



# Antimicrobial resistance in bacterial pathogens of pigeons: A One Health perspective

<sup>1</sup>Zsolt A. Grabán, <sup>2</sup>Tudor Păpuc

<sup>1</sup> National Association of Pigeon and Small Animal Breeders of Hungary, Budapest, Hungary; <sup>2</sup> Faculty of Animal Science and Biotechnologies, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Cluj-Napoca, Romania. Corresponding author: T. Păpuc, tudor.papuc@usamvcluj.ro

**Abstract.** Antimicrobial resistance (AMR) in bacterial pathogens associated with pigeons (*Columba livia*) has emerged as a significant concern within the One Health framework, reflecting the interconnectedness of human, animal, and environmental health. This mini-review synthesizes current evidence on the prevalence, diversity, and molecular determinants of antimicrobial-resistant bacteria in both feral and domestic pigeon populations. Pigeons are frequently colonized by clinically relevant bacterial species, including *Escherichia coli*, *Salmonella enterica*, *Staphylococcus aureus*, *Enterococcus* spp., and *Klebsiella pneumoniae*, many of which exhibit multidrug-resistant (MDR) phenotypes. Resistance is commonly mediated by mobile genetic elements carrying genes such as CTX-M, mcr-1, mecA, and others, often associated with globally disseminated clonal lineages shared across humans, livestock, and wildlife. Environmental interfaces, including urban settings, healthcare facilities, and livestock farms, facilitate the acquisition and dissemination of these resistant strains. Evidence indicates that pigeons can act as reservoirs, sentinels, and potential vectors of AMR, contributing to the environmental circulation of resistance determinants. Overall, the findings underscore the importance of integrated surveillance and coordinated antimicrobial stewardship strategies to mitigate the spread of AMR within and beyond avian populations.

**Key Words:** *Columba livia*, ESBL, *Escherichia coli*, MRSA, multidrug resistance, *Salmonella enterica*, zoonotic pathogens.

**Introduction.** Due to their outstanding navigational skills, varied phenotypic expression, and thoroughly studied physiological traits, pigeons (*Columba livia*) serve as a valuable model organism for integrative research encompassing behavior, morphology, and metabolic processes (Ionescu & Oroian., 2015; Ionescu et al., 2015; Ionescu & Oroian, 2019; Popescu & Cimpean, 2026; Popescu et al., 2026).

Pigeons, both feral and domestic, live in close contact with humans, livestock, companion animals and the urban environment. Across several regions, they carry antimicrobial resistant and multidrug resistant (MDR) bacteria of major clinical importance, making them relevant in a One Health context (Horn et al., 2018; Vasconcelos et al., 2018; Aslantaş & Gövce, 2020; Kaczorek-Łukowska et al., 2020; Chrobak-Chmiel et al., 2021; Bueno et al., 2022; Freire et al., 2022; Sano et al., 2022; Souguir et al., 2023; Wilson et al., 2024; Zhang et al., 2024; Kerek et al., 2025a,b).

The aim of this mini-review is to provide a comprehensive synthesis of current knowledge regarding antimicrobial resistance in bacterial pathogens associated with pigeons (*Columba livia*) within a One Health context. Specifically, the study seeks to (i) identify the major bacterial taxa of clinical and zoonotic relevance present in pigeon populations, (ii) characterize their antimicrobial resistance profiles and underlying molecular determinants, including resistance genes and clonal lineages, and (iii) evaluate the role of pigeons as reservoirs, sentinels, and potential disseminators of antimicrobial resistance across human, animal, and environmental interfaces. Additionally, the review aims to highlight epidemiological links and risk factors associated with AMR transmission, as well as to identify critical gaps in surveillance and research.

**Major Bacterial Pathogens and Zoonotic Relevance.** *Escherichia coli* is the most frequently reported species, with high carriage rates in cloacal or fecal samples (often >90%) (Horn et al., 2018; Aslantaş & Gövce, 2020; Karim et al., 2020; Bueno et al., 2022; Ahmed & Gulhan, 2024; Wilson et al., 2024; Kowalczyk & Wójcik-Fatla, 2025; Kerek et al., 2025a,b). Many isolates belong to pathogenic pathotypes such as STEC, EPEC, APEC, or carry EAST1 toxin genes, intimin (*eae*) and other virulence factors (Horn et al., 2018; Vasconcelos et al., 2018; Carvalho et al., 2020; Karim et al., 2020; Bueno et al., 2022; Sano et al., 2022; Santana et al., 2022; Kowalczyk & Wójcik-Fatla, 2025; Kerek et al., 2025a,b). *Salmonella enterica*, particularly serovar Typhimurium (including monophasic 1,4, (Karim et al., 2020),12:i:-), is repeatedly detected, often with multiple virulence genes and sometimes associated with outbreaks in pigeons (Horn et al., 2018; Vasconcelos et al., 2018; Carvalho et al., 2020; Kaczorek-Łukowska et al., 2020; Santana et al., 2022; Zhang et al., 2024). Clinically relevant *Staphylococcus aureus*, including methicillin resistant (MRSA), and other staphylococci, as well as *Enterococcus* spp., *Klebsiella pneumoniae* and *Clostridioides difficile* have been found in pigeons, sometimes as MDR or extensively drug resistant strains (Chrobak-Chmiel et al., 2021; Santana et al., 2022; Freire et al., 2022; Wilson et al., 2024; Zhang et al., 2024; Kerek et al., 2025a,b; Zhao et al., 2025) (Table 1).

Table 1  
Antimicrobial resistance profiles in key taxa/representative resistance patterns in pigeon-associated bacteria

Bacterial group / context	Main resistance findings	References
<i>E. coli</i> – urban/feral pigeons	16–63% MDR; resistance to tetracycline, ampicillin, nalidixic acid, fluoroquinolones; detection of <i>mcr-1</i> , ESBL (CTX-M) genes in some settings	Horn et al., 2018; Aslantaş & Gövce, 2020; Karim et al., 2020; Bueno et al., 2022; Freire et al., 2022; Sano et al., 2022; Souguir et al., 2023; Ahmed & Gulhan, 2024; Wilson et al., 2024; Kowalczyk & Wójcik-Fatla, 2025; Kerek et al., 2025a,b
<i>Salmonella enterica</i> (mainly Typhimurium)	High resistance to cefazolin, aminoglycosides in China; frequent genotypic resistance to tetracyclines, sulfonamides, aminoglycosides in Poland; often phenotypically MDR, though some series remain fully susceptible	Horn et al., 2018; Carvalho et al., 2020; Karim et al., 2020; Kaczorek-Łukowska et al., 2020; Zhang et al., 2024
<i>Staphylococcus aureus</i>	Very high MDR prevalence (≈80%); frequent resistance to doxycycline, enrofloxacin, amoxicillin; methicillin-resistant and highly MDR strains in feral pigeons near hospitals	Chrobak-Chmiel et al., 2021; Santana et al., 2022; Kerek et al., 2025a,b
<i>Enterococcus</i> spp.	≈60% MDR; high resistance to tylosin, florfenicol, enrofloxacin; full susceptibility to neomycin and potentiated sulfonamides in one survey	Aslantaş & Gövce, 2020; Kerek et al., 2025a,b
<i>Klebsiella pneumoniae</i> (oral, farm pigeons)	Multidrug resistance to cephalosporins and aminoglycosides; TEM, SHV, CTX-M-9 ESBLs and plasmid-mediated <i>qnrB</i> , <i>tetA</i> , <i>aac(6)-Ib</i>	Zhao et al., 2025
Carbapenemase/ESBL producers (various <i>Enterobacteriales</i> , <i>Pseudomonas</i> )	CTX-M-15/27 <i>E. coli</i> and VIM-2 <i>Pseudomonas putida</i> in free-living pigeons on livestock farms; ESBL <i>E. coli</i> with human-associated sequence types in urban pigeons	Bueno et al., 2022; Freire et al., 2022; Souguir et al., 2023; Kerek et al., 2025a,b

**Molecular Determinants and Clonal Lineages.** Across taxa, resistance is driven by classic acquired genes, often on plasmids or integrons. In *E. coli*, CTX M ESBLs, mcr 1 colistin resistance, and a wide array of tetracycline, sulfonamide and aminoglycoside resistance genes are reported (Aslantaş & Gövce, 2020; Karim et al., 2020; Freire et al., 2022; Bueno et al., 2022; Sano et al., 2022; Souguir et al., 2023; Ahmed & Gulhan, 2024; Wilson et al., 2024; Kerek et al., 2025a,b). Pigeon derived *E. coli* include international “One Health” clones (e.g. ST10, ST131, ST155, ST206, ST224, ST457) that are also found in humans, livestock and the environment (Bueno et al., 2022; Sano et al., 2022; Freire et al., 2022; Kerek et al., 2025a,b). *Salmonella* Typhimurium isolates from pigeons often harbor multiple virulence genes (*invA*, *hilA*, *avrA*, *lpfA*, *sivH*, *agafA*, *sitC*, *pefA*) together with *sul1*, *tet(A)*, *floR*, *strA/strB* and other resistance markers, frequently combined with biofilm capacity (Carvalho et al., 2020; Kaczorek-Łukowska et al., 2020; Zhang et al. 2024). MRSA and MDR staphylococci from pigeons carry *mecA* and other resistance determinants against beta lactams, aminoglycosides, macrolides, tetracyclines and phenicols (Chrobak-Chmiel et al., 2021; Santana et al., 2022; Kerek et al., 2025a,b). Enterococci and *K. pneumoniae* isolates also show diverse resistance genes, including TEM, SHV, CTX M 9 and plasmid mediated *qnr*, *tet*, and aminoglycoside modifying enzymes (Aslantaş & Gövce, 2020; Kerek et al., 2025a,b; Zhao et al., 2025).

**One Health Implications and Environmental Interfaces.** Multiple lines of evidence show that pigeons can act as environmental sentinels and reservoirs for clinically important resistance determinants. Free living urban pigeons carry MDR *E. coli* and ESBL producers, including clones and plasmids shared with humans and domestic animals, highlighting possible bidirectional transmission routes (Vasconcelos et al., 2018; Bueno et al., 2022; Freire et al., 2022; Sano et al., 2022; Souguir et al., 2023; Ahmed & Gulhan, 2024; Wilson et al., 2024; Kerek et al., 2025a,b). Pigeons near hospitals and veterinary centers have yielded MRSA, MDR *E. coli*, *Salmonella* and *C. difficile*, suggesting that healthcare and veterinary facilities may be important sources and sinks of resistant strains that are then redistributed by birds (Chrobak-Chmiel et al., 2021; Santana et al., 2022; Sano et al., 2022; Wilson et al., 2024; Zhang et al., 2024). On livestock farms, pigeons harbor CTX M ESBL *E. coli* and VIM 2 carbapenemase producing *Pseudomonas*, with evidence for both clonal spread and plasmid mediated gene transfer (Souguir et al., 2023). High MDR burdens in domestic racing or farm pigeons point to selection from veterinary antibiotic use and raise concerns about occupational exposure, food chain contamination (e.g. feed silos), and environmental dissemination via feces (Aslantaş & Gövce, 2020; Carvalho et al., 2020; Kaczorek-Łukowska et al., 2020; Karim et al., 2020; Zhang et al., 2024; Kerek et al., 2025a,b; Zhao et al., 2025).

From a One Health standpoint (Gavriloaie, 2023; Petrescu-Mag, 2023), the convergence of human associated lineages, mobile resistance elements (ESBLs, carbapenemases, mcr 1), and zoonotic pathogens (STEC, ETEC, APEC, *Salmonella* Typhimurium, MRSA, *C. difficile*) in pigeon populations supports their recognition as important nodes in the human–animal–environment antimicrobial resistance network and underlines the need for integrated surveillance, biosecurity and prudent antimicrobial use across sectors (Horn et al., 2018; Vasconcelos et al., 2018; Aslantaş & Gövce, 2020; Kaczorek-Łukowska et al., 2020; Chrobak-Chmiel et al., 2021; Bueno et al., 2022; Freire et al., 2022; Santana et al., 2022; Sano et al., 2022; Souguir et al., 2023; Ahmed & Gulhan, 2024; Wilson et al., 2024; Zhang et al., 2024; Kerek et al., 2025a,b; Zhao et al., 2025).

**Conclusions.** Current evidence clearly demonstrates that pigeons harbor a wide range of antimicrobial-resistant and multidrug-resistant bacterial pathogens of significant clinical relevance. High prevalence rates of MDR *Escherichia coli*, *Salmonella enterica*, and methicillin-resistant *Staphylococcus aureus* (MRSA), along with resistant *Enterococcus* spp. and *Klebsiella pneumoniae*, indicate that pigeon populations represent important reservoirs of resistance.

The presence of mobile genetic elements, including extended-spectrum  $\beta$ -lactamases (ESBLs), carbapenemases, and plasmid-mediated resistance genes such as

mcr-1, highlights the potential for horizontal gene transfer and rapid dissemination across ecological compartments. The identification of globally distributed clonal lineages shared between pigeons, humans, and livestock further reinforces the interconnected nature of antimicrobial resistance within the One Health framework.

Environmental interfaces, particularly urban ecosystems, healthcare-associated environments, and livestock production systems, play a critical role in shaping resistance patterns and facilitating bidirectional transmission. Consequently, pigeons function not only as passive carriers but also as active participants in the environmental spread of antimicrobial resistance.

Future efforts should prioritize integrated, cross-sectoral surveillance systems, combining microbiological, molecular, and ecological data. Strengthening antimicrobial stewardship, improving biosecurity measures, and monitoring wildlife–human–livestock interactions are essential steps toward mitigating the global threat posed by antimicrobial resistance.

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**Conflict of Interest.** The authors declare that there is no conflict of interest.

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Authors:

Zsolt Attila Grabán (ZAG), National Association of Pigeon and Small Animal Breeders of Hungary, 1433 Budapest, Pf. 575, Hungary, e-mail: grabanzsolt@gmail.com

Tudor Păpuc (TP), Faculty of Animal Science and Biotechnologies, University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Calea Mănăştur 3-5, 400372 Cluj-Napoca, Romania, e-mail:

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