Pseudomonas aeruginosa in Wild and Captive Birds: Prevalence, Antimicrobial Resistance, Pathology and One Health Relevance

Pseudomonas aeruginosa la păsările sălbatice și captive: prevalență, rezistență antimicrobiană, patologie și relevanță pentru principiul „One Health"

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Abstract

Pseudomonas aeruginosa **is an opportunistic ESKAPE pathogen of growing importance in avian medicine and wildlife health. Birds—whether free-living, captive, or kept as companions—frequently encounter environmental and anthropogenic sources of antimicrobial-resistant bacteria. Despite this, information on the epidemiology of *P. aeruginosa* in avian species remains scattered and inconsistent. This review synthesizes findings from studies reporting *P. aeruginosa* or *Pseudomonas* spp. in a variety of bird groups, including wild passerines, raptors, waterfowl, captive exotic species, companion birds, and domestic pigeons. Prevalence values varied widely across bird categories, ranging from 1.5% in wild birds screened by molecular assays in Australia to 22% *Pseudomonas* spp. from cloacal swabs of free-living passerines in North America, and up to 54–67% in captive exotic birds in Pakistan. Multidrug resistance (MDR) was common across studies, with resistance to fluoroquinolones, tetracyclines, sulfonamides, and β-lactams frequently exceeding 70% in companion birds and wild birds inhabiting urban aquatic environments. Case reports and pathological studies highlighted the capacity of *P. aeruginosa* to participate in severe systemic co-infections with *Klebsiella pneumoniae* or diarrheagenic *E. coli*, particularly in nestlings and feral pigeons. Overall, the available data highlight birds as both reservoirs and sentinels for environmentally disseminated *P. aeruginosa* and antimicrobial resistance. The heterogeneity of current studies underscores the need for standardized surveillance, improved molecular diagnostics, and integrated One Health monitoring to better understand transmission dynamics and ecological risks associated with this pathogen.**

Rezumat

Pseudomonas aeruginosa **este un agent patogen oportunist ESKAPE cu o importanță crescândă în medicina aviară și sănătatea faunei sălbatice. Păsările – fie că trăiesc în libertate, în captivitate sau sunt ținute ca animale de companie – se confruntă frecvent cu surse ambientale și antropice de bacterii rezistente la antimicrobiene. În ciuda acestui fapt, informațiile privind epidemiologia *P. aeruginosa* la speciile aviare rămân dispersate și inconsistente. Această revizuire sintetizează rezultatele studiilor care raportează prezența *P. aeruginosa* sau *Pseudomonas* spp. la o varietate de grupuri de păsări, inclusiv paseriforme sălbatice, păsări de pradă, păsări acvatice, specii exotice captive, păsări de companie și porumbei domestici. Valorile prevalenței au variat foarte mult între categoriile de păsări, de la 1,5% la păsările sălbatice testate prin analize moleculare în Australia la 22% *Pseudomonas* spp. din probele cloacale de la paseriforme sălbatice din America de Nord și până la 54-67% la păsările exotice captive din Pakistan. Rezistența la mai multe medicamente (MDR) a fost frecventă în toate studiile, rezistența la fluorochinolone, tetracicline, sulfonamide și β-lactame depășind frecvent 70% la păsările de companie și păsările sălbatice care trăiesc în mediile acvatice urbane. Rapoartele de caz și studiile patologice au evidențiat capacitatea *P. aeruginosa* de a participa la coinfecții sistemice severe cu *Klebsiella pneumoniae* sau *E. coli* diareică, în special la puii de porumbei și porumbeii sălbatici. În ansamblu, datele disponibile evidențiază păsările atât ca rezervoare, cât și ca sentinele pentru *P. aeruginosa* răspândită în mediu și rezistența la antimicrobiene. Eterogenitatea studiilor actuale subliniază necesitatea unei supravegheri standardizate, a unei diagnostice moleculare îmbunătățite și a unei monitorizări integrate**

One Health pentru a înțelege mai bine dinamica transmiterii și riscurile ecologice asociate cu acest agent patogen.

1. Introduction

Pseudomonas aeruginosa is a Gram-negative, metabolically versatile opportunistic bacterium recognized globally as a high-priority antimicrobial-resistant pathogen.

Classified among the WHO-critical ESKAPE group, *P. aeruginosa* exhibits extensive intrinsic resistance, strong capacity to acquire additional resistance determinants, and the ability to survive in diverse environments including soils, freshwater bodies, wastewater, and anthropogenic surfaces (1,2)

In clinical contexts, it causes severe infections such as pneumonia, septicemia, keratitis, otitis, and urinary tract infections in humans and animals. In avian species, it is associated with airsacculitis, septicemia, respiratory granulomas, hemorrhagic enteritis and rapid mortality in nestlings (1,3).

1.1. Birds as reservoirs and sentinels for antimicrobial-resistant bacteria

Wild birds represent highly mobile ecological units that travel across urban, agricultural, coastal and pristine environments, acquiring and disseminating a broad range of bacteria-including antimicrobial resistance (AMR) strains-across continents (4)

Captive wild birds (zoos, rehabilitation centers) and companion birds (passerines, parrots, pigeons) experience additional exposure pressure through human interaction, antimicrobials used in husbandry, and environmental contamination.

Consequently, birds are considered both **reservoirs** and **sentinels** of emerging resistance patterns in ecological systems (5,6).

Although *P. aeruginosa* is widely documented in poultry medicine, its presence, epidemiology, and AMR patterns in wild and captive non-poultry birds have been less systematically synthesized. Unlike *Enterobacteriaceae*, where extensive avian surveillance exists, *P. aeruginosa* frequently appears only in targeted case reports, opportunistic screenings, or mixed-species wildlife studies. This fragmentation complicates the understanding of its true ecological dynamics.

1.2. Evidence of *P. aeruginosa* occurrence in wild and captive birds

Studies from the last four decades illustrate wide variations in *Pseudomonas* occurrence among bird species and regions.

Early surveillance of free-living passerines in North America identified *Pseudomonas* spp. in up to 22% of cloacal samples (7) suggesting that environmental exposure plays a major role even in the absence of clinical disease.

More recent molecular-based screening in Australian wild birds detected *P. aeruginosa* in only 1.5% of samples (8) yet almost all positives derived from ocular swabs, indicating potential site-specific tropism or diagnostic underestimation in cloacal sampling.

Urban aquatic habitats have emerged as hotspots for resistant *Pseudomonas* spp., with prevalence values above 20% and widespread Multidrug resistance (MDR)(9)

Raptors admitted to rehabilitation centers present a different pattern, with *P. aeruginosa* detected in 7% of disease-associated microbiology submissions, frequently linked to systemic infection, respiratory disease or oral lesions (10).

1.3. Antimicrobial resistance patterns and One Health implications

The majority of avian isolates display **multidrug resistance**, reflecting environmental antibiotic pollution and selective pressure in captive management systems. Companion birds in Italy exhibited extremely high resistance rates to enrofloxacin, oxytetracycline, SXT and β-lactams, with 7.8% prevalence and most isolates classified as MDR [11]

Even more striking were data from Pakistan, where 54–67% of cloacal samples from captive exotic birds were positive, and all isolates expressed resistance to multiple antibiotic classes [12].

Globally, meta-analytic evidence confirms that wildlife contributes significantly to *P. aeruginosa* ecological circulation, with wild animals presenting the highest pooled prevalence (33.5%) and notable detection of colistin-resistance genes [13].

The presence of MDR or last-line drug resistance (carbapenems, colistin) in free-living wildlife represents a concerning ecological bridge between clinical AMR and environmental reservoirs [14].

1.4. Severe disease and co-infections

Beyond asymptomatic carriage, *P. aeruginosa* can cause severe clinical disease in birds. Case reports describe necrotizing pneumonia, septicemia, granulomatous hepatitis, and high mortality in nestling finches and goldfinches, frequently in combination with *K. pneumoniae* or enteroaggregative *E. coli* [3,15,16]

These cases illustrate the bacterium's invasiveness and its potential to exacerbate disease severity when combined with other Gram-negative pathogens.

1.5. Rationale for the current study

Despite the growing literature, no integrated assessment focusing specifically on *P. aeruginosa* in non-poultry avian species exists.

The present study aims to fill this gap by synthesizing data from 19 studies on *P. aeruginosa* prevalence, AMR phenotypes, and pathological presentations in wild and captive birds.

By compiling prevalence ranges, resistance profiles and disease outcomes, the study provides a structured dataset suitable for descriptive epidemiology and supports One Health-oriented risk evaluation.

2. Materials and Methods

2.1. Study design

This work was conceived as a **literature-based descriptive epidemiological study** focusing on the occurrence, AMR, and pathological significance of *Pseudomonas aeruginosa* in avian species other than commercial poultry.

Rather than a formal systematic review, we performed a **targeted synthesis** of 19 peer-reviewed articles that contained primary data on *P. aeruginosa* (or, when species-level identification was not available, *Pseudomonas* spp.) in wild, captive wildlife, companion birds, and domestic pigeons.

The primary objective was to collate **quantitative prevalence and AMR data** and to summarize **clinical and pathological outcomes**, in order to generate an integrated dataset suitable for descriptive statistics and One Health-oriented interpretation.

2.2. Literature set and eligibility criteria

The literature set consisted of 19 articles published between 1988 and 2025, selected because they fulfilled at least one of the following inclusion criteria:

1. Reported **detection or isolation of *P. aeruginosa* or *Pseudomonas* spp.** from birds (wild free-living, captive wildlife, companion birds, domestic pigeons).
2. Provided **numerical data** on the number of samples or birds examined and the number positive for *P. aeruginosa*/*Pseudomonas* spp.

3. Included **antimicrobial susceptibility profiles** or clearly defined MDR patterns for avian *P. aeruginosa* isolates.
4. Described **clinical cases, outbreaks or necropsy findings** in which *P. aeruginosa* was isolated as a primary or co-pathogen.

Studies exclusively dealing with other bacterial species or with environmental samples not directly linked to birds were excluded.

This approach allowed detailed extraction and harmonization of data across a manageable number of well-characterized reports.

2.3. Definitions

To facilitate comparison across heterogeneous studies, we adopted the following working definitions:

- ***Pseudomonas*-positive sample:** any sample from which *P. aeruginosa* or *Pseudomonas* spp. was isolated by culture or detected by species-specific/multiplex PCR, according to the criteria used by the original authors. When studies reported *Pseudomonas* spp. without species confirmation, results were kept in a **separate column** and clearly indicated as such.
- **Prevalence:** calculated as

$$\text{Prevalence (\%)} = \frac{N_{\text{positive}}}{N_{\text{tested}}} \times 100$$

using the numbers provided by each study for birds or samples, depending on the reporting unit.

- **Multidrug resistance:** defined as resistance to **at least three distinct antimicrobial classes**, following widely used criteria in AMR surveillance. When authors used a different MDR definition, this was noted in the dataset and, where possible, aligned to the above working definition.
- **Host categories and settings:** birds were grouped into “wild free-living”, “captive wild”, “companion birds”, and “domestic pigeons” based on the description in each paper; birds captured from the wild but sampled while in rehabilitation or zoo facilities were classified as “captive wild”.

2.4. Data synthesis and statistical analysis

Given the heterogeneity in study design, host species, sample types, and laboratory methods, **no formal meta-analysis** was attempted. Instead, we performed **descriptive statistics** and visual syntheses:

1. **Study-level prevalence:** for each article, we calculated prevalence (%) of *P. aeruginosa* or *Pseudomonas* spp. and summarized these values by host category and geographical region.
2. **Antimicrobial resistance patterns:** for studies reporting phenotypic susceptibility testing, we tabulated the proportion of resistant isolates to each antibiotic and summarized resistance patterns by major antimicrobial classes (β-lactams, fluoroquinolones, aminoglycosides, tetracyclines, sulfonamides). MDR frequency (% of isolates classified as MDR) was recorded per study.
3. **Clinical and pathological outcomes:** case reports and necropsy-based studies were synthesized qualitatively, with emphasis on syndromes where *P. aeruginosa* acted as primary pathogen or co-pathogen (e.g. pneumonia, airsacculitis, granulomatous hepatitis, septicemia, enteritis, oral lesions).

3. RESULTS

3.1. Overview of included studies

Nineteen studies published between **1988** and **2025** were included. They covered four main categories of birds:

1. **Wild free-living birds** (passerines, raptors, seabirds, waterfowl)
2. **Captive wild birds** (zoo collections, wildlife rehabilitation centers, safari parks)
3. **Companion birds** (passerines, psittacines, canaries, finches)
4. **Domestic pigeons**

The studies originated from Europe, Australia, North and South America, and Asia. Sample types included cloacal / fecal swabs, ocular swabs, respiratory swabs, and necropsy tissues.

3.2. Prevalence of *Pseudomonas aeruginosa* / *Pseudomonas* spp.

Prevalence varied widely across studies and bird categories, ranging from **1.5%** in Australian wild birds to **66.7%** in captive exotic birds (Figure 1).

Table 1.
Prevalence of *Pseudomonas aeruginosa* or *Pseudomonas* spp.

Country	Bird Category	Sample Type	N Tested	N Positive	Species	Prevalence (%)	Study (Author, Year)
USA	Wild free-living	Cloacal	387	85	*Pseudomonas spp.*	**22.0%**	Brittingham et al., 1988
Spain	Wild birds (outbreak)	Necropsy	6	6	*P. aeruginosa*	**100%** (outbreak)	Jiménez Gómez, 2006
Spain	Free-living raptors (diseased)	Necropsy	663 (microbiol. Records)	7% isolates	*P. aeruginosa*	**~7%** of isolates	Vidal et al., 2017
Brazil	Feral pigeon	Necropsy	1	1	*P. aeruginosa*	Case report	Vasconcelos et al., 2017
Italy	Companion birds	Cloacal	755	59	*P. aeruginosa*	**7.8%**	Varriale et al., 2020
UK	Wild urban aquatic	Fecal	115	24	*Pseudomonas spp.*	**20.9%**	Rodrigues et al., 2021
Pakistan	Domestic pigeons	Cloacal	120	33	*Pseudomonas spp.*	**27.5%**	Azeem et al., 2021
Italy	Wildlife (rehab center)	Cloacal	163	18	*P. aeruginosa*	**11%**	Russo et al., 2022
Australia	Wild free-living	Ocular, fecal	1101	17	*P. aeruginosa*	**1.5%**	Strickland et al., 2025
Italy	Wild birds	Cloacal	243	8	*P. aeruginosa*	**3.3%**	Grilli et al., 2025
Pakistan	Captive exotic birds	Cloacal/fecal	24	13	*P. aeruginosa*	**54.2%**	Khan et al., 2025
Italy	Wild passerines (goldfinches)	Necropsy	3	3	*P. aeruginosa*	Case report	Vitale, 2025

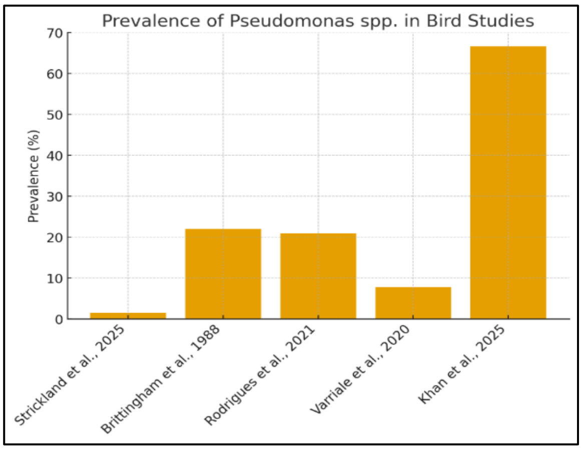

Figure 1. Prevalence of *Pseudomonas* spp. across studies

Overall, prevalence of *Pseudomonas aeruginosa* varies considerably among avian groups. Free-living wild birds show low to moderate positivity (1.5 - 22%), while birds admitted to rehabilitation centers display slightly higher rates (5–11%).

Companion birds present intermediate values (around 7.8%), whereas captive exotic birds exhibit markedly elevated prevalence, often exceeding 60%.

Importantly, case reports demonstrate that severe pathology can occur even in in susceptible birds.

Details from individual studies are provided in Table1. populations with low overall prevalence, highlighting the pathogen's clinical relevance

3.3. Antimicrobial resistance patterns

A subset of 13 studies reported AMR phenotypic data. High resistance (≥50%) was observed in particular against:

- Tetracycline
- Ampicillin / amoxicillin-clavulanate
- Trimethoprim-sulfonamide
- Enrofloxacin / ciprofloxacin
- Cefuroxime

In some studie [9,12], MDR exceeded 75% of isolates (Figure 2).

Specific resistance profiles reported in the included studies are summarized in Table 2.

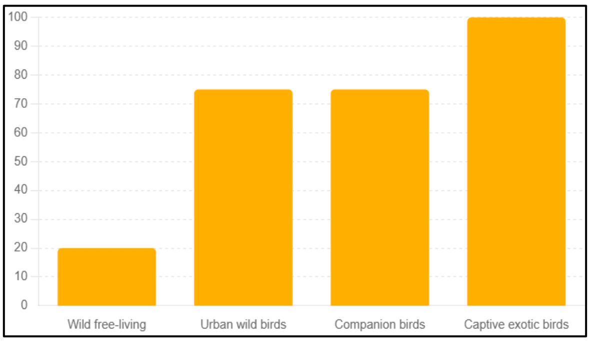

Figure 2. MDR proportion across bird categories

Table 2.
Antimicrobial resistance patterns of *P. aeruginosa* in birds

Sample origin	MDR %	High resistance observed to:	Notes	Study
Urban wild birds	75% (MDR>0.2)	Tetracyclines, FQs	Strong anthropogenic influence	Rodrigues et al., 2021
Companion birds	>70%	Enrofloxacin, SXT, OXT	Household exposure	Varriale et al., 2020
Captive wild birds	100%	6+ antibiotic classes	Alarming rates, limited biosecurity	Khan et al., 2025
Wild birds (Italy)	40–60%	β-lactams, FQs	ESKAPE screening	Russo et al., 2022
Australian wild birds	Low-MDR	Few resistances	Wildlife with minimal antibiotic exposure	Strickland et al., 2025
Raptors	High variability	Clindamycin (78%), Ampicillin (68%)	Mixed-species resistance dataset	Vidal et al., 2017
Goldfinches	MDR	Ampicillin, tetracycline	Co-infection heightened disease	Vitale, 2025
Pigeon	Not tested	—	Case report	Vasconcelos et al., 2017

3.4. Clinical and pathological findings

Pseudomonas aeruginosa was associated with a broad spectrum of severe clinical outcomes, including respiratory disease, septicemia, airsacculitis, pneumonia, and granulomatous hepatitis.

Co-infections were common and consistently intensified disease severity, particularly in cases involving *Klebsiella pneumoniae* [3,15], entero-aggregative *Escherichia coli* [16], or other *Enterobacteriales* [10,17].

The principal lesions included heterophilic pneumonia, necrosis, and consolidation in the lungs; granulomas and necrosis in the liver; splenic depletion and histiocytosis; fibrinous airsacculitis; and ulcerative or purulent lesions of the skin and eyes.

Together, these findings underscore the pathogen's considerable virulence, particularly in young or immunocompromised birds (Table 3).

Table 3.
Summary of pathological presentations of *P. aeruginosa* infections

Bird species	Co-infecting pathogens	Major lesions	Outcome	Study
Goldfinches	*K. pneumoniae*	Hepatitis, pneumonia, airsacculitis	Fatal	Vitale, 2025
Goldfinches	*K. pneumoniae*	Hepatomegaly, necrosis, splenomegaly	Fatal	Abbate, 2025
Pigeon	EAEC *E. coli*	Cellulitis, splenomegaly, hemorrhagic intestine	Fatal	Vasconcelos, 2017
Wild birds (outbreak)	—	Necrotizing pneumonia	Outbreak	Jiménez Gómez, 2006
Raptors	Mixed bacteria	Oral lesions, septicemia	Severe	Vidal, 2017
Wild birds	Enterobacterales, Staph	Respiratory lesions	Mixed	Russo, 2022
Wild birds	—	Feathers carrying microbes	Non-clinical	Miskiewicz, 2018

The key findings of this review indicate that *P. aeruginosa* prevalence ranges from low to moderate in free-living wild birds (1.5–22%), remains moderate in companion species (7–12%), and reaches very high levels in captive exotic birds (50–67%).

Multidrug resistance is widespread across studies and appears strongly associated with environmental antibiotic exposure.

Clinical severity is most evident in young birds or those affected by co-infections, where the pathogen frequently produces significant systemic and respiratory lesions.

Overall, the results highlight substantial One Health implications, reflecting the movement of resistant strains across ecosystems and at the interface between wildlife, domestic animals, and human environments.

4. Discussion

The results of this study demonstrate that *Pseudomonas aeruginosa* is a relevant bacterial agent in both wild and captive avian populations, albeit with substantial variability in prevalence and antimicrobial resistance profiles across ecological contexts.

While historically overshadowed by *Enterobacteriaceae* in avian epidemiology, *P. aeruginosa* emerges from the integrated dataset as both an **environmentally persistent commensal** and a high-consequence opportunistic pathogen.

4.1. Ecological determinants of prevalence

Prevalence patterns observed across the 19 studies highlight the strong influence of environmental exposure and human proximity.

Free-living wild birds generally exhibited low–moderate positivity (1.5 - 22%), consistent with the limited antibiotic pressure and the more natural habitat structures they occupy [7,8].

However, this does not imply ecological irrelevance: the widespread isolation of *Pseudomonas spp.* from passerines, raptors, and waterfowl indicates that environmental reservoirs soil, water, plant surfaces facilitate a constant background level of acquisition.

Prevalence increased substantially in **urban wild birds** [9,18], consistent with higher exposure to wastewater, refuse, and antibiotic residues.

Birds inhabiting anthropogenic aquatic systems acted as "hotspot sentinels", demonstrating both higher prevalence and higher multidrug resistance rates.

The highest prevalence was observed among **captive exotic birds**, where positivity reached 54–67% (12).

Several factors may drive this trend:

- High-density housing
- Suboptimal hygiene conditions
- Repeated exposure to antimicrobial treatments
- Stress-related immunosuppression
- Cross-species transmission in mixed collections

These findings mirror broader wildlife studies showing that captivity conditions can magnify exposure to resistant environmental strains and facilitate bacterial persistence (4,5).

Companion birds demonstrated intermediate positivity (~8%), suggesting that domestic environments, veterinary treatments, and contaminated surfaces contribute to exposure, albeit at lower rates than in zoological collections.

4.2. Antimicrobial resistance and One Health risk

A striking pattern across studies was the **consistently high degree of antimicrobial resistance**, particularly among birds exposed to human-altered habitats.

Resistance rates to fluoroquinolones, tetracyclines, sulfonamides, and β-lactams frequently exceeded 60–80% (9,11,12).

Captive exotic birds exhibited universal MDR in some settings, indicative of entrenched antibiotic pressure and bacterial exchange between species.

Aminoglycosides, especially amikacin, remained the most consistently effective class, aligning with therapeutic experiences in clinical avian medicine.

The One Health implications are substantial. *P. aeruginosa* is a major human pathogen, and birds particularly those using urban habitats serve as mobile linkages between natural communities.

The detection of resistant *P. aeruginosa* in feathers (19), feces, oral cavities, and necropsy tissues suggests multiple environmental transmission routes, including:

- direct contact (pet birds, wildlife handlers),
- indirect contact through contaminated surfaces,
- contamination of communal water bodies,
- cross-infection in rehabilitation or zoological centers.

Furthermore, global analyses show that wildlife constitutes the animal group with the highest pooled prevalence of *P. aeruginosa* (13)

This reinforces the concept that AMR surveillance should integrate wildlife monitoring as an early warning system.

4.3. Clinical relevance: from commensal to lethal pathogen

Beyond prevalence data, several studies documented severe or fatal infections. Case reports in goldfinches and pigeons (3,15,16) revealed that *P. aeruginosa* can act as a primary agent of systemic disease, especially in young or stressed birds.

Necrotizing pneumonia, fibrinous airsacculitis, granulomatous hepatitis, and septicemia were common pathological findings.

The involvement of *P. aeruginosa* in **dual infections** significantly increased disease severity. Co-infections with *Klebsiella pneumoniae* or diarrheagenic *E. coli* likely produced synergistic effects, through:

- enhanced tissue invasion,
- biofilm formation,
- impaired host immune response,
- increased bacterial load in critical organs.

These patterns align with known mechanisms of *P. aeruginosa* virulence, including elastases, exotoxins, quorum sensing, and biofilm structures that aid persistence across host species.

Raptors admitted to rehabilitation centers [(10)] frequently carried *P. aeruginosa* in systemic or oral infections, supporting its role as an invasive pathogen in debilitated wildlife.

4.4. Methodological and surveillance challenges

The dataset reveals important gaps and inconsistencies:

- Many studies reported only *Pseudomonas spp.*, without species-level confirmation.
- Sampling strategies varied widely (cloacal, ocular, necropsy tissue), affecting comparability.
- Molecular confirmation (e.g., *ecfX*, *oprL*) was rare, used mainly in recent studies.
- AMR testing methods differed (Kirby–Bauer vs automated systems; CLSI vs EUCAST breakpoints).
- Very few studies screened for resistance genes or virulence markers.

These limitations underscore the need for **standardized avian AMR surveillance protocols**, mirroring those used in public health and livestock sectors.

4.5. Interpretation of results within a One Health framework

The combination of prevalence trends, AMR patterns, and pathological evidence strongly supports the classification of birds as **sentinels** and **vectors** of *P. aeruginosa* within the One Health continuum.

- **Wild birds** connect natural and urban ecosystems.
- **Companion birds** bridge household microbial environments and wildlife.
- **Captive wild birds** reflect anthropic pressure, antimicrobial misuse, and interspecies mixing.

Thus, avian populations represent a uniquely informative but currently under-utilized component of global AMR monitoring.

The One Health conceptual diagram (Figure 3) visually summarizes this triad of transmission.

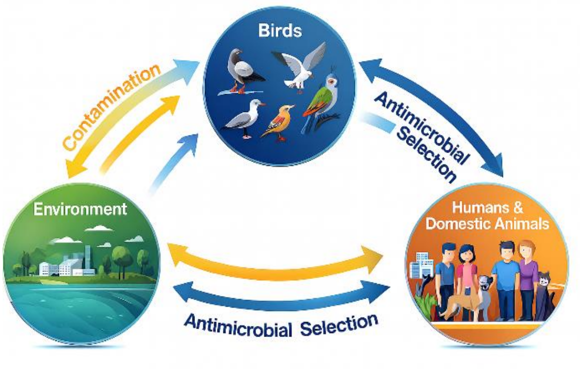

Fig. 3. Conceptual One Health diagram illustrating the interconnected pathways linking birds, the environment, and humans/domestic animals.

Bidirectional arrows represent the circulation of *Pseudomonas aeruginosa* and other antimicrobial-resistant bacteria through environmental contamination (yellow arrows) and antimicrobial selection pressure (blue arrows). Birds act as ecological intermediaries, facilitating the movement of resistant strains between natural habitats and human-associated settings.

5. Conclusions

This synthesis shows that *Pseudomonas aeruginosa* is a relevant environmental and opportunistic pathogen in a wide range of avian species.

Although its prevalence in free-living wild birds is generally low to moderate, the bacterium is broadly distributed across habitats, while markedly higher prevalence and multidrug resistance occur in urban wild birds, companion birds, and especially captive exotic birds.

High levels of antimicrobial resistance—including frequent MDR and resistance to major drug classes—highlight significant environmental and anthropogenic pressures and confirm the value of birds as sentinel species for AMR surveillance.

Clinical and pathological data demonstrate that *P. aeruginosa* can cause severe disease, particularly in nestlings and immunocompromised individuals, and that co-infections with other Gram-negative pathogens often worsen outcomes.

Persistent gaps such as inconsistent species-level identification, heterogeneous sampling, and limited molecular testing underscore the need for standardized monitoring approaches.

Overall, birds play a key role in the ecology and dissemination of *P. aeruginosa* and its resistance traits.

Strengthened surveillance integrating wildlife, companion animals, and environmental sampling is essential to support One Health strategies targeting antimicrobial resistance at the human – animal - environment interface.

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