Perspectives of *K. pneumoniae*'s zoonotic potential from wild birds to human

Perspective ale potențialului zoonotic al *K. pneumoniae* de la păsările sălbatice la om

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Abstract

Research across various regions demonstrates the prevalence of antimicrobial resistance (AMR) *Klebsiella pneumoniae* in wild birds, with notable findings including the detection of carbapenemase-producing strains (*K. pneumoniae* carbapenemase, KPC) in gulls from Spain and Ukraine, and colistin-resistance genes (mcr-1 and mcr-2) in Egyptian migratory waterfowl. Genetic overlaps were observed between avian isolates and human clinical strains, such as indistinguishable *K. pneumoniae* genomes from grey-crowned cranes in Rwanda and human cases. Migratory species, such as Eurasian Blackcaps in Italy, are implicated as sentinels and reservoirs of AMR genes, facilitating global dissemination. Geographic prevalence studies highlight variability, with 11.5% of birds in Spain harboring carbapenem-resistant phenotypes and 8% prevalence in Italian birds. This review examines the role of wild birds as reservoirs of *K. pneumoniae* and its implications for AMR and zoonotic transmission. The goal is to synthesize current knowledge on the prevalence, resistance profiles, and potential transmission pathways of *K. pneumoniae* from avian hosts to humans. Wild birds, including migratory and urban-adapted species, serve as significant reservoirs of AMR genes, potentially transmitting these pathogens to humans through shared environments or migration. The findings underscore the urgent need for a One Health approach to monitor wildlife as part of global AMR surveillance.

Rezumat

Cercetările efectuate în diferite regiuni demonstrează prevalența rezistenței antimicrobiene a *Klebsiella pneumoniae* la păsările sălbatice, constatările notabile incluzând detectarea tulpinilor producătoare de carbapenemază (*K. pneumoniae* carbapenemase, KPC) la pescărușii din Spania și Ucraina și a genelor de rezistență la colistină (mcr-1 și mcr-2) la păsările de apă migratoare din Egipt. Au fost observate suprapuneri genetice între izolatele aviare și tulpinile clinice umane, cum ar fi genomurile *K. pneumoniae* indistincte de la cocorii cu coroană gri din Rwanda și cazurile umane. Speciile migratoare, cum ar fi silviile cu cap negru din Italia, sunt implicate ca santinele și rezervoare ale genelor RAM, facilitând diseminarea la nivel mondial. Studiile privind prevalența geografică evidențiază variabilitatea, 11,5% dintre păsările din Spania prezentând fenotipuri rezistente la carbapenem și o prevalență de 8% la păsările italiene. Această revizuire examinează rolul păsărilor sălbatice ca rezervoare ale *K. pneumoniae* și implicațiile sale pentru RAM și transmiterea zoonotică. Scopul este de a sintetiza cunoștințele actuale privind prevalența, profilurile de rezistență și căile potențiale de transmitere a *K. pneumoniae* de la gazdele aviare la om. Păsările sălbatice, inclusiv speciile migratoare și cele adaptate la mediul urban, servesc drept rezervoare semnificative de gene RAM, putând transmite acești agenți patogeni la om prin medii comune sau migrație. Constatările evidențiază necesitatea urgentă a unei abordări One Health pentru monitorizarea faunei sălbatice ca parte a supravegherii globale a RAM.

Introduction

Wild birds often inhabit areas that overlap with human environments, such as urban settings and agricultural lands. This proximity increases the likelihood of contact between birds and humans, facilitating potential transmission [24, 26].

K. pneumoniae is recognized as an opportunistic pathogen that can infect a variety of hosts, including humans and animals [5, 7]. It is commonly found in the gastrointestinal tracts of both wild and domestic birds, making them potential reservoirs for the bacterium [17, 24, 27].

Isolates of *K. pneumoniae* from wild birds have been found to carry multidrug resistance plasmids that are closely related to those found in human-infecting strains. This raises concerns about the potential for these resistant strains to be transmitted to humans [12, 26, 27].

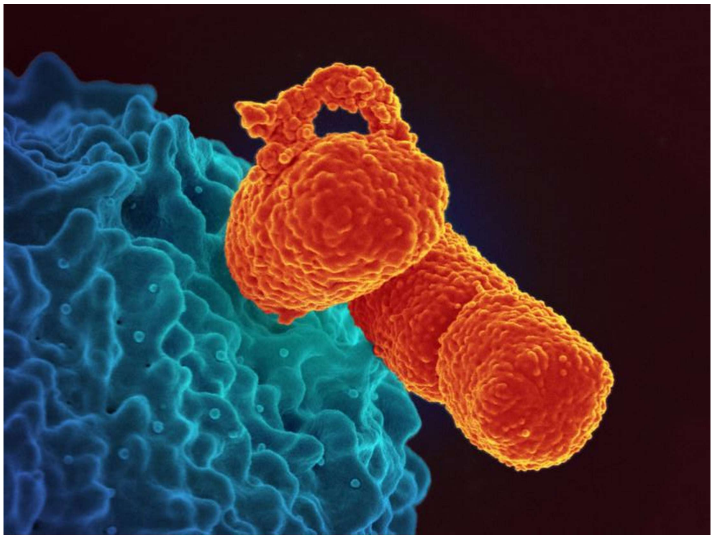

Figure 1. *K. pneumoniae* (NIAID).

Certain bird species are indeed more likely to carry multidrug-resistant bacteria, particularly due to their habitats and interactions with human environments [22,23,25].

Studies have identified specific bird species that frequently harbor multidrug-resistant strains of bacteria, including **gulls**, **pigeons**, **ducks**, **geese** and **birds of prey**.

These species often inhabit areas close to human activity, such as urban environments and agricultural lands, where they are exposed to antibiotic residues and resistant bacteria from waste products [6,10].

Migratory species, such as **black kites** and other migratory birds, have been shown to carry multidrug-resistant **Escherichia coli** and ***K. pneumoniae***. Their migratory patterns facilitate the spread of these resistant strains across regions [8,15,28].

Given their ability to carry and spread multidrug-resistant bacteria, certain bird species pose a risk for public health. The migration of these birds can lead to the introduction of resistant strains into new environments where they may come into contact with humans or domestic animals [6]. Surveillance of these populations is crucial for understanding the dynamics of antibiotic resistance.

The purpose of this literature review is to synthesize current knowledge regarding the prevalence, transmission routes, and antimicrobial resistance of ***K. pneumoniae*** in wild birds, while highlighting the implications for avian health and potential risks to human health.

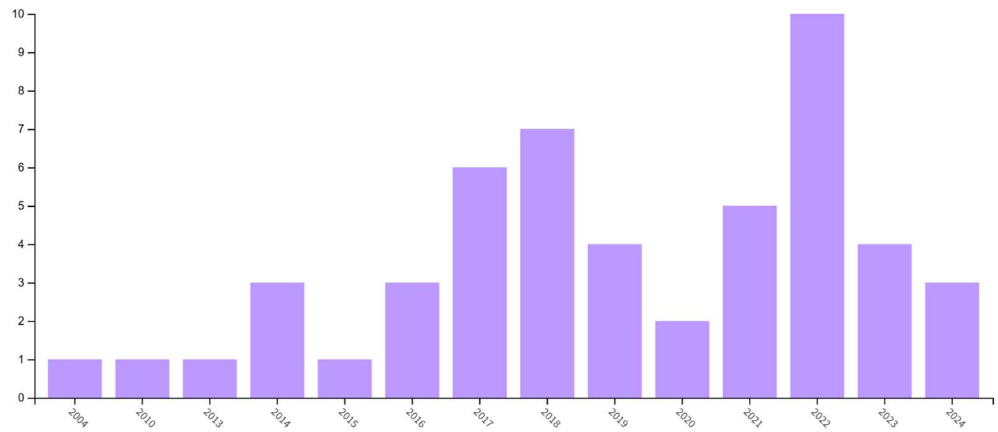

Figure 2. Illustration of the distribution of publication years for 51 articles retrieved from Web of Science, focusing on studies related to *K. pneumoniae* in wild birds and AMR. The data reveals temporal trends in research activity, highlighting an increasing interest in this topic over the years.

Materials and methods

A comprehensive literature review was conducted using the Web of Science database to identify relevant studies on *K. pneumoniae* in wild birds.

The query "*K. pneumoniae*” AND “wild birds" was used to retrieve articles addressing the prevalence, antimicrobial resistance, and zoonotic implications of *K. pneumoniae* in wild bird populations.

Inclusion Criteria

The inclusion criteria for this review encompassed studies that reported the detection or isolation of *K. pneumoniae* in wild birds, investigations into antimicrobial resistance patterns of *K. pneumoniae* isolates from avian hosts, and research examining zoonotic transmission risks or conducting comparative genomic analyses between avian and human *K. pneumoniae* strains.

Additionally, reviews and meta-analyses focusing on the role of *K. pneumoniae* in wildlife and its public health implications were considered.

Exclusion Criteria

The exclusion criteria for this review included studies focusing exclusively on domestic poultry or other non-wild bird species, research not directly related to *K. pneumoniae* or lacking explicit mention of wild birds, as well as conference abstracts, editorials, and non-peer-reviewed sources.

The initial search yielded **51 articles**, which were screened based on their titles, abstracts, and, where necessary, full texts. After applying the exclusion criteria, the focus was narrowed to **36 open-access articles** studied in 28 different regions.

From these, **22 articles** met all the inclusion criteria and were selected for analysis.

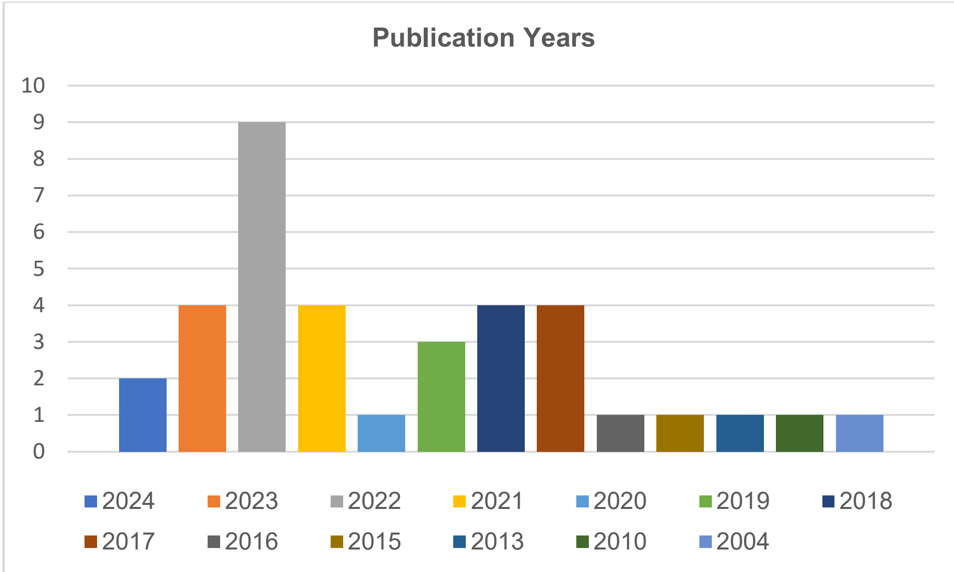

Figure 3. Publication years of 36 open-access articles on *K. pneumoniae* in wild birds (WOS).

The following data were extracted from the selected articles: study location and scope; prevalence data; antimicrobial resistance; zoonotic potential.

The extracted data were synthesized to identify patterns, trends, and gaps in research, with a focus on the public health implications of *K. pneumoniae* in wild birds.

As this study is a literature review, it did not involve the collection of new data from animals or humans. All analyzed data were obtained from publicly available sources.

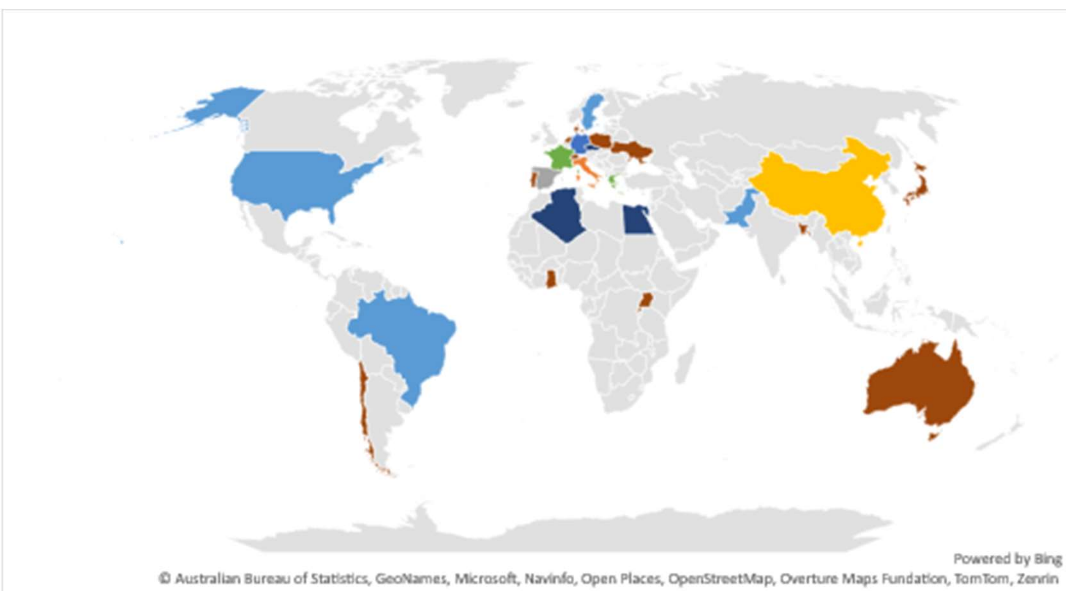

Figure 4. Geographic distribution of relevant publications on *K. pneumoniae* in wild birds. The chart highlights the regions and countries contributing to the research, with the number of studies from each location represented proportionally. This distribution emphasizes the global interest in understanding *Klebsiella* in wild bird populations, with notable contributions from regions such as Germany, Italy, Spain, China, Brazil, and the USA, among others. The chart provides insight into geographic research trends and potential gaps in global coverage.

Results and discussions

The Role of Wild Birds as Reservoirs of Antimicrobial Resistance

The reviewed studies strongly support the role of wild birds as significant reservoirs and potential disseminators of AMR bacteria.

Across various regions and species, wild birds were found to harbor multidrug-resistant pathogens such as *K. pneumoniae*, *E. coli*, and other Enterobacterales [13, 16].

For example, Mansoor et al. (2023) identified phenotypic resistance to tigecycline in *K. pneumoniae* isolates from black kites in Pakistan, emphasizing the risk of tet(X4)-carrying bacteria in wildlife.

Similarly, Darwich et al. (2019) reported a 20% prevalence of carbapenem-resistant (CR) *K. pneumoniae* in Spain, with co-resistance to multiple antibiotic classes, which highlights the potential for wild birds to serve as environmental reservoirs of complex resistance patterns.

Migratory birds further amplify this concern, as demonstrated by studies which revealed the global dissemination of carbapenemase genes (e.g., KPC) in wild bird populations sampled across continents. This evidence underscores the role of migratory routes in the global spread of AMR [1].

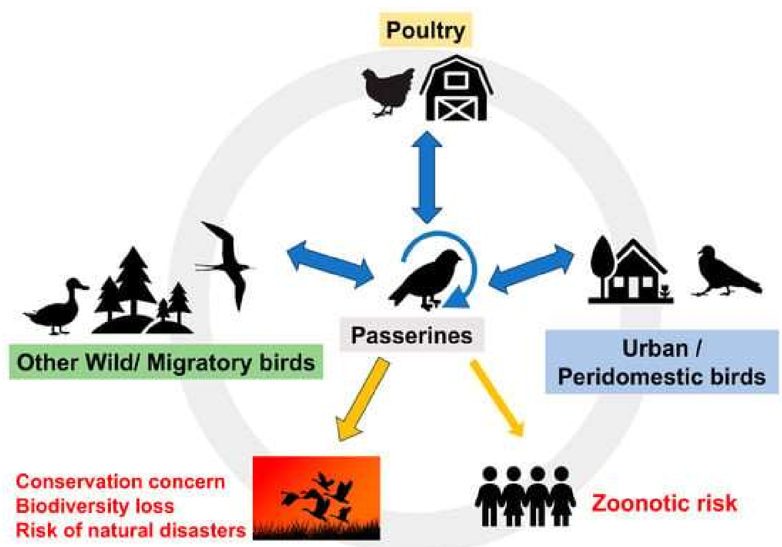

Figure 5. Theoretical role of wild birds in transmitting bacterial pathogens to other birds, domestic animals, and humans (blue and orange arrows), highlighting zoonotic risks and biodiversity threats within the One Health framework (grey ring). Source: Williams et al., 2023 (*Microorganisms, 11*(9), 2355) https://doi.org/10.3390/microorganisms11092355.

Regional Variations in AMR Profiles

The geographical diversity of the studies reflects varying AMR profiles in wild bird populations.

In Egypt, Ahmed et al. (2019) observed colistin resistance genes (mcr-1 and mcr-2) in wild bird isolates, alongside recovery of AMR bacteria from water and human samples. This highlights environmental contamination and possible interspecies transmission.

In Italy, both Foti et al. (2017) and Russo et al. (2022) confirmed the prevalence of multidrug-resistant *K. pneumoniae* and other AMR bacteria, emphasizing the sentinel role of birds in monitoring anthropogenic impacts on microbial resistance.

North and South America present similar concerns, with Kutilova et al. (2021) documenting multidrug-resistant *K. pneumoniae* ST258, a globally distributed nosocomial clone, in American crows.

In Brazil, Matias et al. (2016) reported AMR bacteria in wild birds involved in illegal trade, raising concerns about the impact of wildlife trafficking on AMR dissemination.

Potential Cross-Species and Environmental Transmission

Several studies suggest a strong link between wildlife, humans, and environmental reservoirs of AMR bacteria [3,4,19].

Nsengimana et al. (2022) found that *K. pneumoniae* isolates from captive grey crowned cranes in Rwanda were genetically indistinguishable from those isolated in human clinical cases. This implies the potential for cross-infection between wildlife and humans, possibly through shared environments or direct contact.

Table 1.
Geographic distribution of resistance genes

Region	Bird Species	Resistance genes identified	Significant findings
Pakistan	Black kites (*Milvus migrans*)	tet(X4)	Resistance to tigecycline found in *K. pneumoniae* and *E. coli* isolates
Spain	Various (e.g., Tawny owl, serin)	Multiple (e.g., CR phenotype)	11.5% CR prevalence; multiresistant *K. pneumoniae* isolates
Rwanda	Grey crowned crane	Carbapenemase	Genomic similarity between avian and human isolates
Egypt	Crows, waterfowl	mcr-1, mcr-2	Resistance genes linked to zoonotic risks
USA	Crows	KPC (ST258)	Multidrug-resistant *K. pneumoniae* from crows associated with hospital strains

Wang et al. (China) highlighted the capability of wild birds to carry extended-spectrum beta-lactamase (ESBL) genes, traditionally associated with healthcare settings, thereby emphasizing the potential spillover of AMR determinants between wildlife and human settings.

Implications for Public Health and Zoonotic Risk

Wild birds' capacity to carry and spread AMR bacteria has significant public health implications. Their ability to traverse vast geographical areas and frequent urban, agricultural, and natural environments creates pathways for zoonotic transmission.

Ahmed et al. (2019) and Foti et al. (2017) highlighted that migratory birds could act as sentinels for environmental health while posing risks as zoonotic reservoirs.

Ahlstrom et al. (2022) further emphasized how high genetic diversity in AMR genes (e.g., carbapenemases) in wild bird populations represents a growing challenge to global health.

Monitoring and Future Directions

Monitoring Systems: Expanding surveillance systems that integrate wildlife, human, and environmental health data can help track the dissemination of AMR. Studies like those by Foti et al. (2017) underline the value of birds as environmental health indicators.

Genomic Studies: Advanced genomic tools, as used by Ahlstrom et al. (2022), are critical for understanding the evolution and transmission dynamics of resistance genes across hosts and regions.

Mitigation Strategies: The role of anthropogenic factors in driving AMR, such as agricultural antibiotics and environmental contamination, necessitates stricter regulations and sustainable practices to minimize wildlife exposure.

Addressing Wildlife Trade: The illegal wildlife trade, as highlighted by Matias et al. (2016), represents a critical avenue for AMR spread and requires targeted interventions to mitigate its impacts.

Conclusions

The significance of studying *K. pneumoniae* in wild birds holds considerable implications for bird health and welfare, as well as broader ecological and public health considerations.

Firstly, wild birds can serve as reservoirs for multidrug-resistant strains of *K. pneumoniae*, which can negatively impact their health through increased susceptibility to infections and disease.

The presence of antimicrobial-resistant bacteria in these populations raises concerns about their ability to thrive in natural environments, particularly as they may encounter pathogens that are increasingly difficult to treat. This is especially critical given the ongoing global biodiversity crisis, where many bird species are already facing population declines due to habitat loss and other anthropogenic pressures.

Moreover, the interaction between wild birds and human environments—especially urban settings—can exacerbate the spread of antibiotic resistance. Birds that frequent areas such as landfills or wastewater treatment plants are more likely to carry resistant strains, which can then be transmitted back to humans or domestic animals.

This highlights the need for effective monitoring and management strategies to protect both avian populations and human health. Additionally, understanding the dynamics of *K. pneumoniae* transmission in wild birds can inform conservation efforts and public health policies aimed at mitigating the risks associated with antimicrobial resistance. By recognizing wild birds as potential vectors for disease transmission, stakeholders can develop targeted interventions to reduce environmental contamination and promote healthier ecosystems.

In summary, this study underscores the importance of addressing the health and welfare of wild birds not only for their own sake but also for maintaining ecological balance and safeguarding human health against the backdrop of rising antibiotic resistance.

Wild birds serve as critical reservoirs and potential vectors of AMR bacteria, with implications spanning public health, environmental safety, and wildlife conservation.

Regional differences in resistance profiles, coupled with evidence of interspecies transmission, highlight the need for a One Health approach to address the global AMR crisis. Future research should focus on integrating wildlife surveillance into existing AMR monitoring frameworks, with particular emphasis on genomic analyses and the role of migratory pathways in resistance dissemination.

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