Austropotamobius pallipes*. *A. Astaci* can also disperse quickly through contaminated wet gear that moves between bodies of water. It is noteworthy that the island of Ireland was immune to the crayfish plague pathogen for more than a century, which allowed *A. Pallipes* to thrive there. However, the pathogen was implicated in a large death event in 1987 signaling introduction of this pathogen to the area (Brady et al., 2024).

Historical documents detailing the presence of *A. pallipes* in Spain are limited in comparison to other freshwater species (Alonso et al., 2000). The effects of the 1970s outbreak led to a sharp drop in native crayfish numbers in a spain of less than two years (Cuellar & Coll, 1983).

Swimming zoospore phage, encysted spore phage, and a phase of hyphal development within the host species comprise the life cycle of *A. astaci* (Jussila et al., 2014).

When a crayfish is infected with *A. astaci*, zoospores attach to its cuticle and enter its exoskeleton. From there, they move to deeper tissues and organs, where they cause a deadly disease (Pavić et al., 2020).

A. astaci at least during a crayfish epidemic, transit barriers whether man-made or natural can stop crayfish from moving around, thereby stopping the disease's propagation (Svoboda et al., 2017).

Things that have been exposed to water in certain places where *A. astaci*-infected hosts are present ought to be cleared of infections using hot water. After using the disinfectant sodium hypochlorite or iodophor and completely drying it, the pathogen can be eradicated. This is because the *A. astaci* pathogen is deadly at both low temperatures (1 week at -5 °C) and high temperatures (1 minute at 100 °C) (Pavić et al., 2020).

Peracetic acid can efficiently destroy the *A. astaci* pathogen in water devoid of fish with a concentration of 10 parts per million, while high amounts can also be harmful to aquatic life. Consequently, an environmentally acceptable and sustainable technique of treating *A. astaci* must be developed (Orlić et al., 2021).

Since there is currently no effective cure for the *A. astaci* infection, controlling the infection and stopping the carrier's spread are the recommended courses of action. As a result, constant population surveillance is required to stop the disease's migration and spread among those who may be carriers of *A. astaci* infections (Martín-Torrijos et al., 2017).

Furthermore, to address the issue of invasive species in a fundamental way, a great deal of study is required on risk assessment, the routes of dissemination, and the fundamentals of invasive species (Loureiro et al., 2015).

Conclusion

Most infectious diseases that affect humans have animal roots. Along with causing illness in humans, these infections are a major risk to threatened wildlife species. Different measurements should be taken to avoid the excessive loss of biodiversity of endangered species. In order to minimize human-animal contact and ensure the survival of wildlife species that are at the risk, public awareness is also crucial. Early identification of possible zoonotic disease risks in wildlife also reduces the outbreak timely. Targeted vaccination of domestic and wildlife animals can prevent the spread of diseases to preserve the ecosystem health.

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