

## Role of Wild Migratory Birds as Disease Vectors

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### ABSTRACT

The transmission of infectious organisms from animals to humans is known as zoonosis, and it's a multifaceted and dynamic field of study. Wild birds also play a vital role in it, especially those wild birds which are migratory. They are one of the major causes of genetic mutations when these wild birds, which are reservoirs of zoonotic infections, come into contact with wild birds or animals of another region while migrating. Even humans are affected by these migrations because some birds are consumed by humans. This paper is composed of various research proofs, which show how these infections are modifying and developing the ability to harm other wild birds, livestock, and humans. Mian aims to clarify the ways by which they are affecting how to develop preventive measurements for the future.

### Introduction:

According to the World Health Organization (WHO), zoonosis refers to the transmission of diseases or infections from vertebrate animals to people in a natural manner [1]. Some vertebrate animals can carry those infections as a reservoir and act as a vector for zoonotic diseases [2]. This includes diseases that humans get through direct contact with wild animals, as well as diseases that are transmitted through indirect exposure routes, such as pathogens carried by wild birds or present in the environment and food system during the migration of wild birds. Zoonotic viruses provide a persistent and global risk to the health of both humans, wild animals and livestock. Zoonotic pathogens, exemplified by Covid-19 pandemic, influenza, severe acute respiratory syndrome (SARS) and many more, are responsible for the majority of emerging infectious diseases [3] in human populations. Furthermore, over 75% of developing zoonotic viruses can be traced back to wildlife sources [4]. Zoonotic diseases exert profound effects on both human and animal well-being, as well as on livelihoods and economies. Throughout the last 20 to 30 years, there has been a significant increase in the prevalence of zoonotic illnesses caused by virus, parasites, and bacterial infections through wild birds. These diseases have become a prominent concern on a global scale, resulting in a range of negative impacts, including disease and death, as well as economic and productivity setbacks. The classification of the ongoing COVID-19 pandemic, caused by SARS-CoV-2, as a zoonotic illness has been deemed premature due to the absence of any identified wild animal reservoir thus far [5]. The proposition suggests that COVID-19 should be categorized as an "emerging infectious disease [3] with a likely origin in animals." Over the 30 months since COVID-19 was first recorded in Wuhan, China, there have been more than 543 million cases and more than 6.3 million fatalities globally [6]. Additional instances of zoonotic diseases include the exceptionally few occurrences of Marburg, Crimean-Congo hemorrhagic fever (CCHF), and henipaviruses originating from wildlife, as well as Rift Valley fever (RVF) and Middle East respiratory syndrome (MERS) originating from domesticated animals. Lassa fever is contracted from a peri-domestic rat. At the same time, the origins of the Ebola virus, SARS, and SARS-CoV-2 remain unknown, with the majority of human infections for these diseases being acquired through human-to-human transmission. According to projections, the world human population is anticipated to witness a rise from 6.5 billion in 2008 to approximately 9.2 billion by the year 2050 [7]. The current situation presents significant obstacles to the overall food production industry, as there is a projected surge in demand for almost 50% more food by the year 2030 [8].

In addition, it is worth noting that viruses can infiltrate the human body through the epithelium or superficial mucosa of several anatomical regions, including the respiratory, gastrointestinal, and urogenital tracts. The primary modes of infection commonly observed are the consumption of water or food that has been contaminated (known as the faecal-oral route, exemplified by picornaviruses), inhalation of droplets released by an infected person (known as the respiratory route, presented by herpesviruses and metapneumoviruses),

or contact with contaminated surfaces. In addition to airborne transmission, respiratory viruses can also be spread by direct contact with the mucous membranes of the eye. Airborne transmission refers to the mechanism through which viruses, such as the influenza virus, can disseminate over considerable distances via minute respiratory aerosols that remain suspended in the air [9].

More than two-thirds of viral species that can infect humans are classified as zoonotic, meaning they can also infect non-human animals and potentially persist in non-human reservoirs. Mammals, including rodents, ungulates, other primates, carnivores, and bats, serve as the primary alternative hosts for the majority of zoonotic viruses. Avian species exhibit a comparatively lower significance as reservoirs for zoonotic diseases in comparison to mammals. Although the proportion of zoonotic viruses that utilize avian hosts is below 20%, recent research indicates that birds play a significant role as possible reservoirs for zoonotic viruses [10].

### Wild Birds as Reservoirs of Zoonotic Pathogens

Wild birds are reservoirs of many zoonotic diseases and still we know very few of them. They are affecting human, poultry, livestock animals and even wild animals. It's can be viral, bacterial or parasites. Sometime due to various reasons, these microorganisms, go through genetic mutation which results in zoonosis. The avifauna in natural ecosystems encompasses a diverse array of bird species, each exhibiting distinct characteristics pertaining to their habits, habitats, and feeding patterns. Wild avian species have the potential to carry infections inside their digestive system, leading to the subsequent excretion of these agents via their fecal matter. Consequently, these birds may serve as a reservoir of infection, posing a risk for the transmission of diseases to other avian species. In addition, it should be noted that wild avian species have the potential to transmit infectious and/or parasitic pathogens to mammals, including the human population. Given the frequent presence and habitation of these animals in agricultural regions, it is plausible that they might serve as reservoirs of infections for cattle, hence resulting in significant economic repercussions. The spread of diseases from birds to domestic animals has been linked to the pollution of several environmental elements, including water sources, pastures, and animal feed, due to the presence of avian excrement [11-13].

*Brucella* spp., *Mycobacterium* spp., *Coxiella burnetii*, and *Salmonella enterica* are prominent bacterial pathogens with zoonotic potential that can induce severe diseases in livestock, particularly ruminants. However, it is worth noting that additional bacterial agents such as *Campylobacter* spp., *Staphylococcus* spp., *Chlamydia* spp., and *Escherichia coli* can also pose a threat to the health of animals. Members belonging to the genus *Brucella* are a kind of Gram-negative bacteria that can exist as facultative intracellular organisms. These bacteria are known to infect several species of both domesticated and wild mammals. Brucellosis, a disease caused by *Brucella*, poses a significant threat to the health of livestock. The primary culprits responsible for this disease are *B. abortus* and *B. melitensis*, which may lead to complications such as miscarriage and sterility. There is a lack of evidence

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on the isolation of *Brucella* spp. from avian species. However, the presence of anti-*Brucella* antibodies has been observed in some avian populations in South Africa and Asia [14, 15].

The genus *Mycobacterium* comprises acid-fast bacilli that are categorized into two groups: the mycobacteria responsible for TB, including *M. tuberculosis* and *M. bovis*, and the group of non-tuberculous mycobacteria (NTM). Within the category of nontuberculous mycobacteria (NTM), individuals belonging to the *Mycobacterium avium* complex pose a significant risk in the field of veterinary care. Specifically, *Mycobacterium avium avium* is responsible for avian TB, but it often contributes to infections in mammals, particularly in humans, cattle, and pigs [16]. Furthermore, *M. genavense*, a well-recognized human disease, has often been detected among avian populations [17]. *C. burnetii* is a Gram-negative, intracellular obligate bacterium which may infect several avian and mammal species. It is the etiologic agent of the zoonotic disease Q Fever, which causes reproductive disorders mainly in farm ruminants [18].

*Salmonella enterica*, a bacterium classified as Gram-negative and belonging to the Enterobacteriaceae family, is known to infect both domestic and wild avian species. The manifestation of the infection varies depending on the specific serovar involved. *Salmonella enterica* serovars Gallinarum and Pullorum mostly induce systemic sickness in avian species and do not exhibit pathogenicity towards mammals [19]. The serovars that lack specificity for a particular host can infect avian populations without causing any noticeable illness symptoms. However, these serovars are known to cause enteric, septicemic, and reproductive disorders in several mammal species, including humans and farm animals [20].

Protozoan parasites, such as *Giardia* spp. and *Cryptosporidium* spp., have been identified as potential excretions in the faeces of avian species [4]. *Giardia* spp. and *Cryptosporidium* spp. are often seen as intestinal protozoan parasites with zoonotic potential, capable of infecting a diverse array of vertebrate hosts around the globe, including humans, mammals, as well as domestic and wild animals. Both species are often found in wild avian populations as well [21]. Two distinct species of *Giardia*, namely *G. ardeae* and *G. psittaci*, have been found in avian populations by the examination of trophozoite and cyst morphology [22]. In addition to the species above/assemblages, there have been documented reports of further assemblages, namely A and B, occurring in avian hosts with zoonotic potential [23]. To provide more elaboration, it was observed that *G. duodenalis* assemblage A was detected in Brazil. In contrast, *G. duodenalis* assemblages B, D, and F were identified in the northwest region of Spain [24].

Currently, four known species of *Cryptosporidium* have been identified as causing infection in avian species. These species, namely *C. meleagridis*, *C. baileyi*, *C. avium*, and *C. galli*, are differentiated based on both biological and genetic variations. Furthermore, previous studies have shown the existence of other species, including *C. andersoni*, *C. parvum*, *C. hominis*, *C. muris*, as well as multiple genotypes such as *Cryptosporidium* goose genotypes I–IV, a *Cryptosporidium* duck genotype, and *Cryptosporidium* avian genotypes I–IV [25]. Typically, a considerable number of *Cryptosporidium* species and genotypes exhibit host specificity, hence rendering them of little public health significance. Nevertheless, it is worth noting that some avian species have the potential to harbour and spread zoonotic pathogens [26]. Furthermore, it is noteworthy that *C. meleagridis* is recognised as the third most often seen species responsible for human infections, behind *C. hominis* and *C. parvum* [27].

### Conclusion

In a nutshell, migration of wild avian species for their survival are resulting in the spread of zoonotic diseases all around the world. Some avian species leave their habitat in search of food during harsh environments. This migration facilitates the spread of disease from wild birds to other wild animals and also to humans and livestock. When humans came into the contact with these wild animals, their infection may spread to humans. Corona virus spread is the recent example of it. In this paper, the relation of migration and its impact on disease transmission is explained.

Zoonotic disease may spread through the direct contact and indirect contact of humans with these wild birds species. Sometimes, Local wild species of birds also carry some zoonotic infections and when they came into contact with migratory birds which also carry zoonotic infections, chances of mutation in microorganisms enhances. Due to this mutation, these microorganisms creating more alarming conditions, which should be control by any means. Otherwise, the world may face condition like corona pandemic. Similarly, Proactive approaches should be taken as surveillance of wild birds, interaction of wild birds to other wild birds during migration and interaction of wild birds to humans. Some birds only migrate in short distances and some do very long-distance migration. Those birds which are migrating in long distance and more impacting huge ecosystem.

Such as shorebirds, arctic tern, waterfowl, peregrine falcon, swallow-tailed kite, osprey, blackpoll warbler, yellow warbler, bar-tailed godwit, common swift and many more

Waterfowl and shorebirds often carry avian influenza viruses, which could harm humans and animals. Thus, these species' migratory and ecological traits must be examined to determine their disease transmission potential across regions. Understanding the complex relationships between wildlife, urban development, and zoonotic illnesses requires identifying high-risk avian species. In this paradigm, scientists and public health officials can improve their preparedness for zoonotic outbreaks by studying urban and synanthropic bird species and other migratory organisms. This will ultimately protect human well-being.

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