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The authors have declared that no competing interests exist.

Review

Zoonotic Bridge: Unraveling the Role of Wild Birds in Spreading the Bacterial Pathogenic Diseases

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Abstract

While wild birds contribute significantly to our ecosystem, they also act as carriers for various zoonotic diseases affecting humans. These diseases are often transmitted through international and local migrations, direct contact, and water sources, as well as through droppings and the excretion of spores in their feces. Over time, they present significant risks to the health of humans and animals by serving as carriers and hosts for new strains of pathogens. This review emphasizes the significant zoonotic diseases caused by birds, which include bacterial infections. These pose substantial health risks to both humans and animals. The review delves into their epidemiology and clinical manifestations. Of utmost significance, it underscores the pivotal function of birds as both distributors and reservoirs of potentially significant zoonotic diseases.

Key words: *Avian Pathogens, Birds, Human health risks, Infections, Vectors, Zoonosis*

Wild avian species encompass a diverse array of birds, each characterized by unique behaviors, habitats, and dietary preferences. Wild birds have pathogens in their digestive systems and can spread these infectious agents through their droppings, making them potential sources of infection for other bird species. Moreover, they can also transmit agents that cause infectious and parasitic diseases, which can impact mammals, including humans. The potential exists for these animals to spread a variety of new and recurring diseases to humans, mainly through close contact or by consuming tainted meat, eggs, or water. Considering the ongoing growth of international trade, rising populations, increased human movement, and changing demographic patterns, the prevalence of pathogens has notably risen. These infections persist in presenting risks to human health across the globe and hold notable economic significance (Kumar et al. 2018). Millions of individuals experience the severe impact of enteric pathogens each year, resulting in hundreds of thousands of deaths worldwide (Scallan et al. 2011; Havelaar et al. 2015). Three specific types of bacteria — *Salmonella* spp., *Escherichia coli*, and *Campylobacter spp*. — are predominantly accountable for most gastrointestinal infections (Havelaar et al. 2015).

Salmonella

Salmonella enterica belongs to the Enterobacteriaceae family and has a distinctive rod-shaped structure. It is a Gram-negative bacterium with flagella and can thrive in both aerobic and anaerobic conditions. These unique qualities make it stand out in the microbial world (Ryan et al., 2017). While some species can exist in animals without any noticeable symptoms, others can cause a variety of illnesses in humans, known collectively as salmonellosis.

Salmonellosis is a widespread foodborne illness worldwide. Its symptoms typically encompass fever, diarrhea, abdominal cramps, and vomiting, with the potential to endure for several days (Chanamé Pinedo et al., 2022). As per the World Health Organization (WHO), over 2 billion individuals globally experience diarrheal illnesses each year. Shockingly, it is reported that one out of every four of these cases is attributed to *Salmonella* infections (Popa et al., 2021).

Salmonella enterica exhibits remarkable diversity, boasting over 2600 distinct serovars. The six subspecies show significant genetic similarity. The subspecies categorization includes *S. enterica* subspecies enterica (Group I), *S. enterica* subspecies salamae (Group II), *S. enterica* subspecies arizonae (Group IIIa), *S. enterica* subspecies diarizonae (Group IIIb), *S. enterica* subspecies houtenae (Group IV), and S. enterica subspecies indica (Group VI).

The diverse genetic makeup of *Salmonella enterica* is emphasized by this comprehensive categorization (Brenner et al., 2000). *S. enterica* subspecies enterica, the pathogenic variation, is well-known for its detrimental effects on warm-blooded organisms and comprises over 1580 distinct serovars. Research by Xiong et al. (2018) and Ferrari et al. (2019) has highlighted its significant impact on the health of homeothermic creatures. Globally, an estimated 93.8 million cases of enteric infections caused by non-typhoidal *Salmonella* (NTS) are reported annually, leading to approximately 155,000 deaths, underscoring the substantial public health burden posed by NTS infections worldwide as noted by Eng et al. (2015).

The most frequently identified *Salmonella* serovars in the United States among humans, in order of occurrence, are *S. enteritidis, S. newport, S. typhimurium, S. javiana*, and the monophasic variant of *S. typhimurium* (Table 1). This ranking provides insight into the common prevalence of *Salmonella serovars* in the U.S. population (Hohmann, 2001). The yearly economic impact of foodborne *Salmonella* infections in the United States, which includes healthcare expenses, decreased productivity, and premature deaths, ranges from $4 -11 billion. This significant economic burden emphasizes the widespread effects of these infections on society (Gast and Porter, 2020).

The Bird-Human Connection

Salmonella bacteria can impact not only humans but also domesticated animals and potentially even wild avian species as shown in Figure 1. This raises concern about the potential for infections to spill over into wildlife populations, posing a risk of further (Smith et al., 2020). *Salmonella* spp. infections can affect all types of birds, but the impact can differ significantly. These differences in impact are attributed to variations in species susceptibility, age, and the virulence of the specific serotype, (Table 1). *Salmonella* spp. infections can affect all types of birds,

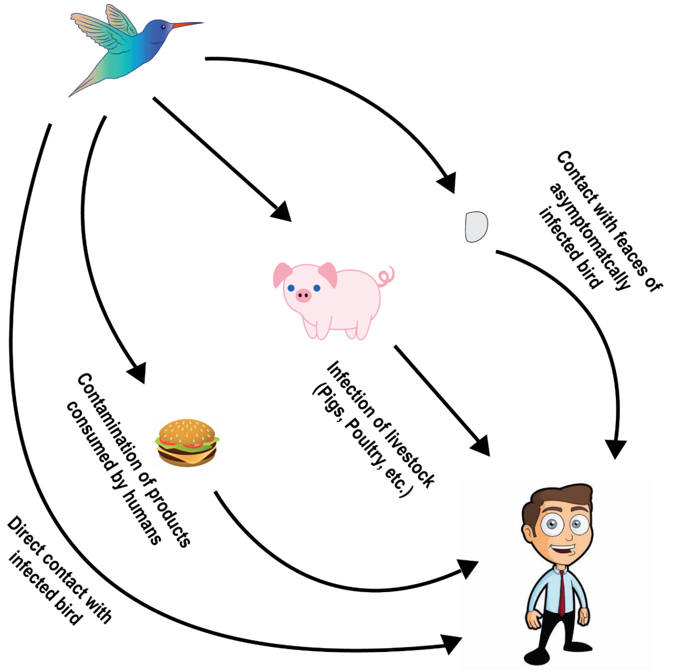

Figure 1: Potential pathways for the spread of Salmonella spp. from wild birds to humans.

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Table 1: Presence of specific Salmonella serovars in the avian populations of the wild.

Country	Effected Birds	Serotype	References
Croatia	*Buteo buteo, Corvus frugilegus, Strix aluco, Columba livia*	*S. ser.* Enteritidis, *S. ser.* Typhimurium	Vlahović et al., 2004
Canada	*Phalacrocorax auratus*	*S.* ser. Typhimurium	Dobbin et al., 2005
Australia	*Threskiornis molucca, Eudyptula minor, Anous Stolidus, Onychoprion fuscatus, Anous tenuirostris*	*S.* ser. Bovismorbificons, *S.* ser. Havana, *S.* ser. Infantis, *S.* ser. Muenchen, *S.* ser. Infantis	Epstein et al., 2006;
United Kingdom	*Sturnus vulgaris, Fringilla coelebs, Turdus merula, Carduelis chloris, Passer domesticus*	*S.* ser. Typhimurium (DT56, DT40)	Grant et al., 2007
United States	*Otus asi, Parabuteo Unicinctus, Bubulcus ibis*	*S.* ser. Saintpau, *S.* enterica houtenae, *S.* ser. Bredeney, *S.* ser. Braenderup, *S.* ser. Mississippi, *S.* ser. Typhimurium, *S.* ser. Oranienburg, *S.* ser. Anatum, *S.* ser. Ibadon	Jijón et al., 2007; Phalen et al., 2010
Belgium	*Passer domesticus, Columba livia*	*S.* ser. Typhimurium (DT99, DT195), S. ser. Enteritidis (PT4)	Haesendonck et al., 2016

but the impact can differ significantly. These differences in impact are attributed to variations in species susceptibility, age, and the virulence of the specific serotype (Table 1). This variability underscores the complex nature of *Salmonella* infections in avian hosts (Connolly et al., 2006). Birds that have acclimated to urban environments face an increased risk of infection and can potentially spread enteric zoonotic pathogens. This phenomenon is influenced by several factors, including the consumption of contaminated food and water, exposure to polluted environments, microclimates with higher temperatures, and diminished seasonal variations. These conditions facilitate the growth of vectors and the persistent presence of certain parasites. Moreover, urban avian populations might encounter immunosuppressive factors and tend to aggregate in confined spaces, thereby increasing the probability of interactions with potential hosts (Bradley and Altizer, 2007). *Salmonella* not only establishes itself in the gastrointestinal tract of birds but also extends its presence to other organs beyond the digestive system. This includes the liver, spleen, ovaries, oviducts, and even the muscular tissues. This broad colonization pattern highlights the wide-ranging impact of *Salmonella* in avian hosts (Ainslie-Garcia et al., 2018).

Migratory birds are believed to be the primary source of *Salmonella* spp. infections in humans. It's interesting to note that a matching strain of *S. bongori* has been found in both migratory birds and cases of human infection in Italy. This finding suggests a potential link between migratory birds and certain *Salmonella* strains affecting humans in the region (Foti et al., 2009).

In cloacal swabs and organ samples from various raptor species (Table 1), different serotypes such as *S. ser.* Typhimurium, *S. ser.* Tuindorp*, S. ser.* Enteritidis*, S. ser.* Newport*, and S. ser.* Pajala have been detected. This range of serotypes highlights the potential for *Salmonella* diversity within avian populations. Certain species, like the peregrine falcon (*Falco peregrinus*), may act as carriers of these pathogens, with their primary diet consisting mainly of birds from the Charadriidae and Laridae families. Given their migratory nature, peregrine falcons traverse considerable distances, potentially spreading these pathogens to diverse regions, including those unaffected by human activities (Hernandez et al., 2012). In a comprehensive study conducted by de Oliveira et al., specimens were collected from the cloacal swabs of 156 urban avian specimens, including synanthropic great egrets (*Ardea alba*) and feral pigeons (*Columba domestica*), residing in the proximity of an urban zoo in Brazil. The aim was to evaluate the impact of shelter and food accessibility on the habitat of these avian species. The investigation unveiled that the act of defecation in these areas could potentially facilitate the transmission of *Salmonella* to captive zoo animals by these birds. Among the sampled avian population, 11 individuals tested positive for *S. enterica ser. Typhimurium*, indicating a prevalence rate of 7%. This discovery highlights the significant role of free-ranging birds as potential vectors of infection for other animals.

Campylobacteriosis

Campylobacter is characterized by a unique spiral or helical shape, deviating from the usual curved rod morphology. Notably, *Campylobacter* demonstrates remarkable adaptability by undergoing shape alterations, adopting filamentous or coccoid forms in response to adverse environmental conditions. This remarkable morphological flexibility is a noteworthy characteristic of the bacterium (Tresse et el., 2017). Within the bacterial genus *Campylobacter*, there exist zoonotic strains, a few of which can present as emergent and notably virulent pathogens (Sahin et al., 2012). *Campylobacter*-induced human campylobacteriosis primarily manifests as gastroenteritis and ranks among the top four culprits of global diarrheal afflictions (Henderson et al., 2009).

Moreover, *Campylobacter* has been associated with serious neuropathological conditions such as Guillain–Barré syndrome (GBS) and Miller Fisher syndrome (MFS), in addition to reactive arthritis. These connections highlight the substantial effect of *Campylobacter* on human health (Keithlin et al., 2014). *Campylobacter*, classified within the Epsilon proteobacteria class, stands as a prominent bacterial agent responsible for global foodborne diarrheal infections (Kirk et al., 2015). The year 2010 witnessed a staggering tally of over 95 million instances of foodborne illnesses directly linked to *Campylobacter* across the globe (Kirk et al., 2010; Tack et al., 2020).

Campylobacter Bacteria and Human Symptoms

Recently recognized, emerging *Campylobacter* species have surfaced as causative agents of illnesses (Kaakoush et al., 2015). This group includes a range of bacteria, such as *C. rectus, C. sputorum, C. gracilis, C. mucosalis, C. concisus, C. upsaliensis, C. showae, C. curvus, C. fetus, C. lari, C. volucris, C. pinnipediorum, and C. ureolyticus.* Their clinical importance and pathogenic capabilities have undergone thorough assessment and scrutiny (Man, 2011; Costa et al., 2019). The available corpus of evidence indicates that these newly identified *Campylobacter* species demonstrate the capacity to attach to and penetrate human epithelial cells. In addition, they have the capability to change the integrity of the intestinal barrier, avoid the immune response of the host, release toxins, and infiltrate macrophages. However, it is not completely clear how these newly discovered *Campylobacter* strains contribute to the development of campylobacteriosis. This lack of clarity is due to the limitations of current cultivation methods. Despite using hydrogen-enhanced microaerobic and anaerobic environments, these methods have not yet led to successful growth of these microorganisms in laboratory conditions (Kaakoush et al., 2015).

Avian Reservoir: Birds as Carriers of Campylobacter

Avian species, including domestic poultry and wild birds, often have *Campylobacter* in their intestinal tracts, where they live as normal commensal organisms. Additionally, these bacteria are commonly found in aquatic environments. Notably, *Campylobacter spp*. exhibit the capacity to withstand and endure for prolonged durations, potentially presenting a threat of pathogenicity (Hald et al., 2015). An alternative study has observed that *C. jejuni*, despite its commensal nature, has the potential to induce prolonged inflammation, resulting in damage to gut tissues and the occurrence of diarrhea in broiler chicks (Humphrey et al., 2014). Furthermore, certain species of wild birds have adeptly acclimated to human-altered environments. They frequently interact closely with livestock, domesticated animals, and humans, potentially serving as a reservoir for *Campylobacter* (Vogt et al., 2020). Additionally, it is important to recognize that many wild bird species are classified as game and their meat is harvested for human consumption. While this practice is widespread, it carries potential health risks (Thomas et al., 2020). The prevalent presence of *Campylobacter* colonization in agricultural chickens is commonly linked to horizontal environmental transmission, often associated with factors like feed or water sources. Upon infiltrating the chicken flock, *Campylobacter* rapidly spreads and establishes itself in the intestinal regions of a large portion of the bird population, including the ceca, small intestine, and colon, within a week (Shanker et al., 1990). The transportation of live birds from farms to processing facilities plays a vital role in the dissemination and establishment of *Campylobacter* (Newell et al., 2011). Therefore, migratory birds act as carriers for numerous pathogenic microbes, either through biological or mechanical transmission. Consequently, antimicrobial-resistant pathogens are transmitted to domestic animals, birds, and various environmental water sources via the fecal droppings of migratory birds. These avian species are widely acknowledged as significant and extensively researched natural reservoirs for *C. jejuni, C. coli*, and *C. lari* (Table 2).

Each year, Egypt serves as a vital rest stop for millions of migratory birds traveling from Europe to Africa due to its mild winter climate and proximity to the Red Sea (Houlihan, 2023). The country's urban areas, farms, and markets commonly host wild birds, which may be carriers of *Campylobacter spp*. These birds can transmit the bacterium to animal and poultry farms by depositing droppings or encountering bacteria in farm waste and contaminated poultry facilities (Mohamed, 2021).

Table 2: The current state and characteristics of Campylobacter spp. found in various types of wild birds.

Bird species (Scientific name)	**Country**	**Overall number of samples.**	**Percentage of positive samples.**	***Campylobacter* spp. prevalence (%)**	**References**
Northern pintail (*Anas acuta*)	Egypt	16	4 / 25%	*C. jejuni (4), C. coli (4)*	Tawakol et al., 2023
Quails, red-crested Pochard, Eurasian coot, European turtle dove, and song thrush.	Spain	689	52 / 7.5 %	*C. lari (3.8), C. coli (3.8), C. jejuni (88.5).*	Mencía-Gutiérrez et al., 2021
Audouin's gull and Yellow-legged gull	Southern Europe.	1,785	93 / 5.2 %	*C. lari (2.12), C. jejuni (94.6), C. coli (2.12).).*	Antilles et al., 2021
Common teal (*Anas crecca)*	Egypt	20	5 / 25.0%	*C. jejuni* (5), *C. coli* (5)	Tawakol et al., 2023
Northern shoveler (*Spatula clypeata*)	Egypt	21	2 / 9.5 %	*C. jejuni* (2), *C. Coli* (2)	Tawakol et al., 2023
Different species of raptors	Spain	387	9 / 2.3 %	*C. lari (11.1), C. coli (33.3), C. jejuni (33.3).*	Jurado-Tarifa et al., 2016
Crow, Eurasian tree sparrow (*Passer montanus*), pigeon.	Japan	173	34 / 19.7%	*C. fetus 1/34 (2.9), C. jejuni 32/34 (94.1), C. coli 1/34 (2.9)*	Shyaka et al., 2015
Black-headed Gulls (*Larus ridibundus*)	Sweden	419	117 / 27.9 %	*C. jejuni, C. coli, C. lari*	Broman et al., 2002

Lyme Disease (LD)

LD is the most common tick-borne infection affecting people in North America and Eurasia (van den Wijngaard et al. 2015). LD is a complicated infectious condition that impacts various systems in the body. It is brought about by bacteria from the *Borrelia burgdorferi* sensu lato (s.l.) species complex, which includes more than 20 different genospecies. Key human pathogens in this complex include *B. burgdorferi* sensu stricto (s.s) in North America, and in Europe, *B. garinii, B. afzelii, B. burgdorferi* s.s., *B. spielmanii, B. bissettii, and B. bavariensis* (Beckers et al., 2016).

Epidemiology of Lyme disease

Between 2008 and 2015, the CDC received reports of 208,834 verified cases, peaking at 29,959 cases in 2009 (Schwartz et al., 2017). During this period, LD accounted for a notable 82% of all documented tick-borne ailments and 63% of all diseases transmitted by vectors in the United States. This firmly establishes it as the most widespread vector-borne ailment in the country, with Ixodes scapularis emerging as the paramount vector (Rosenberg et al., 2018).

Research conducted in Germany emphasizes the important contribution of birds to the spread of LD. One of the key species identified in this regard is *B. valaisiana*, which has been associated with birds (Kipp et al., 2006).

Migratory Birds: Transmission Vector

The movement patterns of specific bird species, such as the Pacific wren (*Troglodytes pacificus*), spotted towhee (*Pipilo maculatus*), Swainson's thrush (*Catharus ustulatus*), and fox sparrow (*Passerella iliaca*), may facilitate the widespread of ticks over large distances (Scott et al., 2015). Consequently, this may leads to the introduction of *B. burgdorferi* s.s. into areas where LD is not commonly present. In the western regions of Canada, both along the coast and inland locations, there have been documented occurrences of limited populations of *Ixodes pacificus* immatures. The presence of these ticks is believed to be attributed to migratory birds transporting them from the western United States (Davis et al., 2015). In addition, it is possible that birds could spread *B. burgdorferi* s.s. across long distances by either carrying spirochetal infections for prolonged periods or reactivating dormant infections because of the stress of migration (Wright et al., 1998). Although avian hosts might play a limited role in the local maintenance and transmission of *B. burgdorferi*, they have the potential to introduce ticks carrying the LD pathogen to regions where it has not yet been established (Dizon et al., 2023).

In Cyprus, research uncovered that the parasitic interaction between larvae and nymphs of *Ixodes ricinus* occurs with migratory passerine birds (Kaiser et al., 1974). Each spring, almost 100 million birds undertake migration to their breeding destinations in or through Sweden. Concurrently, they serve as carriers for a significant population of ticks. Among the 22,998 avian subjects examined, 2% were found to be hosting 967 ticks (Olsén et al., 1995). The dominant tick species identified was *Ixodes ricinus*, accounting for 98.3% of the total population. Each year, researchers calculated that over 6.8 million new ticks were brought into Sweden by migratory birds during the spring season. Furthermore, around 4.7 million ticks were seen leaving the country in the autumn as they migrated southward. Notably, the taiga tick (*Ixodes persulcatus*) was officially recorded in Scandinavia for the first time during the study period. This adaptable tick species feeds on over 200 mammal species and more than 120 bird species. One nymph was found on a willow warbler (*Phylloscopus trochilus*) (Filippova, 1977). Nymphs exhibit a particular preference for birds (Korotkov and Kislenko, 2001). The main stage of *Ixodes persulcatus* that primarily feeds on humans is the adult stage, which is different from *Ixodes ricinus*, where it's the nymphal stage that usually bites humans.

In the USA and Canada, *Ixodes scapularis* is widely present and looks for blood meals from more than 125 different vertebrate species, particularly focusing on 57 of them (Keirans et al., 1996). In a recent study across 11 European countries—Spain, Portugal, Netherlands, Germany, Greece, Estonia, Czech

Republic, Finland, Sweden, Hungary, and Slovenia—data on tick infestation of Passeriformes was compiled. From a sample of 843 birds, researchers collected and examined 2,308 ticks. In a study of 656 Ixodes ticks, 244 were found to carry *B. burgdorferi* s.l., resulting in a prevalence rate of 37.2%. Among the ticks analyzed, 20% of the larvae (22 out of 110) tested positive, while the prevalence increased significantly to 41% in nymphs (214 out of 521), almost doubling the rate compared to the larvae. *Ixodes ricinus* was the most heavily infected species, with an infection rate of 40.2% (210 out of 522). Among the examined avian species, ticks found on the fieldfare (*Turdus pilaris*) had the highest prevalence of Borrelia at 92%, followed by those on the common blackbird at 58%. Examination of flaB gene sequences unveiled that the predominant genospecies was *B. garinii*, making up 60.7% (116 out of 191), followed by *B. valaisiana* at 23.6% (45 out of 191), *B. afzelii* at 9.4% (18 out of 191), *B. turdi* at 5.2% (10 out of 191), *B. lusitaniae* at 0.5% (1 out of 191), and the presence of a novel genospecies at 0.5% (1 out of 191) (Norte et al., 2020).

Future Directions and Research Needs

Safeguarding against diseases, particularly zoonotic ones, demands a collective effort from both domestic and global entities. Ensuring the "One Health approach" is crucial for both public health and animal welfare. To support this approach, the main emphasis should be on spearheading cutting-edge research efforts led by skilled professionals in various scientific fields, with the goal of reducing zoonotic diseases. Additionally, administrative and policy decisions influencing climate shifts, urban development, land utilization, and the impacts of industrial and agricultural contaminants must align with ecological and epidemiological insights into diseases.

Foreseeing and promptly evaluating outbreaks, along with predicting their potential expansion into previously unaffected and potentially unstable areas, represents a crucial principle in managing persistent diseases. The importance of this factor is crucial and essential, especially when considering worldwide animal trade. The key principle of early detection and action is based on the idea that it is not only easier to manage but also less expensive to address a disease epidemic in its early stages than to deal with a large-scale outbreak.

Conclusion

The review covers notable zoonotic diseases originating from birds, including, *Salmonella*, *Campylobacter* and LD. Each presents distinctive challenges concerning manifestation, control, prevention, and treatment. Compelling evidence underscores the diseases' ability to breach species barriers, affecting healthcare workers, veterinarians, as well as individuals of all age groups, thereby incurring significant economic consequences. Swift detection stands as a critical step in countering outbreaks and safeguarding public health. While substantial strides have been made in poultry stock, a gap persists in understanding the intricacies of host-pathogen interactions in wild birds, as well as in the development of their vaccines. Future endeavors should zero in on these aspects to enhance prevention and control strategies against these zoonoses. Heightened surveillance in high-risk areas, prompt reporting of cases, and robust biosecurity measures are imperative interventions for public health in regions where humans and birds coexist. Collaboration between medical professionals and veterinarians is indispensable in the management of zoonotic diseases. In summary, the interplay between humans and wild birds represents a dynamic and intricate field. Hence, by prioritizing research, intensifying surveillance efforts, and fostering collaboration, we can mitigate the risks of zoonoses. Ultimately, both human and avian communities necessitate a united effort grounded in a "One Health approach".

Authors' contributions

MHR, MHA, MIA AND TB designed, conducted the research, and wrote first draft of the manuscript while, NZ AND N wrote revised and final manuscript.

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