Annals of Animal Science
Volume 27 · pp. 304–367 · DOI: 10.2478/aoas-2027-0024

Annals of Animal Science

Current trends in drug resistance of pathogens isolated from poultry and the use of commercial phage preparations to control infections

Review Article

Renata Urban-Chmiel[1], Marta Dec[1], Agnieszka Marek[1], Dagmara Stepień-Pyśniak[1], Anna Nowaczek[1], Klaudia Herman-Ostrzyżek[1], Magdalena Zając[2], Ewelina Pyzik[1]*

[1] *Department of Veterinary Prevention and Avian Diseases, Faculty of Veterinary Medicine, University of Life Sciences in Lublin, Akademicka 12, 20-033 Lublin, Poland*
[2] *Department of Microbiology, National Veterinary Research Institute (PIWetPIWet-PIB), Partyzantów 57, 24-100 Puławy, Poland*

Received 19 June 2026; Accepted 04 September 2026

Abstract: Food safety in poultry products is crucial due to the potential presence of various pathogens causing foodborne diseases. The microbes most commonly isolated from poultry include *Salmonella* spp., *Campylobacter jejuni*, *Campylobacter coli*, *Escherichia coli*, *Staphylococcus* spp., and *Listeria monocytogenes*. A particular threat is posed by drug-resistant pathogens, which significantly limit the possibility of controlling infections and food contamination. In the last 5 years, significant changes have been observed in the acquisition of antimicrobial resistance in pathogens, which is closely linked to the type of drug used. The aim of the present study is to present current trends in acquisition of drug resistance among the bacteria most commonly isolated from poultry and the perspectives of using of experimental and commercial phage preparations as an alternative to antibiotics. Analysis of the literature from various parts of the world, as well as our own research, reveals that drug resistance among bacteria in poultry continues to be a major factor limiting the ability to combat infections. Equally concerning is the fact that over the last 5 years, there has been a significant increase in bacterial resistance to the antibiotics most commonly used in poultry production, mainly tetracyclines, fluoroquinolones, beta-lactams, and macrolides, which is indicative of continuing acquisition of resistance by pathogens. Actions undertaken at many research centres, including in Poland, using bacteriophages as alternatives to antibiotics are met with considerable interest, especially as the efficacy of phage preparations is very high. A measurable result is the increase in the production of commercial preparations containing phages, despite legal restrictions on their use in animal production. Alternatives to antimicrobials for controlling infections must be sought in order to curb drug resistance among bacteria. Increased public awareness and knowledge of bacteriophages are helpful here, as they are conducive to legislative action facilitating the registration process for commercial phage preparations, especially in the European market.

Keywords: *Bacteria* • *Bacteriophages* • *Drug resistance* • *Poultry*

1. Introduction

Food safety in poultry products is crucial due to the potential presence of various pathogens causing foodborne diseases. The main goal of the global poultry industry is to produce safe food for consumers in an economically sustainable environment while applying antibiotics rationally. Poland, as the main poultry producer among European Union (EU) countries, is responsible for about 70% of poultry exports to other countries, including those outside the EU (Eurostat, 2025). This trend has persisted since at least 2023, and according to estimates, Poland will remain the largest poultry meat producer in the EU in 2025, accounting for more than 22% of all EU production (Eurostat, 2025).

The bacteria most frequently isolated from poultry, which due to their significant risks for human health are subject to obligatory antimicrobial resistance (AMR) monitoring in food-producing animals (Commission Implementing Decisions 2013/652/EU and (EU) 2020/1729),

* *E-mail: ewelina.pyzik@up.edu.pl*

Open Access. © 2027 the author(s), published by National Research Institute of Animal Production
This work is licensed under the Creative Commons Attribution-NonCommercial-NoDerivs 4.0 License.

include *Salmonella* spp., *Campylobacter jejuni*, *Campylobacter coli*, and *Escherichia coli* (European Centre for Disease Prevention and Control et al., 2024). Another major threat is posed by *Staphylococcus* spp. and *L. monocytogenes* strains, which can also contaminate poultry during processing, leading to serious health problems after consumption. *Salmonella* and *Campylobacter*, for example, are classified as common bacteria in poultry and humans causing gastrointestinal diseases with diarrhoea, high fever, and severe abdominal cramps (Dlamini et al., 2024).

Pathogens counted among drug-resistant bacteria pose a particular threat to effective control of infections. These include *Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp., known as the ESKAPE pathogens (Hao et al., 2024). Bacteria belonging to this group are able to rapidly acquire resistance to commonly used antimicrobials, including broad-spectrum antibiotics, such as beta-lactams, carbapenems, glycopeptides, fluoroquinolones, and aminoglycosides, as well as certain biocidal solutions (Hao et al., 2024).

The phenomenon of drug resistance is particularly pronounced in intensive poultry production, and in some countries, the use of antimicrobials for this purpose can reach even 70–80% of their total consumption in animal production (Tiseo et al., 2020). According to the latest literature data, the lowest drug resistance among pathogens isolated from poultry in EU countries is noted for macrolides and aminoglycosides, ranging from 0% to 14%, while by far, the highest drug resistance was noted against quinolone and tetracycline (TET), ranging from 41% to 70% (Abou-Jaoudeh et al., 2024).

Under the One Health strategy developed and implemented by EU countries, the EU Council Recommendation "on stepping up EU actions to combat antimicrobial resistance in a One Health approach" (Council of the European Union (2023)/C 220/01) was adopted in 2023. These recommendations cover 10 core areas for fighting drug resistance among bacteria, including introducing national action plans for curbing resistance to antimicrobials; preventing and controlling infections through continual monitoring, preventing the spread of resistant pathogens, and undertaking measures to improve animal health and welfare; management and rational use of antimicrobials, e.g. limiting their widespread application in animal production, replacing metaphylaxis with prophylaxis aimed at improving animals' natural immunity, and also developing alternatives to antibiotics; raising public awareness and education regarding the threats arising from the uncontrolled use of antimicrobials, as well as conducting and funding research aimed at developing modern methods for counteracting the development of antimicrobial resistance; and continual cooperation with EU member states, e.g. by sending current data on resistance to antimicrobials and their sale and consumption to the global antimicrobial resistance surveillance system. The recommendation recognized that it was crucial for EU countries, as well as developing and highly developed countries, to carry out global measures for developing and implementing international standards and guidelines, e.g. on the responsible and prudent use of antimicrobials in veterinary medicine, rational use of antimicrobials for phytosanitary purposes, and minimization and containment of drug resistance in bacteria present in food (2023/C 220/01 – Council Recommendation; World Organisation for Animal Health, 2024).

In 2024, all countries sent data on the use of these preparations for chickens at the category level (Figure 1). According to ESVAC reports (2020), European Medicines Agency (2021), European Medicines Agency (2022a), European Medicines Agency (2022b) Poland, as the main poultry producer in the EU, consumed the largest quantity of antimicrobials in poultry production among European countries up to 2022 (Pyzik et al., 2024). In 2023, however, this level had significantly decreased to 53.1 tonnes of active substance, and further decreased to 41.2 tonnes in 2024. This currently places the country sixth among EU member states, with the highest rate of consumption of antibacterial substances recorded for Germany (142.4 tonnes of active substance in 2023 and 139.6 in 2024; Figure 2).

Under the farm-to-fork strategy implemented by the EU, aimed at reducing the overall use of antimicrobials by 50% in farm animals and aquaculture by 2030, comprehensive legislative action has been undertaken, resulting in Regulation (EU) 2021/1756 on official controls, aimed at ensuring compliance with the ban on the use of certain antimicrobial agents. The objectives of the regulation include the introduction of a ban on the preventive use of antibiotics in various animal species, including poultry. On 28 January 2022, a new legal framework was implemented for Regulation (EU) 2019/6 on veterinary medicinal products (VMP), focusing on establishing a modern, innovative, and tailored legal framework for VMP, providing incentives to stimulate innovation in VMP and increase their availability, and strengthening EU measures for preventing the spread of drug resistance among bacteria (USDA, 2024). These measures were continued by Commission Delegated Regulation (EU) 2021/1760 of 6 October 2021, establishing the criteria to designate the antimicrobials to be reserved for human use. The European Commission followed this up by adopting Implementing Regulation (EU) 2022/1255 of July 2022, listing antimicrobials reserved for treatment of infections in humans. In February 2023,

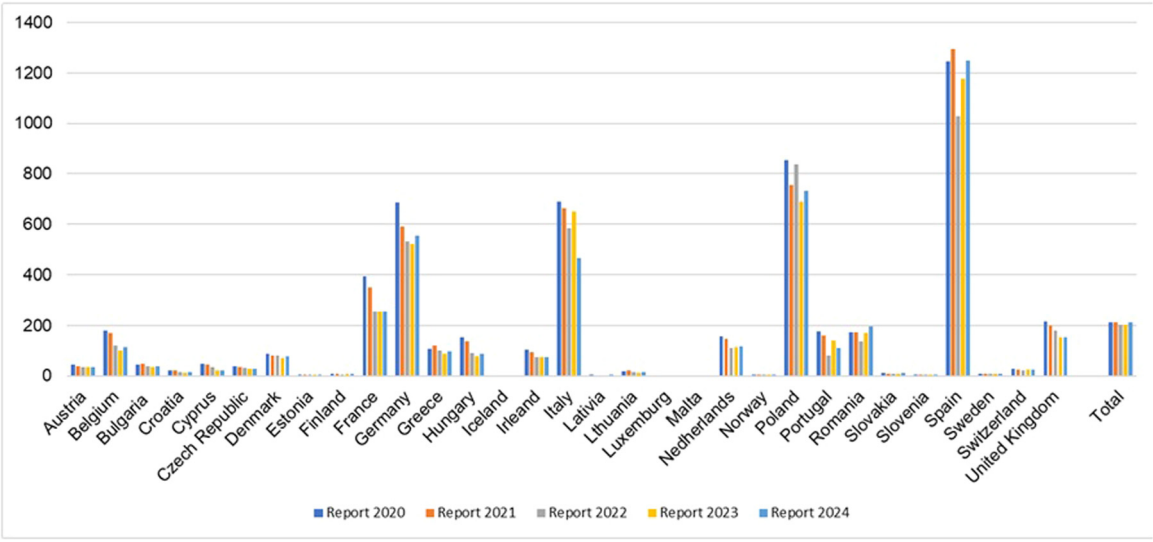


Figure 1. Sales report of antimicrobial active substances for food-producing animals of (tonnes).
Source: European Medicines Agency – ESVAC reports 2020, 2021, 2022.

the European Commission adopted Delegated Act 2023/905 implementing Article 118 of the VMP Regulation, which imposes restrictions on the use of antimicrobials in animals transported from third countries into the EU (USDA, 2024).

In the era of the global crisis of multidrug resistance (MDR) to antimicrobials, alternative methods of controlling infections have begun to play an important role in animal production. One such approach is the use of bacteriophages, natural bacterial viruses exhibiting affinity for specific species of bacteria. Bacteriophages are ubiquitous, simple bacterial viruses and the most commonly occurring microbes in various natural ecosystems, including fresh water and seawater (Wessels et al., 2021). The total number of bacteriophages is estimated at about 10^{32}, which is ten times the number of bacteria (Alomari et al., 2021). The presence of bacteriophages has also been confirmed in many available products, e.g. in fermented

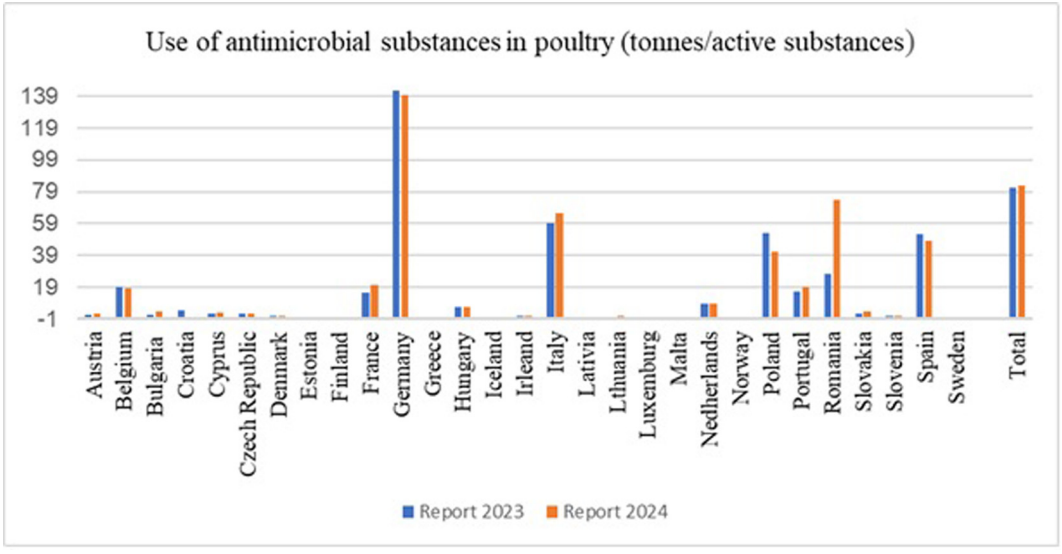


Figure 2. Average consumption (in tonnes) of antimicrobial active substances in poultry production in EU countries in 2023–24 (European Sales and Use of Antimicrobials for Veterinary Medicine ESUAvet, 2023, 2024).

food and fresh vegetables, and in soil. Their presence has also been demonstrated in simple and more complex living organisms, such as reptiles, amphibians, birds, and mammals, including primates. This means that both animals and humans are constantly exposed to bacteriophages, e.g. through consumption of foods of plant and animal origin or direct contact with the natural environment. Moreover, bacteriophages make up a significant part of the microbiota of living organisms and ecosystems, regulating its homeostasis (Łusiak-Szelachowska et al., 2017; Urban-Chmiel & Pyzik, 2025). The mechanism of action of bacteriophages involves lysis of the target bacterial cell hosting a given phage by attaching to specific phage receptors present on the surface of bacterial cells (Endersen & Coffey, 2020).

2. Trends in drug resistance among the most commonly occurring bacteria in poultry production

2.1 *E. coli*

Pathogenic strains of *E. coli* exhibit a high level of drug resistance, most often to several groups of antimicrobial agents simultaneously. Our own research (Stępień-Pyśniak et al., 2025) determining the drug resistance profiles of avian pathogenic *Escherichia coli* (APEC) strains isolated from laying hens, breeding hens, broiler chickens, and turkeys in Poland revealed a high rate of resistance to the drugs tested, including amoxicillin (AMX, 100%), doxycycline (100%), enrofloxacin (ENR, 85%), chloramphenicol (75%), AMX + clavulanic acid (55%), sulfamethoxazole/trimethoprim (STX, 45%), and neomycin (NEO, 40%) (Table 1). Another of our studies (Nowaczek et al., 2021), using *E. coli* strains isolated from wild birds in Poland, confirmed resistance to three or more groups of antibiotics in more than 31% of strains tested. The most common resistance profile was simultaneous resistance to TET, STX, and ampicillin (AMP). It should be stressed that wild birds are most often reservoirs of pathogenic microbes, including *E. coli* strains, and are a very important vector in the transmission of drug resistance.

Earlier research conducted in Poland (Racewicz et al., 2022), in which commensal *E. coli* strains were isolated in 2019–2020 from litter swabs taken in poultry litter, showed the highest resistance against AMP and doxycycline (100%). In the case of *E. coli* isolate obtained from cloacal swabs, the highest resistance was observed against AMP (100%) and ciprofloxacin (CIP) (92%). The highest resistance to AMP (100%) and STX (94.7%) was observed in the case of strains isolated from chicken meat from slaughterhouses, while the lowest resistance was shown for gentamicin (GEN 12.5%, 36%, and 36.8%, respectively). Other research (Majewski et al., 2021) using pathogenic *E. coli* strains isolated from poultry in Poland, including APEC strains, confirmed high resistance to AMX (73.64%) and doxycycline (52.08%), whereas a high percentage of strains were susceptible to colistin (85.64%), NEO (80.62%), and AMX + clavulanic acid (73.05%).

Findings from Poland are largely consistent with the results of studies carried out by other research centres within and outside of Europe. For example, a study conducted in Portugal (Oliveira et al., 2022) using APEC strains from broiler chickens in the years 2009–2018 showed that resistance to the antimicrobials most often used in poultry ranged from 32.6% to 78%, i.e. 78% for AMX, 73.5% for AMP, 63.3% TET, 68.2% NEO, and 32.6% for ENR (Table 1). A study conducted in 2023–2024 in Spain, using *E. coli* strains isolated from broiler chickens, layers, and breeders (the drug susceptibility of 898 isolates in total was tested, among which 59.5% were classified as APEC), showed a high percentage of strains resistant to colistin (58.3%), β-lactams (99.1%), macrolides (99.2%), lincosamides (98.9%), and TETs (38%) (Monroy et al., 2025). A concerning finding is that as many as 99.3% of strains were classified as MDR, showing resistance to at least three families of antibiotics – β-lactams, macrolides, and lincosamides – at a rate of nearly 100%.

In Asian countries such as Nepal, the problem of drug resistance in *E. coli* from poultry was analysed in a study conducted on strains isolated from broiler chicken carcasses in 2021, which confirmed the presence of strains showing high resistance to GEN (90.2%), TET (67.2%), and AMP (54.1%) (Ranabhat et al., 2024). A study carried out in India (Patel et al., 2024), using *E. coli* strains isolated in 2019–2021 from chickens that had died with colibacillosis symptoms, confirmed high resistance to ENR (72.46%), levofloxacin (69.56%), ciprofloxacin (66.66%), AMX + clavulanic acid (63.77%), and TET (59.42%). Lower resistance was observed in the case of AMP + sulbactam (34.78%) and ceftriaxone + sulbactam (36.23%). The latest research conducted by Chinese scientists on APEC strains obtained in 2024 (Tian et al., 2025) also confirmed high resistance of isolates to TET (95%), AMP (84.6%), ceftiofur (73.1%), florfenicol (FLO, 80%), sulfisoxazole (80%), and STX (63.3%). MDR was observed in 74% of APEC strains (Table 1).

An equally high rate of drug resistance among APEC strains was observed by researchers in Brazil in 2022–2023, based on samples obtained from birds that

Table 1. Current trends in drug resistance among *E. coli* strains isolated from poultry in the years 2021–2025

Type of strain/ type of infection	Species of bird	Country	Most frequently detected resistance genes	Antibiotic resistance	Most effective antibiotics	References
E. coli APEC/ colibacillosis	Broiler chickens	Poland	nd	AMX, AMX + clavulanic acid, colistin, ENR, NEO, norfloxacin, spectinomycin, and STX	Colistin (84.64%), NEO (80.62%), AMX + clavulanic acid (73%)	Majewski et al. (2021)
E. coli APEC/ colibacillosis	Laying hens, breeding hens, broiler chickens, turkey broilers	Poland	*blaTEM*, *tetB*, *sul2*, *tetA*, *tetB*, *strA/strB*, *aphA1*, *floR*, *catA1*, *aadA*	AMX, AMX + clavulanic acid, doxycycline, ENR, chloramphenicol	NEO STX	Stępień-Pyśniak et al. (2025)
Pathogenic *E. coli* strains	Mallard, white-tailed eagle, common buzzard, Eurasian sparrow hawk, Eurasian tawny owl, mute swan, little bittern, little owl, short-eared owl, great spotted woodpecker, lesser spotted woodpecker, European green woodpecker, Bohemian waxwing, western capercaillie, grey heron, Eurasian golden oriole	Poland	*sul2*, *blaTEM*; *tet*(A), *aphA1*	TET (50%), ciprofloxacin (46.8%), GEN (34.3%), AMP (28.1%)	Chloramphenicol	Nowaczek et al. (2021)
E. coli APEC/ colibacillosis	Broilers, layers and breeder chickens	Spain	*mcr-1*, *mcr-2*,	colistin (58.3), β-lactams (99.1%), macrolides (99.2%), lincosamides (98.9%), TETs (38%)	nd	Monroy et al. (2025)
E. coli APEC/ colibacillosis	Necropsied chickens	India	*blaTEM* *blaCTX-M-G9 g*	ENR (72.46%), levofloxacin (69.56%), ciprofloxacin (66.66%), AMX + clavulanic acid (63.77%), TET (59.42%)	Ceftriaxone + sulbactam (63.77) AMP + sulbactam (65.22%)	Patel et al. (2024)

Table 1: *Continued*

Type of strain/ type of infection	Species of bird	Country	Most frequently detected resistance genes	Antibiotic resistance	Most effective antibiotics	References
E. coli APEC/ colibacillosis	Necropsied chickens	Brazil	nd	AMX (66.1%), ceftiofur (56.9%), norfloxacin (47.7%), TET (33.9%), ciprofloxacin (31.2%), FLO (25.7%), doxycycline (23.9%), ENR (22.9%)	GEN (97.1%), NEO (85.3%), ENR (77.1%)	Lúcio et al. (2025)
E. coli strains	Broiler meat	Nepal	nd	GEN (90.2%), TET (67.2%), AMP (54.1%)	Ciprofloxacin (93.4%), amikacin (98.4%)	Ranabhat et al. (2024)
APEC	Chicken samples	Algeria		AMP (97.96%), AMX + clavulanic acid (96.94%), nalidixic acid (94.90%), TET (90.82%), ciprofloxacin (79.59%), trimethoprim/ sulfamethoxazole (67.35%), kanamycin (61.22%)	Chloramphenicol (78.60%), GEN (79.60%), cefotaxime (82.70%)	Boulbair et al. (2025)
APEC	Broilers, layers, broiler breeders	Ukraine	nd	AMX (78.4%), AMX + clavulanic acid (69.3%), doxycycline (58.3%), oxytetracycline (75.6%), flumequine (78.5%) ENR (55.9%)	Colistin (91.6%), GEN (85.6%), ceftiofur (63.9%), FLO (61.0%)	Nechypurenko et al. (2024)
E. coli	Broilers	Sweden	bla_{TEM}-1B, bla_{TEM}-1C *dfrA1, dfrA5* *tet*(A) *sul2* *aadA1* *aph(3')-Ia, aph(3'')-Ib* *aph(6)-Id* *qnrS1* *gyrA* (p.S83L) *parC* (p.S57T), *parE* (p.I355T)	AMP 34.0%, sulfamethoxazole 32.1%, Trimethoprim 28.4%, TET 18.3%	Ciprofloxacin 92.7% Nalidixic acid 93.6%	Davam et al. (2026)

Table 1: *Continued*

Type of strain/ type of infection	Species of bird	Country	Most frequently detected resistance genes	Antibiotic resistance	Most effective antibiotics	References
APEC	Birds	Italy	nd	AMP (45%), nalidixic acid (45%), TET (43%), sulfonamide (41%), flumequine (33%)	Cefotaxime (100%) Cefepime (100%) Cefoxitin (98%) Ceftazidime (98%)	Sgariglia et al. (2019)
APEC	Laying hens	China	tet(A), *floR, sul2, aph(3'')-Ib, aph(6)-Id,* bla_{TEM}1B, *qnrS1*	TET (95.0%), AMP (84.6%), FLO (80.0%), sulfisoxazole (80.0%), ceftiofur (73.1%)	Colistin (100%) AMX + clavulanic acid (95%)	Tian et al. (2025)
APEC	Broiler breeder hens	USA	B-lactamase inhibitors (*blaTEM*), cephalosporins (*blaCTX-M*), aminoglycosides (*aac3Vla, aph3IA,* and *aadA*), TETs (*tetA*), sulfonamides (*dfr7, sul1*), quinolones (*qnr*), phenicols (*cat1*)	TET (28.6%) Streptomycin (18%) Kanamycin (14.3%) GEN (7.1%)	STX 96.4%	Joseph et al. (2023)
E. coli	Broiler chickens	Canada	nd	Sulfisoxazole (57.3%) Streptomycin (51.6%) AMP (51.2%) TET (46.1%) Ceftriaxone (36.2%), cefoxitin (35.9%), AMX + clavulanic acid (35.8%), GEN (30.2%)	Azithromycin (99.9%) Ciprofloxacin (99.8%)	Romero-Barrios et al. (2020)
APEC	Birds	Iran	*blaCTX-M-15, blaTEM-1A, blaVEB,* and *blaSHV tetA, tetB,* and *tetC, sul1* and *sul2, dfrA1, ereA, qnrA*	AMP (84.2%), STX (65.70%), TET (62.80%), Cefoxitin (60.00%), Nalidixic acid (60.00%)	Imipenem (100%) GEN (97.2%)	Ghorbani et al. (2022)
E. coli strains	Broilers	Egypt	*bla*TEM, *bla*SHV, *bla*CTXM, *mcr*1, *qnrA*, *qnrB, papC*	AMP 97.8%, doxycycline 85.5%, chloramphenicol 80.9%, Ciprofloxacin 73.5%, danofloxacin 84.3%, fosfomycin 85.5%,	Colistin sulphate 50.7%	Abdel-Rahman et al. (2023)

Table 1: *Continued*

Type of strain/ type of infection	Species of bird	Country	Most frequently detected resistance genes	Antibiotic resistance	Most effective antibiotics	References
E. coli strains	Broiler poultry	China	nd	Levofloxacin 69.7%, Nalidixic acid 92.2%, norfloxacin 73.2%, PEN 95%, streptomycin 82.5%, TET 94.8%, STX 88.5%, ENR 82.4%, Cefotaxime 86.7%, imipenem 72.8%, AMX + clavulanate 89% AMX (95.47%), AMP (95.08%), FLO (85.43%), Chloramphenicol (84.06%), TET (84.06%), cefotaxime (80.12%), cefazolin (85.43%) GEN (36.81%)	Ofloxacin (24.41%)	Liu et al. (2025a)
APEC	Broiler and layer farms	Java Yogyakarta Indonesia	nd	AMX (66.7%), ENR (57.1%), streptomycin (52.4%), STXazole (52.4%), nalidixic acid (47.6%), oxytetracycline (47.6%), TET (42.9%), GEN (42.9%)	NEO (23.8%)	Timur et al. (2025)

nd – not detected.

had died with colibacillosis symptoms. The most frequently observed MDR profile was simultaneous resistance to β-lactams, fluoroquinolones, TETs, and aminoglycosides (Lúcio et al., 2025). The highest drug resistance was recorded for AMX (66.1%), ceftiofur (56.9%), and norfloxacin (47.7%), while resistance to FLO (25.7%), doxycycline (23.9%), and ENR (22.9%) was markedly lower (Table 1).

The problem of drug resistance in pathogenic *E. coli* strains isolated from poultry has also been demonstrated in Australia and Thailand (Thomrongsuwannakij et al., 2020). In that study, more than 60% of APEC strains isolated in Thailand were resistant to more than three antibiotics, whereas the percentage of MDR strains isolated in Australia was 10.7%. The highest drug resistance in strains isolated in Thailand was observed for TET (84.5%), AMX (70.2%), and STX (51.2%). In the case of Australian strains, the rates of resistance to these antibiotics were 36.9%, 29.8%, and 17.86%, respectively (Thomrongsuwannakij et al., 2020).

In a study using samples obtained in Algeria in 2019–2020 (Boulbair et al., 2025), 98 APEC strains isolated from chicken samples with characteristic colibacillosis signs showed the highest resistance rates for AMP (97.96%), AMX + clavulanic acid (96.94%), nalidixic acid (94.90%), TET (90.82%), and ciprofloxacin (79.59%). It is concerning that 92.86% of APEC strains showed resistance to at least three of the antibiotics tested, which is indicative of the serious problem resulting from the common use of antimicrobials on poultry farms in Algeria and the need for changes in flock health management, especially in poultry production.

Comparison of research results on the drug resistance of *E. coli* strains isolated from poultry in Poland and around the world reveals that the acquisition of resistance to antibiotics commonly used in poultry is trending upward (Table 1). In Poland as well, as the largest poultry producer in the EU, studies indicate a significant increase in the resistance of *E. coli*, including APEC strains, to the most important antibiotics in poultry production, such as TET, AMX, AMX + clavulanic acid, and colistin (Majewski et al., 2021). A similar opinion is shared by Ukrainian researchers (Nechypurenko et al., 2024), whose study of APEC strains isolated from broilers in 2015–2022 showed that the number of isolates resistant to colistin decreased in the years 2017–2018, but again increased from 2021 to 2022. In the case of AMX, AMX + clavulanic acid, spectinomycin, and doxycycline, a pronounced upward trend in drug resistance was observed in the years 2015–2022. The highest percentage of APEC strains exhibited resistance to flumequine (78.5%), AMX (78.4%), amoxiclav (69.3%), oxytetracycline (75.5%), and doxycycline (58.3%). This concerning phenomenon was again observed in 2022 in more than 40% of isolates, which showed MDR to more than ten antibiotics among polypeptides, aminoglycosides, TETs, beta-lactams, quinolones, and cephalosporins (Nechypurenko et al., 2024).

2.2 *Campylobacter* spp.

Infections caused by *Campylobacter* spp., especially *Campylobacter jejuni* (*C. jejuni*) and *Campylobacter coli* (*C. coli*), are a significant public health problem around the world. According to the World Health Organization (WHO), *Campylobacter* spp. are one of the four main causes of diarrhoeal diseases in the world, leading to gastroenteritis in humans, as well as extraintestinal complications such as Guillain-Barré syndrome, Miller Fisher syndrome (Yuki, 2001), and reactive arthritis (Keithlin et al., 2014). A report published by the European Food Safety Authority (EFSA) in November 2025 and a report created by the Foodborne Diseases Active Surveillance Network (FoodNet) in cooperation with the Centres for Disease Control and Prevention (CDC) in 2023 confirmed that campylobacteriosis is the most common zoonosis in EU countries and the United States (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2025c; Delahoy et al., 2023). The main reservoirs for the microbes are poultry, pigs, and cattle (Al Hakeem et al., 2022; Wieczorek et al., 2021). The first-line drugs for treatment of *Campylobacter* spp. infections are usually macrolides (erythromycin, ERY and azithromycin), which have largely displaced fluoroquinolones. Fluoroquinolones, due to their widespread use in veterinary medicine, their non-selective use in treatment of humans, and the possibility of inducing drug resistance, are used as second-line drugs (Nunes et al., 2023).

Mechanisms of resistance transfer in *Campylobacter* spp., including both chromosomal mutations and horizontal gene transfer (HGT), have been described in detail in the literature (Urban-Chmiel et al., 2022). However, trends in the resistance of *Campylobacter* spp. strains to specific groups of antibiotics are continually changing. For example, a study conducted by Australian researchers using *C. jejuni* and *C. coli* strains isolated from chicken broilers showed that most strains of both *C. jejuni* (63%) and *C. coli* (86.5%) were susceptible to the antibiotics used in the study, i.e. FLO, GEN, azithromycin, ERY, clindamycin, and telithromycin, with *C. coli* strains shown to be much more susceptible than *C. jejuni.* A large discrepancy in resistance was noted for TET, 22.2% for *C. jejuni* but only 3.1% in *C. coli*. The level of resistance to both

ciprofloxacin and nalidixic acid was 14.8% for *C. jejuni* and 5.2% for *C. coli*. The results also confirmed the presence of strains resistant to fluoroquinolones, which are not approved for use in poultry production in Australia. The authors emphasize that the ban on the use of fluoroquinolones in poultry farming does not itself guarantee that bacteria will not be resistant, if there are other routes by which resistant strains can be introduced, such as humans, pests, or wild birds. Genetic analysis of the isolates showed that the most frequently detected resistance gene was bla_{OXA}, determining resistance to β-lactam antibiotics. Its presence was confirmed in 64.8% of *C. jejuni* isolates and in 72% of *C. coli* isolates (Table 2). A mutation in the gene encoding the DNA gyrase A subunit (*gyr*A) was detected in all *C. jejuni* and *C. coli* strains resistant to fluoroquinolones. The *tet*O gene, determining resistance to TETs, was identified in 28.4% of *C. jejuni* isolates, which was correlated with the phenotypic assessment of resistance to TET (22.2%). In *C. coli*, the TET resistance gene was detected in only one isolate (Abraham et al., 2020).

Another study, conducted in China (Tang et al., 2020) using 70 strains of *Campylobacter* spp., confirmed a high rate of resistance to fluoroquinolones, in which the resistance of *C. jejuni* to ciprofloxacin and nalidixic acid was high, at 66.7% and 80%, respectively. For *C. coli* strains, the values were 100% and 92%, respectively (Table 2), which is an alarming phenomenon and, as stressed by the authors, directly linked to the intensive use of these drugs in the poultry sector. High resistance to ERY, clindamycin, azithromycin, GEN, and TET was also noted among *Campylobacter* spp. strains, ranging from 60% to 80% (Table 2). Genetic testing identified key mechanisms of resistance in *Campylobacter* spp., such as a point mutation in the *gyr*A gene (C257T), detected in all strains that were phenotypically resistant to ciprofloxacin and/or nalidixic acid, mutation A2075G in the V domain of the 23S rRNA gene in both *C. jejuni* and *C. coli* isolates that were highly resistant to macrolides, and the presence of the gene *erm*B in nearly 65.7% of strains (Table 2). Among genes responsible for TET resistance, the genes *tet*O and *tet*A were detected (Abraham et al., 2020). Similar drug resistance results in *Campylobacter* spp. strains were obtained in a study carried out in Brazil (Paravisi et al., 2020) on 54 strains of *C. jejuni*, obtained from bird carcasses, cloacal swabs, and environmental samples. One strain was shown to be susceptible to all antimicrobials tested: ciprofloxacin, nalidixic acid, ERY, TET, GEN, and chloramphenicol. The study showed an extremely high level of resistance to ciprofloxacin (94.4%) and nalidixic acid (94.4% according to CLSI criteria), which was linked to specific mutations in the *gyr*A gene. In the case of other antimicrobials, the level of resistance varied depending on the standards used Clinical and Laboratory Standards Institute (CLSI) vs European Committee on Antimicrobial Susceptibility Testing (EUCAST) and ranged from 46.3% to 51.8% for TET and from 42.6% to 48.1% for ERY (Table 2). Only 42.8% of strains phenotypically resistant to TET possessed the gene *tet*O, which suggests that other mechanisms, such as efflux pumps, may be responsible for resistance in the remaining strains (Paravisi et al., 2020). All strains were shown to be clinically susceptible to GEN and chloramphenicol, which the authors link to bans or restrictions on their use in poultry production in Brazil. A particularly concerning phenomenon is the high resistance to ERY and ciprofloxacin shown in the study, as both of these substances are first-line drugs for campylobacteriosis treatment in humans. In addition, the multiple antibiotic resistance (MAR) index of 0.5 suggests high selection pressure in the study area resulting from frequent use of antibiotics in poultry farming (Paravisi et al., 2020). The results are also similar to those of a study conducted in Chile on 118 *Campylobacter* strains (*C. jejuni n* = 75, *C. coli n* = 43) isolated from poultry carcasses (Concha-Toloza et al., 2023). *C. jejuni* strains showed the highest resistance to ciprofloxacin (37.3%) and TET (20%), and 5.3% of strains were resistant to both antibiotics (Table 2). *C. coli* strains showed the highest rate of resistance to ciprofloxacin (55.8%), while by far the lowest percentage of strains were resistant to TET (4.7%). In addition, 16.3% of isolates were resistant to ERY, and all of these strains were also resistant to ciprofloxacin. A much lower percentage of *C. coli* strains showed simultaneous resistance to ciprofloxacin and TET (2.3%) than in the case of *C. jejuni*, but all strains of *Campylobacter* spp. were susceptible to GEN, and *C. jejuni* was additionally susceptible to ERY (Table 2). The genetic analysis detected molecular determinants of resistance to antibiotics; in all *Campylobacter* spp. strains resistant to ciprofloxacin, the C257T mutation was detected in the quinolone resistance-determining regions (QRDR) of the *gyr*A gene. The *tet*O gene was also present in all TET-resistant strains. In addition, determinants of resistance to antimicrobials that were not tested phenotypically were present: *lnu*C determining resistance to lincomycin (LIN), bla_{OXA-61}, which encodes the enzyme oxacillinase responsible for *Campylobacter* resistance to β-lactam antibiotics, *aph*(3')-III and *aadE*-C*c*, responsible for resistance to some aminoglycoside antibiotics, and *cfr*C, associated with resistance to linezolid and phenicols (Concha-Toloza et al., 2023).

In a study conducted in the United States, Poudel et al. (2022) tested 414 samples from conventional chicken farming and farming without antibiotics for the presence of *Campylobacter* spp. The overall prevalence of *Campylobacter* was 25.4%. *C. jejuni* was the dominant species,

Table 2. Current trends in drug resistance among *Campylobacter* spp. strains isolated from poultry

Type of strains	Type of sample	Number of samples	Country	Most frequently detected resistance genes	Resistance to antibiotics	Most effective antibiotics	References
Campylobacter jejuni	Caecal samples from chickens	*n* = 108	Australia	*Tet*O, $bla_{OXA,}$ *gyr*A	Ciprofloxacin (14.8%), nalidixic acid (14.8%), TET (22.2%)	FLO (100%), ERY (99.1%), GEN (100%), azithromycin (99.1%), clindamycin (99.1%), telithromycin (99.1%)	Abraham et al. (2020)
Campylobacter coli	Caecal samples from chickens	*n* = 96	Australia	*Tet*O, bla_{OXA}, *gyr*A	TET (22.22%)	FLO (100%), ERY (94.8%), ciprofloxacin (94.8%), nalidixic acid (94.8%), GEN (100%), TET (96.9%), azithromycin (94.8%), clindamycin (94.8%), telithromycin (95.8%),	Abraham et al. (2020)
C. jejuni	Chickens	*n* = 45	China	*Gyr*A, *Tet*O, *Tet*A, *erm*B	Ciprofloxacin (66.7%), nalidixic acid (80%), ERY (62.2%), azithromycin (60%), TET (71.1%), clindamycin (62.2%), GEN (68,9%)	FLO (93.3%)	Tang et al. (2020)
C. coli	Chicken	*n* = 25	China	*Gyr*A, *Tet*O, *tet*A, *erm*B	Ciprofloxacin (100%), nalidixic acid (92%), ERY (76%), azithromycin (64%), TET (88%), clindamycin (64%), GEN (60%)	FLO (92%)	Tang et al. (2020)
C. jejuni	Carcass, chicken cuts, cloacal swabs, pre-chiller water	*n* = 54	Brazil	*Gyr*A, *tet*O	Ciprofloxacin (94.4%), nalidixic acid (94.4%), ERY (51.9-53.7%)[a], TET (51.9-57.4%)[a]	GEN (100%), chloramphenicol (100%)	Paravisi et al. (2020)
Campylobacter jejuni	Chicken meat samples	*n* = 75	Chile	$bla_{OXA-61,}$*lnuC, gyrA, tet(O)*	Ciprofloxacin (37.3%), TET (20%)	ERY (100%), GEN (100%)	Concha-Toloza et al. (2023)
Campylobacter coli	Chicken meat samples	*n* = 43	Chile	*aph(3')*-III, *aad*E-Cc, *cfr*C, bla_{OXA-61}, *gyr*A,*tet*O	Ciprofloxacin (55.8%), ERY (16.3%), TET (4.7%)	GEN (100%)	Concha-Toloza et al. (2023)
C. jejuni	retail raw chicken samples, Farm samples: litter, faeces, cloacal swabs	*n* = 59	United States	*Gyr*A, *tet*O*aph(3')-IIIa,* $bla_{OXA-184}$, bla_{OXA-61}	nalidixic acid (49.2%)	ERY (83.1%) Ciprofloxacin (84.7%), GEN (93.2%), TET (76.3%), clindamycin (83.1%)	Poudel et al. (2022)
C. lari	Retail raw chicken samples, farm samples:	*n* = 7	United States	bla_{OXA-61}	Nalidixic acid (71.4%), ciprofloxacin (57.1%), TET (57.1%)	ERY (85.3%), GEN (85.3%), azithromycin (85.3%)	Poudel et al. (2022)

Table 2: *Continued*

Type of strains	Type of sample	Number of samples	Country	Most frequently detected resistance genes	Resistance to antibiotics	Most effective antibiotics	References
	litter, faeces, cloacal swabs						
Campylobacter spp.	Chicken faeces	*n* = 26	Ukraine	nd	Ciprofloxacin (57.7%), ERY (73%), TET (88.5%)		Shchur et al. (2023)
Campylobacter spp.	Poultry caecal swabs	*n* = 36	Iraq	nd	Nalidixic acid (100%), ciprofloxacin (100%) , TET (88.8%), AMP (83.3%), sulfa/trimethoprim (80.5%), ERY (50%), ceftriaxone (50%)	GEN (69.5%), chloramphenicol (77.8%), AMX/clavulanic acid (72.3%)	Shakir et al. (2021)
C. jejuni	Swab samples from broiler carcasses	*n* = 525	Poland	nd	Ciprofloxacin (92.0%), nalidixic acid (90.3%), TET (64.8%)	ERY (98.9%), GEN (98.7%), streptomycin (79.8%)	Wieczorek et al. (2020)
C. coli	Swab samples from broiler carcasses	*n* = 738	Poland	nd	Ciprofloxacin (93.9%), nalidixic acid (93.8%), TET (75.3%)	ERY (93.6%), GEN (99.6%), streptomycin (72.9%)	Wieczorek et al. (2020)
C. jejuni	Cloacal swabs from laying hens	*n* = 76	Germany	nd	Ciprofloxacin (81.6%), nalidixic acid (86.9%), enrofloksacin (88.2%), sulfa/trimethoprim (86.9%)	ERY (98.7%), gentamycin (100%), TET (94.7%), azithromycin (100%), chloramphenicol (98.7%)	Casalino et al. (2022)
C. coli	Cloacal swabs from laying hens	*n* = 63	Germany	nd	Ciprofloxacin (79.4%), nalidixic acid (82.5%), ENR (84.1%), TET (60.3%)	ERY (100%), GEN (100%), azithromycin (98.5%), chloramphenicol (100%), sulfa/ trimethoprim (90.5%),	Casalino et al. (2022)

[a]Depending on the criteria (CLSI or EUCAST).

accounting for 78.1%. *C. lari* and *C. volucris* were isolated as well, accounting for 6.7% and 1.9%, respectively. *C. coli* was not detected in that study. Among the *C. jejuni* isolates, 13.6% were resistant to three or more classes of antibiotics. *C. jejuni* showed the highest resistance to nalidixic acid (49.2%) and the highest susceptibility to GEN, ciprofloxacin, ERY, clindamycin, and TET, ranging from 76% to 93%. In *C. lari*, the highest rate of resistance was noted for nalidixic acid (71.4%) and for ciprofloxacin and TET (57.1%), and the lowest for ERY, azithromycin, and GEN (14.3%). Among 82 *C. jejuni* isolates, 52.4% possessed the *gyr*A gene. Other resistance genes were detected as well: *tet*O, *aph(3')*-IIIa, $bla_{\text{OXA-184}}$, and $bla_{\text{OXA-61}}$. Only $bla_{\text{OXA-61}}$ was identified in *C. lari*. The study demonstrated that *Campylobacter* spp. is present on farms without antibiotics, and antibiotic resistance, while lower than in conventional farming, still occurs; the absence of antibiotics reduces but does not fully eliminate the problem of resistance (Poudel et al., 2022).

Findings obtained by researches from Iraq (Shakir et al., 2021) for 36 *Campylobacter* spp. strains isolated from 179 samples (including 150 faecal samples and 29 cloacal swabs) also revealed an alarmingly high level of resistance to commonly used drugs, including 100% resistance to representatives of quinolones – nalidixic acid – and fluoroquinolones – ciprofloxacin (Table 2). High resistance to TET (88.8%), AMP (83.3%), and STX (80.5%) was noted as well. Half of the strains were resistant to ERY (50%) and ceftriaxone (50%). The study confirmed MDR among the *Campylobacter* spp. strains. The researchers also determined the MAR index, which was 0.3 or higher in 97.2% of isolates, suggesting that these bacteria come from environments in which antibiotics are overused (Shakir et al., 2021).

A large study using 2,367 swabs collected from broiler chicken carcasses in Poland (Wieczorek et al., 2020) showed a very high (>50%) prevalence of *Campylobacter* spp. strains, among which the dominant species was *C. coli* (n = 738). Among *C. jejuni* isolates, 108 (20.6%) were resistant to three or more classes of antibiotics; for most strains (17.9%), the resistance profile included ciprofloxacin, nalidixic acid, streptomycin, and TET. In the case of *C. coli*, 25.1% of isolates exhibited MDR; the resistance pattern was identical to that of *C. jejuni* and was found in 18.8% of strains. Only two *C. jejuni* isolates and one *C. coli* strain proved to be resistant to all antimicrobials used in the study (Wieczorek et al., 2020). In another study (Casalino et al., 2022), German researchers demonstrated high prevalence of *Campylobacter* spp. strains (90.4%), which were isolated from 177 of samples collected from layers. *C. jejuni* was identified in 43.5%, *C. coli* was detected in 38.9%, and mixed infections were shown in 7.9% of birds. Resistance to antimicrobials was considerable and more often observed in *C. coli* than in *C. jejuni*. Higher values for fluoroquinolones were noted in *C. coli*, amounting to 20.6% for ciprofloxacin, 17.5% for nalidixic acid, and 15.9% for ENR. In *C. jejuni*, resistance to this group of antibiotics was lower: 18.4% for ciprofloxacin, 13.1% for nalidixic acid, and 11.8% for ENR. Significant differences were also observed for TET resistance, which was much higher in *C. coli* (39.7%), while only 5.3% of *C. jejuni* strains were not susceptible to this antibiotic. Resistance to STX was detected in 13.1% of *C. jejuni* strains and 9.5% of *C. coli* strains. In the case of ERY, chloramphenicol, and azithromycin, resistance was only observed in single strains, and resistance to GEN was not found in either species. Despite the fact that resistance was higher in *C. coli*, MDR was shown in more strains of *C. jejuni* (19.7%) than *C. coli* (17.5%) (Casalino et al., 2022). A high rate of resistance to TET: 88.5%, ERY (73%), and ciprofloxacin (57.7%) was also observed in a study conducted on 26 *Campylobacter* spp. isolates from samples of caecal contents collected from poultry in Ukraine (Shchur et al., 2023).

To sum up, resistance of *Campylobacter* spp. to antimicrobials is dynamic, changing constantly depending on the region, time, and type of antibiotic use. The findings of research conducted in the last 5 years in various parts of the world show a clear upward trend in the acquisition of drug resistance among *Campylobacter* spp. strains, particularly to ciprofloxacin and nalidixic acid, for which it often exceeds 80–90%, and in some cases, even reaches 100%. This is indicative of the global nature of the problem of drug resistance among *Campylobacter* spp. isolated from poultry. At present, studies indicate that the efficacy of macrolides remains relatively high, but the appearance of localized cases of resistance indicate that it will gradually decline in the future. Differences in resistance profiles between countries (very high values in Asia vs lower ones in parts of Europe and Australia) confirm the impact of local farming practices and antibiotic policies. The presence of resistant strains is observed even in countries with restrictive antibiotic policies (Australia), which suggests the role of alternative routes of transmission among bacteria. Especially increasing occurrence of MDR strains indicates a growing treatment problem and may limit available treatment options. The trends observed suggest that without effective control measures (rational antibiotic therapy, epidemiological supervision, and biosecurity), the level of resistance may continue to rise.

2.3 *Enterococcus* spp.

Bacteria of the genus *Enterococcus* are part of the gut microbiota in poultry. Due to high genome adaptability

and plasticity, they are an important reservoir of resistance genes in the animal production environment. In recent years, the role of enterococci in the epidemiology of resistance to antimicrobials has been clearly highlighted in both the scientific literature and reports of European institutions functioning within the framework of the integrated One Health approach (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2023b, 2025b). Despite the decrease in selection pressure associated with the use of antibiotics, resistance to many classes of antimicrobial agents among *Enterococcus* spp. isolated from poultry remains high. This is due to several overlapping mechanisms, i.e. the durability of resistance determinants encoded on mobile elements (plasmids and transposons), the capacity of enterococci for horizontal transfer of resistance genes, and their natural adaptation to the environment of the digestive tract of animals (Clewell et al., 2014; Partridge et al., 2018). In addition, the phenomenon of co-selection makes exposure to factors other than antibiotics (e.g. heavy metals) conducive to the persistence of resistance genes. In consequence, restricting the use of antibiotics does not always eliminate resistance, which may persist in bacterial populations for a long time (Seiler & Berendonk, 2012). This underscores the need for continued monitoring and the implementation of comprehensive measures within the framework of the One Health approach, encompassing the health of animals, humans, and the environment.

Enterococcus faecalis and *Enterococcus faecium* are among the enterococcal species most commonly isolated from the gut of poultry. In recent years, other species have increasingly been identified as well, including those of clinical importance in poultry, such as *Enterococcus cecorum*, *Enterococcus hirae*, *Enterococcus durans*, *Enterococcus gallinarum*, and *Enterococcus thailandicus* (Stępień-Pyśniak et al., 2016; Velhner et al., 2024; Wigmore et al., 2024). Enterococci are used as indicator bacteria to assess the selection pressure of antibiotics, which results from their ability to accumulate and transfer resistance genes (Hollenbeck & Rice, 2012). Reports by the European Food Safety Authority and the European Centre for Disease Prevention and Control from the years 2020 to 2023 indicate significant geographic variation in levels of resistance in *Enterococcus* spp. in EU member states (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2023a, 2024a, 2025c). This may be linked to differences in antibiotic use practices, animal production systems, and degrees of implementation of surveillance programmes. Nevertheless, a common feature observed in all regions is the high occurrence of MDR strains, defined as resistant to at least three classes of antibiotics. Especially high MDR levels are noted in isolates from poultry farms, where environmental selection and stocking density are conducive to the persistence and spread of resistance. In many cases, genes of resistance to antibiotics of critical importance for human medicine co-occur, which underscores the importance of the One Health approach in monitoring and curbing this phenomenon.

3. TETs, macrolide–lincosamide–streptogramin B (MLS_B), and aminoglycosides – phenotypic and molecular analysis

The dominant resistance phenotypes observed in populations of enterococci associated with poultry production are resistant to TETs, macrolides, and aminoglycosides, often occurring together, creating MDR profiles. Among these groups of drugs, the most common phenotype is TET resistance. Numerous epidemiological studies carried out in Europe and in other parts of the world have shown that the percentage of *Enterococcus* strains resistant to this group of antibiotics often exceeds 70–80% (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2023a; Garcia-Llorens et al., 2024; Velhner et al., 2024). A high frequency of resistance is observed irrespective of the type of biological material, including isolates from intestinal contents, faeces, swabs from the cloaca and other internal organs, and the poultry farm environment. Analysis of isolates from broiler cloacae in turkey revealed TET resistance in 81.3% of *Enterococcus* spp. strains and ERY resistance in 77.1% (Aslantaş, 2019). Similar observations were made in a study carried out on poultry farms in Zambia, in which TET resistance was found in 89.2% of *E. faecalis* and *E. faecium* isolates, and resistance to AMP and ERY was shown in 68.9% (Mwikuma et al., 2023). Clinical isolates from internal organs (mainly hearts of broilers up to 10 days of age) were resistant to tylosin (71.4%) and doxycycline (67.3%) (Stępień-Pyśniak et al., 2016). Similar results were obtained in a study in turkeys in Hungary, which showed high phenotypic resistance to tylosin (62.6%), FLO (51.1%), doxycycline (48.7%), and ENR (45.5%) (Kerek et al., 2025a). Together, the data indicate that resistance to TETs and co-occurring mechanisms of resistance to other groups of antimicrobials persist,

irrespective of geographic location, the source of isolation, or the type of production system.

At the molecular level, determinants belonging to the *tet* gene family, mainly *tet*(M) and *tet*(L), play a key role in TET resistance. The *tet*(M) gene encodes a ribosomal protection protein responsible for reducing the ability of TET to inhibit the translation process, while *tet*(L) is involved in active removal of the antibiotic from the bacterial cell by efflux systems. Other determinants are identified as well, such as *tet*(O), *tet*(K), and *tet*(S), which indicates that a wide variety of genetic mechanisms are responsible for resistance within the animal-derived *Enterococcus* population (Rehman et al., 2018; Ahmed et al., 2020).

At the same time, resistance to macrolides and antibiotics of the MLS_B group is the second dominant resistance phenotype observed in enterococci associated with poultry production. ERY resistance is commonly identified both within and outside of Europe, attaining values exceeding 40–60% of all isolates tested (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2023a; Garcia-Llorens et al., 2024; Velhner et al., 2024). The dominant molecular mechanism remains methylation of 23S ribosomal RNA, encoded mainly by genes of the *erm* family, primarily *erm*(B) and less often *erm*(A) and *erm*(TR). Expression of these determinants leads to the MLS_B phenotype, i.e. cross-resistance to macrolides, lincosamides, and streptogramin B. The occurrence of *erm* genes has been widely documented in *E. faecalis*, *E. faecium*, and other species of enterococci isolated from poultry, and their spread remains closely linked to selection pressure occurring in intensive production systems (Molechan et al., 2019).

A particularly important aspect of the epidemiology of resistance in enterococci is the frequent co-localization of determinants of resistance to TETs and macrolides, represented mainly by *tet* and *erm* genes, on shared mobile genetic elements (MGEs) such as plasmids and conjugative transposons. This phenomenon plays a key role in the co-selection and horizontal transfer of resistance genes, promoting the simultaneous spread of multiple determinants within bacterial populations. This mechanism is confirmed by Fatoba et al. (2022), who used genome analyses to show the presence of the *tet*(M), *tet*(L), and *erm*(B) genes located on plasmids, at the same time indicating their role in the transmission of resistance determinants from poultry farm litter to soil. These findings indicate that mobile resistance determinants are an important factor responsible for preserving and spreading MDR phenotypes in enterococci populations of animal origin.

Another important component of the MDR phenotype of enterococci isolated from poultry is resistance to aminoglycosides, especially a high level of resistance to GEN and streptomycin (high-level aminoglycoside resistance, HLAR). The dominant molecular mechanism responsible for this phenotype is enzymatic modification of the antibiotic molecule, including acetylation, phosphorylation, and adenylation. Key epidemiological importance is ascribed to genes encoding aminoglycoside-modifying enzymes, including *aac(6′)-Ie-aph(2″)-Ia*, *aph(3′)* and *ant(6)-Ia* (Arias & Murray, 2012; Lebreton et al., 2014). The gene *aac(6′)-Ie-aph(2″)-Ia*, determining resistance to most aminoglycosides, except for streptomycin, is of particular clinical importance.

Studies conducted in Europe in recent years indicate a persistently high prevalence of the HLAR phenotype in enterococci isolated from poultry. In Serbia and Hungary, 20–30% of isolates tested showed a high level of resistance to aminoglycosides (Kerek et al., 2024; Velhner et al., 2024), while in Czechia this percentage reached 20–40% in isolates from chicks of various production types (Bzdil et al., 2023). Even higher values have been observed outside Europe, especially in intensive production systems in Asia and South America, where the percentage of strains resistant to high concentrations of GEN exceeded 60–70% (Hammerum, 2012). The study also showed frequent co-occurrence of determinants of the HLAR phenotype with the *erm*(B) and *tet*(M) genes, which additionally increases the potential for the spread of MDR.

4. Glycopeptides and vancomycin resistance status in enterococci (VRE)

Glycopeptides, i.e. vancomycin and teicoplanin, are antibiotics of key clinical importance, as last-resort drugs used to treat severe infections induced by multidrug-resistant gram-positive bacteria. Therefore, the development of resistance to this group of antimicrobial compounds is considered a serious public health problem, reaching beyond the clinical environment and affecting the animal production sector as well. In the case of enterococci, mechanisms of resistance to glycopeptides are most often associated with the presence of *vanA* and *vanB* operons, which encode an alternative pathway of peptidoglycan biosynthesis leading to modification of the final structures of cell wall precursors, thus reducing the antibiotic's affinity for the target site (Palmer & Gilmore, 2010; García-Solache & Rice, 2019).

Data from European antimicrobial resistance monitoring systems indicate that the prevalence of

vancomycin-resistant enterococci in poultry is currently relatively low and stable (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2025c). It is also markedly lower than that observed in clinical human isolates (EFSA Panel on Biological Hazards BIOHAZ et al., 2021). The withdrawal of avoparcin used as a growth promoter in animal production was particularly important. The elimination of this antibiotic has led to a significant reduction in selection pressure and a lasting reduction in the spread of glycopeptide-resistant enterococci in livestock populations. This effect has been documented in detail in Scandinavian countries, mainly Denmark, where a significant decline in the number of VRE isolates was noted following the withdrawal of avoparcin (Bager et al., 1997; Aarestrup et al., 2001). Despite the improvement in the epidemiological situation, determinants of resistance to glycopeptides have not been fully eliminated (Bortolaia et al., 2015; Ünal et al., 2020; Ben Yahia et al., 2024). Studies conducted in various EU countries indicate the persistence of sporadic cases of VRE and locally varied patterns of their occurrence. Woźniak-Biel et al. (2019) reported vancomycin resistance in 15.69% of strains isolated from turkeys, additionally identifying the *vanA* gene in some isolates. The presence of vancomycin-resistant *E. faecium* has also been shown in samples collected from broilers and from farm environments (Bortolaia et al., 2015; Ünal et al., 2020). In contrast, other European studies have shown only a marginal level of resistance or the complete absence of the *vanA* and *vanB* genes (Kasimoglu-Dogru et al., 2010; Aslantaş, 2019; Stępień-Pyśniak et al., 2021). These data suggest that the current European epidemiological situation is significantly regionally varied and does not reflect a uniform pattern of VRE prevalence. On a global scale, the epidemiological situation is even more diverse. In Zambia, for example, most enterococcal isolates have been shown to be susceptible to vancomycin (Mwikuma et al., 2023). Similar observations have been made in Australia, where no significant spread of resistance to last-resort antibiotics was shown (Wigmore et al., 2024). In contrast, in parts of the world with less restrictive policies on antibiotic use, the VRE rate remains high. Particularly concerning data are reported in Egypt, where an increased prevalence of vancomycin-resistant strains and numerous resistance determinants, including *vanB* and *vanC1*, have been observed (Ahmed et al., 2020).

The epidemiological significance of even sporadically detected resistance determinants is mainly due to their location on MGEs, such as transposons of the *Tn1546* family and conjugative plasmids, which enable effective horizontal transfer between gut-colonizing bacteria (López et al., 2010). In addition, VRE isolates from animals often co-occur with determinants of resistance to other groups of antibiotics (Garcia-Llorens et al., 2024; European Food Safety Authority, & European Centre for Disease Prevention and Control, 2025c). This is also confirmed by the latest molecular research, in which apart from genes associated with glycopeptide resistance, determinants of resistance to oxazolidinones, TETs, macrolides, and aminoglycosides were identified as well (Ben Yahia et al., 2024). This phenomenon is indicative of the important role of co-selection, in which pressure exerted by various classes of antibiotics can favour the persistence of MGEs containing numerous resistance determinants even when there is no direct exposure to glycopeptides (García-Solache & Rice, 2019). In consequence, vancomycin resistance, despite its currently limited prevalence in poultry populations, remains one of the important epidemiological markers used to monitor the long-term consequences of selection pressure and potential transfer of clinically important lines of *Enterococcus* in the food chain.

5. New challenges: amphenicols, oxazolidinones, and the Phenicols–Lincosamides–Oxazolidinones–Pleuromutilins–Streptogramin A (PhLOPSA) phenotype

FLO is a fluorinated derivative of thiamphenicol used exclusively in veterinary medicine. Resistance to amphenicols in bacteria, including *Enterococcus* spp., can develop via various molecular mechanisms. The most important of these is reducing intracellular accumulation of the antibiotic through active transport systems (efflux). Resistance may also result from enzymatic inactivation of the antibiotic, modification of its target site within the ribosome, and ribosomal protection mechanisms associated with the presence of specific genetic determinants of resistance to this group of drugs (Schwarz et al., 2004).

An increase in the prevalence of genes associated with amphenicol resistance, especially *fexA* and *floR*, has recently been observed in various parts of the world among bacteria isolated from livestock, including poultry (European Food Safety Authority, & European Centre for Disease Prevention and Control 2023a; Tyson et al., 2018). In addition, studies conducted on *Enterococcus* isolates from animals have shown frequent co-occurrence of determinants of resistance to amphenicols and genes

determining resistance to other classes of antimicrobials (Li et al., 2022; Ben Yahia et al., 2024). The simultaneous presence of the *fexA*, *optrA*, *tet*(M), *tet*(L), and *erm*(B) genes has been shown among isolates from poultry and other farm animals. These observations indicate that selection pressure exerted by specific groups of antibiotics can lead to the persistence and spread of genes of resistance to various classes of antibacterial drugs simultaneously, even in the absence of direct exposure to a given substance. Particular epidemiological importance is ascribed to the co-occurrence of determinants of amphenicol resistance and genes determining oxazolidinone resistance, primarily *optrA* and *poxtA*. The *optrA* gene encodes a protein belonging to the ABC-F family, whose mechanism of action involves protecting the ribosome against the action of oxazolidinones and phenicols, while *poxtA* encodes a protein with a similar function, additionally associated with TET resistance. These determinants are often located on MGEs, such as conjugative plasmids, transposons, and insertion sequences, which increases their potential for horizontal transfer between bacteria belonging to different species and colonizing different ecological niches (Antonelli et al., 2018; Elghaieb et al., 2019; Li et al., 2022).

An important epidemiological issue is the possibility of indirect co-selection of determinants of linezolid resistance due to the use of FLO. Despite the fact that oxazolidinones are not used in veterinary medicine, the use of FLO can generate selection pressure conducive to the persistence and spread of determinants of resistance to this group of drugs. An additional factor increasing the clinical importance of this phenomenon is the presence of the *cfr* gene and its variants, which can lead to the development of the PhLOPSA MDR phenotype. The *cfr* gene encodes 23S rRNA methyltransferase, responsible for modifying the binding site of antibiotics in the 50S ribosomal subunit, which decreases the affinity of many classes of antibacterial drugs to the target site, thus leading to the development cross-resistance (Tang et al., 2023). Studies on *Enterococcus* isolates from livestock, including poultry, have shown the co-occurrence of the gene *optrA* with genes *fexA*, *cfr*, *cfr*(D), and *poxtA2* within the same MGEs (Li et al., 2022; Tang et al., 2023; Meng et al., 2025). This increases the risk of simultaneous transfer of multiple resistance determinants and is conducive to the spread of multidrug-resistant strains in the food chain (Elghaieb et al., 2019).

A review of recent literature confirms that *Enterococcus* spp. isolated from poultry are an important and lasting reservoir of antimicrobial resistance determinants, including genes of critical importance for the effectiveness of treatments used in human medicine. The persistence of a high level of resistance to macrolides and TETs, as well as the increasing occurrence of genes of resistance to oxazolidinones, such as *optrA*, *poxtA*, and *cfr* variants (including *cfr(D)*), indicate the progressive complexity of resistance profiles in populations of enterococci isolated from poultry. This underscores the need for further enhancement of integrated antimicrobial resistance monitoring systems, strict rationalization of antibiotic use in poultry production, and the implementation of strategies consistent with One Health objectives.

5.1 *Listeria* spp.

Antibiotic resistance in *Listeria* spp., as described in earlier works (Charpentier & Courvalin, 1999; Urban-Chmiel et al., 2022), is primarily determined by the presence of resistance genes in mobile fragments and by plasmid transfer through conjugation with plasmids present in bacteria, mainly *Enterococcus* spp., *Staphylococcus* spp., and *Streptococcus* spp. Drug resistance in *Listeria* is also associated with transposons carrying resistance genes from the above-mentioned bacterial species to *Listeria*, or between *Listeria* species. Changes in determinants of drug resistance acquisition in those bacterial species also influence resistance in *Listeria*. These mechanisms, known as efflux pumps, are significantly linked to the occurrence of resistance to fluoroquinolones, macrolides, and cefotaxime in *L. monocytogenes*.

Drug resistance in *Listeria* spp. is highly varied, and as shown in the studies cited below, depends on the part of the world where the bacteria are isolated. A recent study conducted by Chinese researchers in 2024 (Chen et al., 2024) showed a considerable decrease in the percentage of strains resistant to β-lactams, whose resistance was at a level of 5.26% in 2020 but is currently zero. Similarly, in the case of ERY, representing macrolides, previous research showed a resistance rate of 15.79%, but current values are close to 0 (Chen et al., 2024). In the case of LIN and TET, resistance rates have increased, amounting to 36.36% and 18.18%, respectively, while earlier resistance was at 10.53% for LIN and 15.70% for TET.

Previous research by Hailu et al. (2021) showed that *L. monocytogenes* strains obtained from poultry manure were 100% resistant to kanamycin, nalidixic acid, and levofloxacin, with MDR to cephem, LIN, antitubercular drugs, folic acid antagonists, penems, and macrolides. Research conducted previously in Poland (Skowron et al., 2020) also confirmed high resistance of *L. monocytogenes* to cotrimoxazole (45.8%), meropenem (43.3%), ERY (40.0%), penicillin (PEN, 25.8%), and AMP (17.5%).

In Spain, the latest research (Panera-Martínez et al., 2022; Martinez-Laorden et al., 2024) has demonstrated very high resistance of *L. monocytogenes* strains to cephalosporins and beta-lactams (Table 3). The prevalence of resistance to oxacillin, cefoxitin, cefotaxime, cefepime, ciprofloxacin, ENR, and nitrofurantoin in the *Listeria* isolates ranged from 97.3% to 100%. The authors cited (Panera-Martínez et al., 2022) suggest that the increase in drug resistance observed in these strains in recent years in comparison to the period before 2020 seems to be due in part to the activation of MGEs associated with plasmids or transposons, through horizontal transfer mechanisms. A fairly concerning phenomenon is the appearance of *L. monocytogenes* resistance to nitrofurantoin, a substance whose use in livestock has been banned for many years. The authors cited indicate that this may be due to mechanisms of cross-resistance or co-resistance, which could have contributed to the persistence of resistance genes over time. The latest research (Martinez-Laorden et al., 2024) revealed a significant increase in the drug resistance of *L. monocytogenes* to oxacillin, to 100%, in contrast to data from 2015, in which drug resistance ranged from 75% to 93.3% (Aras & Ardıç, 2015). These findings clearly indicate a concerning phenomenon of intensive acquisition of resistance to an increasingly large group of antimicrobials among *Listeria* spp. strains.

5.2 *Staphylococcus* spp.

Bacteria of the genus *Staphylococcus* are ubiquitous in the environment, including in the water, soil, and air, and are isolated from various animal species, including poultry, in which they colonize the digestive and respiratory systems and are present as physiological flora on the skin and mucous membranes. In the external environment, they can be present in the air, dust, soil, water, and wastewater (Götz et al., 2006). The latest phylogenetic analysis of *Staphylococcus* led to the separation of a new genus, *Mammaliicoccus*, within this group of bacteria. The species previously called *Staphylococcus sciuri*, *S. fleurettii*, *S. lentus*, *S. stepanovicii*, and *S. vitulinus* were assigned to the new genus *Mammaliicoccus*, with *M. sciuri* as the type species (Lory, 2014; Madhaiyan et al., 2020). Coagulase-negative species belonging to both genera can be harmless commensals in poultry and wild birds or invasive opportunistic pathogens with varying virulence potential (Becker, 2020). Among coagulase-positive staphylococci, *Staphylococcus aureus* is regarded as the most pathogenic, causing a wide range of illnesses, not only in birds, from superficial skin infections to life-threatening conditions such as toxic shock syndrome and sepsis (Mehrotra et al., 2000). Infections caused by *S. aureus* are a worldwide problem in poultry production and encompass arthritis, synovitis, chondronecrosis, osteomyelitis, gangrenous dermatitis, subcutaneous abscesses, and sepsis (Meyer et al., 2021; Mohibbullah et al., 2022). In addition, strains producing enterotoxins can cause food poisoning in consumers of poultry meat (Franjus et al., 2026). Of particular concern, however, is the growing frequency of isolation of multidrug-resistant *Staphylococcus* strains, both coagulase-positive and coagulase-negative, including methicillin-resistant *Staphylococcus aureus* (MRSA) and methicillin-resistant coagulase-negative *Staphylococcus* (CoNS) strains (Gómez-Sanz et al., 2013; Katkowska et al., 2025). Poultry is currently regarded as an important reservoir of livestock-associated MRSA (LA-MRSA) strains (Hado & Assafi, 2021). According to the latest estimates, the prevalence of LA-MRSA is 2.5% in chickens and 5% in turkeys (Chen & Wu, 2021). LA-MRSA strains have also been isolated from poultry products, which indicates that LA-MRSA can spread between humans and animals (da Silva et al., 2020; Tuominen et al., 2022). The local environment is also a significant factor. According to research carried out in Denmark by Friese et al. (2013), residents living in the vicinity of poultry farms are at 15% greater risk of LA-MRSA exposure. One reason for this is undoubtedly the use of poultry manure to fertilize crop fields, but various insects and rodents can also be vectors for these bacteria (Hamza et al., 2020).

An alternative PEN-binding protein 2a, encoded mainly by the gene *mec*A and displaying low affinity for β-lactam antibiotics, underlies resistance to methicillin in staphylococci (Katayama et al., 2000). The *mec*A gene is part of the *mec* complex located on MGEs known as staphylococcal chromosomal cassette *mec* (SCCmec) (Lakhundi & Zhang, 2018). In 2011, a new type of *mec* gene was discovered in *S. aureus*, showing about 70% overlap with the nucleotide sequence of *mec*A (Shore & Coleman, 2013). This *mec* homologue was initially called *mec*ALGA251, and later renamed *mec*C. A plasmid-borne *mec*B gene has also recently been identified in *S. aureus* (Becker et al., 2018). The presence of the methicillin resistance gene *mec*C in coagulase-negative bacteria of the genera *Staphylococcus* spp. and *Mammaliicoccus* spp. is rare. In practice, the fact that phenotypic resistance to cefoxitin and oxacillin has been demonstrated in *Staphylococcus aureus* isolates suggests methicillin resistance (MRSA), which can be confirmed by the detection of *mecA* or *mec*C at the molecular level (Fernandes et al., 2005). A much less common and less known phenotype is borderline oxacillin-resistant *Staphylococcus aureus*

Table 3. Current trends in drug resistance among *Listeria* spp. strains isolated from poultry

Type of strain/type of infection	Species of bird	Country	Most frequently detected resistance genes	Antibiotic resistance	Most effective antibiotics	References
L. monocytogenes	Chicken and turkey	Spain	nd	Oxacillin (98.5%), cefotaxime (97.5%), cefoxitin (93%), cefepime (97.3%)	Chloramphenicol (97.5%), AMP (97.5%), TET (~94%), gentamycin (~89%)	Panera-Martínez et al. (2022)
L. mobocytogenes, L. innocua, L. welshimeri	Chicken, duck, quail, turkey	Spain	nd	Cefotaxime (100%), oxacillin (100%)	Vancomycin (100%), SXT (98.31%), AMP (96.62)	Martinez-Laorden et al. (2024)
L. monocytogenes	Poultry meats: goose, chicken, pigeon, duck	China	nd	Cefoxitin (100%), oxacillin (17.7%), clindamycin (17.7%)	STX(SXT 100%), GEN (100%), AMP (100%), chloramphenicol (100%), ciprofloxacin (100%)	Chen et al. (2024)
L. monocytogenes L. welshimeri L. innocu	Broiler chickens	Zambia	nd	Clindamycin (61%), TET (30%), ERY (13%)	GEN (100%), chloramphenicol (100%), levofloxacin (100%)	Mpundu et al. (2022
L. monocytogenes	Chicken meat	Indonesia	nd	AMX + sulbactam (100%), STX (100%), AMP (100%),	Sefotaxime (100%), meropenem (66.67%)	Aksono et al. (2020)
L. monocytogenes	Broiler meat	Egypt	nd	PEN (100%), AMP (100%), TET (88.8%), AMX/clavulanic acid (55.5%), ERY (66.6%)	STX (88.8%), streptomycin (77.7%), chloramphenicol (66.6%)	Aziz & Mohamed (2020)

nd – not detected.

(BORSA). BORSA strains show reduced oxacillin susceptibility, with minimum inhibitory concentrations (MICs) ranging from 1 to 8 mg/l. While *S. aureus* strains with MIC > 2 mg/l are generally considered methicillin-resistant due to the presence of *mec*A or *mec*C, BORSA strains do not possess these genes (Hryniewicz & Garbacz, 2017).

One of the factors that can contribute to an increase in bacterial resistance is the widespread use of subtherapeutic doses of antibiotics in poultry production. This is often referred to as "metaphylaxis" and is aimed at preventing the consequences of infections before clinical symptoms or a reduction in production are observed in the flock. The antibiotics most commonly used in high-risk situations, such as transport or the post-vaccination period, include TETs, aminoglycosides, macrolides, and quinolones, which may explain the high rate of resistance to them in *Staphylococcus* strains isolated from poultry (Van Cuong et al., 2021; Singh et al., 2025). Due to the conditions mentioned above, the level of resistance in both commensal and pathogenic *Staphylococcus* and *Mammaliicoccus* strains of various species isolated from birds and from henhouse environments varies depending on geographic location, the degree of development of a given region, and awareness among farmers and veterinarians. It most likely also depends on the source of the samples (henhouse environment, dead birds, healthy birds, or slaughterhouse) and on poultry species and production types, probably due to differences in antibiotic use practices and management systems. Another factor is the legal provisions in force in a given country, particularly discrepancies in regulations between the EU and countries outside the EU. These determinants underscore the importance of regional programmes for monitoring antibiotic resistance in bacteria and the need to tailor strategies for combating antimicrobial resistance to local conditions. The collection and analysis of data on antibiotic resistance is a difficult challenge given the large number of *Staphylococcus* and *Mammaliicoccus* species, which can constitute microflora colonizing the skin and mucous membranes or can be pathogens in poultry. Currently available literature from various parts of the world indicates that the frequency of isolation of *Staphylococcus* bacteria in samples from farming environments and from birds has ranged from 29% to 64%, with *S. aureus* being the dominant species. The percentage of MRSA strains on poultry farms ranged from about 30% in Algeria to 95% in samples collected in Egypt (Benrabia et al., 2020; Ahmed et al., 2021). Analysis of samples of retail poultry meat has shown widespread contamination with *Staphylococcus aureus* (34–57% of samples), with MRSA strains identified in 1.8–21% of isolates, depending on the country and the study. The typical resistance patterns in staphylococci isolated from poultry show a high percentage (53–97%) of strains resistant to β-lactam antibiotics (PEN G, AMP, and oxacillin), and in most cases, these were MRSA strains in which the gene *mec*A was detected. Many MRSA strains and coagulase-negative *Staphylococcus* strains possessing the *mec*A gene also harboured other genes of resistance, to TETs (*tet*K/L/M/O) and macrolides (*erm*A/B/C and *mph*C). The percentage of strains resistant to antibiotics of the TET group (TET and doxycycline) ranged from 60% to 95%. A similar percentage (~50–95%) was shown for strains resistant to macrolides and lincosamides (ERY and clindamycin), while the percentage of staphylococci resistant to fluorinated quinolones (ciprofloxacin and ENR) ranged from 23% to 66%. Moreover, several studies have shown MDR (≥ 3 classes of antibiotics) in 39–95% of isolates. The examples of data presented in Table 4 reveal higher rates of resistance among staphylococci isolated from poultry or poultry products and from the environment. For example, studies of retail chicken and turkey meat samples in Czechia in 2017–2018 showed a very high percentage (36.4%) of methicillin-resistant *S. aureus* strains (Tegegne et al., 2021). Data gathered in 2022 by the EFSA indicate that a high percentage of *Staphylococcus* and *Mammaliicoccus* strains in EU countries are resistant to TETs (even 96.7%), clindamycin (95%), trimethoprim (88.3%), and ERY (85%) (Annex E – EUSR on AMR, 2025). A similar high percentage of tiamulin (TIA)-resistant strains (90%) was reported, particularly in turkey samples (Kovács et al., 2025). European strains showed the lowest rate of resistance to vancomycin and chloramphenicol. The low resistance to vancomycin is most likely due to the fact that its use has been highly restricted in veterinary practice, as it has never been approved for use in poultry and is currently banned for use to protect animal health due to its critical importance in human medicine. Strains isolated from poultry and poultry products in other parts of the world (Asia, the Near East, and Africa) have also showed varying degrees of resistance to antibiotics. A study conducted in Egypt showed a 95% MRSA rate in strains isolated from samples from broiler farms, poultry hatcheries, and slaughterhouses (Ahmed et al., 2021). Available data also indicate a high percentage of strains resistant to β-lactam antibiotics. For example, a study of samples collected from poultry carcasses in Nigeria in 2018–2019 showed 100% resistance to PEN and other β-lactam antibiotics among *S. aureus* isolates (Igbinosa et al., 2023). The high prevalence of resistance to AMX, an antibiotic commonly used to treat bacterial infections in humans, raises particular concern. Troubling data from 2025 from South America indicated that 100% of *S.*

Table 4. Antimicrobial resistance in *Staphylococcus* and *Mammaliicoccus* bacteria isolated from poultry

Country	Years	Type of material	Number of flocks/ samples	Isolated strains		Phenotypic resistance	Resistance genes	References
				CoPS	CoNS			
Poland	2016–2017	Broiler chickens, turkeys –internal organs	173 flocks		*S. cohnii, S. saprophyticus, S. epidermidis, S. xylosus, M. lentus, M. sciuri, S. chromogenes, S. simulans, S. haemolyticus, S. hominis*	TET 59%, PEN G 54%, AMP 49.6%, AMX 21.3%, GEN 25.2%, cefoxitin 16.5%, ERY 14.1%, AMX/clavulanic acid 7.9%, STX 7.1%, clindamycin 5.5%, chloramphenicol 3.1%	tetK, tetL, tetM, tetO, ermA, ermB, aac (6')-Ie, aph (2")-Ia, msr, A/B, Cfr, BlaZ, mecA 27.5%	Pyzik et al. (2019)
Hungary	2022–2023	Layers, breeding flocks, broilers	8 flocks, 7 flocks, 8 flocks	*S. aureus, n* = 227		TIA 82.8%, doxycycline 74.4%, ENR 68.7%, STX 60.2%, AMX 58.6%, ENR 55.1%, AMX/clavulanic acid 35.7%	No data	Szabó et al. (2025)
	2022–2023	Turkeys	7 breeding farms, 14 broiler farms	*S. aureus n* = 166		TIA 90.4%, doxycycline 79.5%, AMX 63,3%, AMX/ clavulanic acid 60.8%, tylosin 41%, vancomycin 18.1%	No data	Kovács et al. (2025)
Czechia	2017–2018	Turkey and chicken meat	33 flocks	*S. aureus*		MRSA 36.4%	No data	Tegegne et al. (2021)
Belgium	2023	Chicken broilers Commercial layers Meat turkeys	96 flocks 33 flocks 27 flocks	MRSA *n* = 1 nd MRSA *n* = 5	nd	MRSA 1% nd MRSA 18.5%	No data nd	EFSA (2022, 2023)
Germany	2022	Chicken broilers – carcasses	—	MRSA *n* = 60		TET 96.7%, clindamycin 95%, trimethoprim 88.3%, ERY 85%, TIA 76.7%, quinupristin/dalfopristin 75%, GEN 11.7%, ciprofloxacin 10%, streptomycin 8.3%,	No data	

Table 4: *Continued*

Country	Years	Type of material	Number of flocks/ samples	Isolated strains		Phenotypic resistance	Resistance genes	References
				CoPS	CoNS			
		Meat turkeys – carcasses		MRSA *n* = 219		rifampicin 1.7%, sulfamethoxazole 1.7%, chloramphenicol 0% TET 92.2%, clindamycin 80.8%, trimethoprim 77.6%, ERY 79.5%, TIA 79%, quinupristin/dalfopristin 69.4%, GEN 6.4%, ciprofloxacin 38.4%, streptomycin 9.1%, rifampicin 0.5%, sulfamethoxazole 1.8%, kanamycin 5.9%, chloramphenicol 0%	No data	
Autonomous Province of Vojvodina in Serbia	2021	Chicken broilers – meat		*S. aureus n* = 34		Cloxacillin 100%, AMX 100%, AMX/clavulanic acid 100%, ERY 82.35%, chloramphenicol 61.77%, STX 38.24%, TET 34%, GEN 23.53%	No data	Lika et al. (2021)
Portugal	2020	Swabs from slaughterhouses	100 quails; 50 commercial chickens; 70 homebred chickens		Methicillin-resistant, *M. lentus, S. urealyticus, M. sciuri, S. haemolyticus*	73 (97.3%) isolates MDR (resistant to at least 3 or more classes of antibiotics): 11 strains of *S. lentus*, 21 *S. urealyticus*, 14 *S. sciuri*, and 3 *S. haemolyticus* with phenotypic resistance to PEN; 40% of isolates were	- *mecA*, - *aph(3)-IIIa, ant(4)-Ia, -ermA, -ermB, -ermC, -mphC, -tetK, -tetL, -tetM, -tetO*, - cat_{p194} in one *S. lentus* isolate, *-dfrK, -dfrD,*	Silva et al. (2022)

Table 4: *Continued*

Country	Years	Type of material	Number of flocks/ samples	Isolated strains		Phenotypic resistance	Resistance genes	References
				CoPS	CoNS			
						resistant to aminoglycosides. All strains of *S. lentus* and *S. urealyticus*, 14 *M. sciuri* and 2 *S. haemolyticus* resistant to macrolides and lincosamides.All strains of *S. urealyticus*, *S. sciuri* ,and *S. haemolyticus* and 25 (69.4%) of *S. lentus* resistant to TET.No resistance to vancomycin	*-cfr* one *M. sciuri* strain	
Iran	2023	523 samples of meat and edible viscera from broiler chickens	Thigh and breast meat, liver, stomach, heart, shank	*S. aureus n* = 267		TET (94.37%), AMP (88.73%), PEN (71.83%).	*-mecA* 53.2%	Seyedeh Mozhgan et al. (2025)
Pakistan – Khyber Pakhtunkhwa province	2017	100 small-intestinal samples from broiler chickens	50 samples from farm chickens, 50 samples from household chickens		*S. carnosus*, *S. xylosus*, *S. cohnii S. lentus*, *S. saprophyticus*, *S. simulans*, *S. gallinarum*, *S. chromogenes*, *S. warneri.*	Over 50% isolates resistant to four antimicrobials, including, ERY 66.7% and 69.8%, clindamycin 68.6% and 72.1%, TET 66.7% and 65.1% and tygecycline 74.5% and 58.1%, for breeding and homebred chickens, respectively.	*-mecA* 15.8%, *-ermC, -ermA, -tet K, -tetM, -aacA-aphD.*	Syed et al. (2020)
Egypt	2020	396 samples from broiler chickens	Samples from broiler farms, runs, hatcheries, slaughterhouses	*S. aureus* (*n* = 40)	nd	Clindamycin (97.5%), ERY (95%), TET (90%), PEN and oxacillin (82.5%), 95% strains MRSA,	No data	Ahmed et al. (2021)

Table 4: *Continued*

Country	Years	Type of material	Number of flocks/ samples	Isolated strains		Phenotypic resistance	Resistance genes	References
				CoPS	CoNS			
Algeria	2011–2018	4,248 nasal swabs from birds	840 poultry farms, breeding hens (*n* = 654 samples), layer hens (*n* = 838 samples), chicken broilers (*n* = 1,614), turkeys (*n* = 1,142)	*S. aureus*, *n* = 1,276	nd	MRSA: 100% MRSA isolates (*n* = 252) resistant to PEN G, AMX/clavulanic acid, oxacillin, and cefoxitin. TET (82.5%). ERY (70.6%). Clindamycin (68.6%), ciprofloxacin (50%). All MRSA isolates susceptible to vancomycin, mupirocin and rifampicin, except 2 isolates from turkeys, which were resistant to rifampicin. About 82.3% of strains were susceptible to chloramphenicol, 76.1% to GEN, 75.8% to streptomycin, 72.6% to STX and 58.73% to kanamycin. 50% susceptible to ciprofloxacin. All isolates were MDR.	No data	Benrabia et al. (2020)
Nigeria	June 2018 to April 2019	Frozen turkey samples Broiler chickens, *n* = 368		MRSA *n* = 110		PEN G 110 (100%), clarithromycin 53 (48.2%), doxycycline 58 (52.7%), minocycline 53 (48.2%), TET 64 (58.2%), ciprofloxacin 71 (64.6%), levofloxacin 84 (76.4%), moxifloxacin 88	No data	Igbinosa et al. (2023)

Table 4: *Continued*

Country	Years	Type of material	Number of flocks/ samples	Isolated strains		Phenotypic resistance	Resistance genes	References
				CoPS	CoNS			
						(80%), clindamycin 62 (56.4%), sulfonamides 53 (48.2%), trimethoprim 71 (64.6%) and rifampicin 103 (93.6%), ceftaroline 54 (49.1%), GEN 51 (46.4%), amikacin 64 (58.2%), kanamycin 56 (50.9%), nitrofurantoin 100 (90.9%), STX 58 (52.7%), chloramphenicol 78 (70.9%), linezolid 83 (75.5%). All isolates were susceptible to vancomycin, oritavancin, teicoplanin, daptomycin, and tedizolid. 89 (80.9%) MDR isolates in total		
	2017	Faecal samples from healthy broiler chickens	Four broiler chicken farms		14 strains of *S. epidermidis*, *S. saprophyticus*, *M. sciuri*	*M. sciuri* PEN 87.5%. *M sciuri* cefoxitin 37.5%	*-mecA, -blaZ*	Jesumirhewe et al. (2024)
South Africa	2019	384 samples from poultry farms, transport, abattoir, and retail outlets		*S. aureus n* = 120: farm (40 strains), transport (15 strains), abattoir (30 strains), retail outlet (35 strains)		TET (61.67%), PEN G (55.83%), ERY (54.17%), clindamycin (43.33%), doxycycline (36.67%), AMP (34.17%), moxifloxacin (30.83%), amikacin		Amoako et al. (2020)

Table 4: *Continued*

Country	Years	Type of material	Number of flocks/ samples	Isolated strains		Phenotypic resistance	Resistance genes	References
				CoPS	CoNS			
						(30.83%), STX(30.00%), levofloxacin (23.33%). All isolates were 100% susceptible to tigecycline, teicoplanin, vancomycin, nitrofurantoin, chloramphenicol, and linezolid. Mdr 39.17%		
Ethiopia	2021	222 samples: 101 cloacal swabs, 90 tracheal swabs, 17 pooled litter swabs	Broiler chickens	40 *S. aureus* strains	11 strains of *S. hyicus* 13 strains of other CoNS species	PEN G (96.9%), TET (78.1%), AMX 65.6%, ERY 65.6%. Most isolates were highly susceptible to ciprofloxacin (95.3%). SFX (85.9%) 95.3% resistant to three or more drugs	No data	Abunna et al. (2022)
USA	2010	Retail chicken and turkey broiler carcasses	114 samples from chicken broilers and 53 from turkeys	168 *Staphylococcus aureus* isolates (101 from chickens and 67 from turkeys)		12 MRSA isolates (7.1%), AMP (94.6%), TET (72%). PEN (70.8%). doxycycline (62.5%). oxacillin with 2% NaCl (47.6%). azithromycin (44.6%). ERY (44.6%). vancomycin (36.8%). cyprofloxacin (32.1%). cefoxitin with 2% NaCl (31%). GEN (25.6%). kanamycin (26.8%). clindamycin (20.8%).	*mecA* 1.8%	Abdalrahman et al. (2015)

Table 4: *Continued*

Country	Years	Type of material	Number of flocks/ samples	Isolated strains		Phenotypic resistance	Resistance genes	References
				CoPS	CoNS			
Canada	2022–2024	Air samples from chicken barns, chickens aged 7–15 weeks, and layers from 44 to 64 weeks	15 chicken barns		*S. equorum n* = 7, *S. shinii n* = 5, *S. cohnii n* = 1, *S. pseudoxylosus n* = 1, *S. gallinarum n* = 1	rifampicin (14.9%). STX. chloramphenicol (5.4%). LIN 73.3%,, TET 66.7%,, streptomycin 33.3%,, ERY 20%,, GEN 6.25%. All isolates susceptible to ciprofloxacin, chloramphenicol, daptomycin, nitrofurantoin, linezolid, PEN, synercid, vancomycin, and tigecycline., 40% of isolates were MDR	*tetk* 66.7%, *LnuA* 66.7%, *mphC* 66.7%, *str* 33.3%, *msrA* 20%, *fosD* 13.1%, *aac (6')-aph* (2'') 6.67%, *fusF* 6.7%	Ghaffar et al. (2025)
Brazil		Chicken meat samples		*S. aureus*		ERY 100%, GEN 100%, clindamycin 100%, doxycycline 100%, TET 100%	*norC, tet, nora, blaZ.*	da Silva et al. (2025)

aureus strains isolated from samples of retail chicken meat sold on street markets and in butcher shops in Brazil were resistant to several groups of antibiotics (macrolides, aminoglycosides, lincosamides, and TETs). In contrast, a low percentage of strains (Table 4) were resistant to fluorinated quinolones, sulfonamides with trimethoprim, and chloramphenicol (da Silva et al., 2025). The authors of most of the studies cited also demonstrated the presence of isolates resistant to more than three groups of antibiotics, which indicates MDR in these strains and suggests high selection pressure resulting from long-term or improper exposure to antibiotics. This finding additionally underscores the possibility of horizontal transfer of resistance genes via plasmids, transposons, and various other MGEs. Molecular detection of resistance genes reveals the common occurrence of *mec*A, *bla*Z, *erm*A, *erm*B, *erm*C, *msr* (A), and *tet*(K/L\M\O), which mediate resistance to these antibiotics, in staphylococci (Krupa et al., 2015; Silva et al., 2022; Syed et al., 2020; Seyedeh Mozhgan et al., 2025).

5.3 *Salmonella* spp.

Salmonellosis is globally reported as a major foodborne gastrointestinal infection in humans, with an estimated 90 million cases of gastroenteritis worldwide annually and approximately 155,000 deaths (Majowicz et al., 2010). In 2024, salmonellosis was the second most frequently reported zoonotic disease in Europe, with 79,703 confirmed cases in the EU The overall trend for *Salmonella* infections in Europe showed a significant increase in the years 2020–2024 (European Food Safety Authority, & European Centre for Disease Prevention and Control 2025c). Poultry and its products continue to be the primary source of *Salmonella*, with eggs and egg products identified as infection vehicles in strong-evidence outbreaks (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2023a, 2024a, 2025c).

The *Salmonella* genus consists of over 2,600 serovars, classified into typhoidal (*S. enterica* subspecies *enterica* serovar Typhi) and non-typhoidal serotypes (NTS) (Grimont & Weill, 2007). All serovars have pathogenic potential and are considered potentially harmful to human health. NTS are the most predominant zoonotic pathogens and can easily adapt to a wide range of hosts. Various *Salmonella* serovars are identified in various poultry species, among which *S.* Gallinarum and *S.* Pullorum are host-adapted and cause disease in chickens. In *Gallus gallus* (chickens), several *Salmonella enterica* serovars are especially common and important for both poultry health and human food safety. The distribution varies by region, production system, and control programmes, but *S. enteritidis*, *S. typhimurium*, and *S. infantis* consistently rank among the most significant globally (European Food Safety Authority, & European Centre for Disease Prevention and Control 2023a, 2024a, 2025c; Borges et al., 2019). In Europe, *S. enteritidis* is associated with laying hens, whose eggs are the source, while *S. infant* is is strongly associated with chicken consumption (Table 5) (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2025a, 2025c). Turkeys are more commonly linked with *S. agona*, *S. infantis*, or *S. kentucky*, but *S.* Reading was commonly noted in the USA (Cason et al., 2024). In China, *S. enteritidis* is associated with broilers (Wang et al., 2024, Liu et al., 2025a), whereas *S. kentucky* was the dominant serovar in the USA (Table 1) (Obe et al., 2023). Duck production is mainly associated with Asian countries, where *S. typhimurium* and *S. indiana* are frequently isolated (Song et al., 2024; Chu et al., 2024).

AMR has contributed to the emergence and proliferation of individual NTS serovars and strains within animal and human populations (Ao et al., 2015) The occurrence of resistance in *Salmonella* depends on several important factors, including the serovar, selective pressure from antimicrobial use in animal populations, the clonal spread of resistant strains within production sectors, and the horizontal transfer and dissemination of resistance determinants, such as resistance plasmids. The importance of resistance to last-resort antimicrobials such as cephalosporins, carbapenems, quinolones, or polymyxins was underlined in the WHO Bacterial Priority Pathogens List (World Health Organization 2024). Fluoroquinolone-resistant *Salmonella enterica* is classified as a high-priority pathogen because of its increasing resistance trends, global disease burden, and limited treatment options. Moreover, isolates resistant to cephalosporins or carbapenems are ranked as a “critical group” on the priority pathogens list (World Health Organization 2024). Levels of antimicrobial resistance remain consistently high, varying between regions and countries. Resistance levels in laying hens are generally lower than in broilers, but infections may persist longer because laying hens remain in production for extended periods (Table 5).

In Europe, *Salmonella* most commonly shows resistance to ciprofloxacin, TET, and AMP, ranging from moderate to very high in isolates from food-producing animals and imported poultry meat (Table 6). The exception was in laying hens, where low levels of resistance were reported. Large differences in resistance levels between countries were observed, especially in *Salmonella* isolates from broilers (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2025a, 2025c). At the

Table 5. Percentage of MDR *Salmonella*, the most common antimicrobial resistance, and the most prevalent *Salmonella* serovars in different poultry sectors from selected countries

Poultry sector	Country	MDR *Salmonella* prevalence (%)	Common resistance	Reference	Dominant *Salmonella* serovar (%)	References
Broiler chickens	EU	35.1–43%	Ciprofloxacin, sulfonamides, TET	European Food Safety Authority, & European Centre for Disease Prevention and Control (2025a, 2025b)	Infantis (57.9%)	EFSA & ECDC (2024)
	China	61.6–70.6%	Sulfisoxazole, nalidixic acid, TET	Wang et al. (2024); Liu et al. (2025b)	Enteritidis (34.3%–37.5%)	Wang et al. (2024); Liu et al. (2025b)
	USA	47.4%	TET, sulfamethoxazole-sulfisoxazole, ciprofloxacin	Food and Drug Administration (2026)	Kentucky (nd)	Obe et al. (2023)
	Egypt	100%	Ceftazidime, cefepime, and ERY	Salem et al. (2025)	Kentucky (52.6%)	Salem et al. (2025)
	Brazil	50.7–77.3%	Ciprofloxacin	Rau et al. (2021)	Heidelberg (37.7%–54.6%)	Rau et al. (2021)
	Thailand	29.1%	Doxycycline, colistin	Noenchat et al. (2023)	Enteritidis (73.36%)	Noenchat et al. (2023)
	Japan	0%	Not detected	Noenchat et al. (2023)	Schwarzengrund (100%)	Noenchat et al. (2023)
Laying hens	Europe	6.0–7.5%	Ciprofloxacin, sulfonamides, TET	European Food Safety Authority, & European Centre for Disease Prevention and Control (2025a, 2025b)	Enteritidis (38.5%)	EFSA & ECDC, 2024
	China	5.1%	Sulfisoxazole, nalidixic acid, TET	Wang et al. (2024)	Newport (51.2%)	Wang et al. (2024)
	Egypt	100%	NEO, nalidixic acid, cefoxitin	Elsayed et al. (2024)	Enteritidis (nd)	Elsayed et al. (2024)
	Brazil	51.1%	Sulfamethoxazole, sulfonamides, ceftiofur	Moraes et al. (2024)	Agona (31.1%)	Moraes et al. (2024)
Turkey	Europe	22.9–38,9%	Ciprofloxacin, AMP, TET	European Food Safety Authority, & European Centre for Disease Prevention and Control (2025a)	Agona (46.1%)	EFSA & ECDC, 2024
	USA	16.2%	TET, sulfamethoxazole-sulfisoxazole, AMP	FDA, 2026	Reading (11.3%)	Cason et al. (2024)
Ducks	China	97.3%	AMP, TET, ciprofloxacin	Chu et al. (2024)	Indiana (29.0%), Typhimurium (30.15%)	Chu et al. (2024); Song et al. (2024)

Table 6. Percentage of *Salmonella* isolates resistant to selected antimicrobials isolated from poultry and tested in the harmonized AMR monitoring in Europe (https://www.efsa.europa.eu/en/microstrategy/dashboard-antimicrobial-resistance)

Antimicrobial	AMP		Ciprofloxacin		Colistin		TET		Cefotaxime	
Year	2022	2024	2022	2024	2022	2024	2022	2024	2022	2024
Broilers	19%	17%	55%	50%	4%	4%	40%	32%	1%	1%
Laying hens	5%	5%	25%	22%	5%	7%	9%	7%	0%	0%
Turkeys	50%	28%	58%	33%	0%	1%	41%	26%	2%	0%

EU level, a statistically significant decreasing trend in TET resistance was observed in *Salmonella* from broilers. Between 2022 and 2024, a decreasing trend in AMP resistance was identified in isolates from turkeys and broilers, while in the case of laying hens, no changes in resistance to these antimicrobials were observed. A significant decrease in ciprofloxacin resistance was also noted in broilers and turkeys. In contrast, laying hens showed a statistically significant increasing trend in ciprofloxacin resistance (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2025c). For cefotaxime and ceftazidime, representing third-generation cephalosporins, resistance levels were generally low among *Salmonella* spp. The occurrence of presumptive extended spectrum beta lactamases (ESBL)-/AmpC beta-lactamases (AmpC)-producing *Salmonella* was low in 2024, ranging from 0.2% in turkeys to 1.2% in broilers. Only a few countries, mainly Italy and Malta, reported moderate cephalosporin resistance. Analysis of WGS data for *Salmonella* spp. reported by Germany, Italy, and the Netherlands revealed the $bla_{\text{CTX-M-1}}$ gene to be the most common resistance determinant. No carbapenem-resistant isolates derived from poultry have been identified thus far in European countries (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2025a, 2025c). In the USA in 2024, resistance among *Salmonella* chicken isolates was most commonly reported against TET (60.7%), sulfamethoxazole-sulfisoxazole (46.8%), AMP (15.6%), and ceftriaxone (15.6%), as compared to 51.4%, 17.6%, 16.2%, and 6.8%, respectively, in turkey isolates. A total of 4.5% chicken and 2.7% turkey isolates were resistant to cefoxitin (Food and Drug Administration, 2026). Isolates were frequently resistant to at least one antibiotic (91.2%) or MDR (45.5%). Resistance was observed to TET (82.8%), minocycline (42.3%), nitrofurantoin (40.3%), cefazolin (38.3%), AMP (32.1%), and ceftriaxone (26%). All isolates were susceptible to fluoroquinolones, carbapenems, and glycylcyclines (Food and Drug Administration 2026).

Research conducted on the Brazilian poultry production chain demonstrated a high prevalence of resistance in *Salmonella* isolates, with the highest resistance percentage noted for sulfamethoxazole (91%), followed by sulfonamides (51%) and ceftiofur (28.9%). The serovars showed no resistance to ciprofloxacin (Moraes et al., 2024). In the case of China's study, research from broiler farms, layer farms, slaughterhouses, and retail chicken meat consistently shows high levels of *Salmonella* resistance to sulfisoxazole (100%), nalidixic acid (54.3%), TET (47.8%), streptomycin (39.86%), AMP (39.1%), and chloramphenicol (30.4%) (Wang et al., 2024). Other studies have found that 41–62.5% of isolates were ESBL-producing strains (Shu et al., 2023; Zhou et al., 2025). Three serotypes of carbapenem-resistant *Salmonella* from chickens, *S.* Kentucky, *S.* Indiana, and *S.* Idikan, were shown to carry $bla_{\text{NDM-5}}$ (Zhou et al., 2025). In India, AMR was observed across regions, revealing substantial variation. Studies have reported high resistance to antibiotics such as AMP, TET, and colistin (Shil et al. 2026).

Research in Bangladesh found that *S. enterica* prevalence in layers was significantly higher than in broilers. Broiler isolates showed considerable resistance, particularly to sulfamethoxazole (100%), streptomycin/sulfonamide (88.9%), nitrofurantoin (66.7%), and AMP (55.6%). Layer isolates demonstrated lower resistance overall, though resistance to AMP (52%) and sulfonamide/sulfamethoxazole (92%) was still prevalent (Popy et al. 2025). Most *Salmonella* isolated from Thai poultry samples were phenotypically resistant to doxycycline (84.4%) and colistin (68.75%), while the same study showed no resistance in isolates obtained in Japan (Noenchat et al., 2023). Interestingly, higher NTS prevalence in Vietnam was reported in ducks (94.3%) than in chickens (64.7%), with a high rate of resistance to TET (58.5%), STX (58.1%), streptomycin (47.3%), AMP (39.8%), and chloramphenicol (37.3%). The diversity of *Salmonella* serotypes may reflect differences in geographic location, collection time, or identification methods (Starkova et al., 2025).

Among African countries, AMR testing of *Salmonella* serovars in Egypt revealed that all isolates were completely resistant (100%) to ceftazidime, cefepime, and ERY. High resistance was also observed against AMX (94.7%), AMX + clavulanic acid (94.7%), ceftriaxone (84.2%),

chloramphenicol (84.2%), doxycycline (84.2%), ciprofloxacin (89.5%), GEN (89.5%), streptomycin (89.5%), and STX (94.7%). In contrast, a high level of sensitivity to meropenem was observed (Salem et al., 2025). In another Egyptian study, *S. enteritidis* isolates from broiler and layer farms were found to be extremely resistant to NEO (100%), nalidixic acid and cefoxitin (95.4%), norfloxacin (86.3%), cefotaxime (81.8%), AMX (77.2%), amikacin (72.7%), and ERY (68.1%). The presence of the $bla_{\text{CTX-M}}$ gene and *gyrA* mutation was high (Elsayed et al., 2024). In Uganda, *Salmonella* species isolated from broiler samples were highly resistant to AMP (80%), ERY (70%), TET (67.5%), and ciprofloxacin (62.5%) (Ssemakadde et al., 2025). Similarly, in Tanzania, the highest resistance was also observed against AMP (92.9%), followed by TET (71.43%), ciprofloxacin (42.9%), sulfonamide (42.85%), GEN (35.7%), and azithromycin (28.9%) (Mwambene et al., 2025).

The widespread use of antimicrobials to enhance poultry meat production has facilitated the increase in MDR *Salmonella* spp. Studies show significant differences among MDR *Salmonella* spp. strains isolated from various poultry species and geographic regions (Di Taranto et al., 2025). In general, Asian and African countries have reported increasing levels of MDR *Salmonella* on poultry farms and in poultry meat. Broilers consistently show the highest MDR prevalence globally. *S.* Infantis, *S.* Enteritidis, *S.* Typhimurium, and *S. Heidelberg* are the dominant poultry MDR *Salmonella* serovars worldwide. In European countries, a slight decrease in MDR *Salmonella* was observed between 2022 and 2024 (European Food Safety Authority, & European Centre for Disease Prevention and Control 2025a, 2025c). MDR was observed at high levels in *Salmonella* spp. recovered from broilers and turkeys in 2024 (35.1% and 22.9%, respectively). *Salmonella* spp. isolates from laying hens showed a markedly lower MDR level (6.0%). The highest levels of MDR were observed in *S.* Infantis isolates, particularly those derived from broilers and turkeys (European Food Safety Authority, & European Centre for Disease Prevention and Control, 2025c). In the USA, the MDR *Salmonella* rate in 2024 was higher in isolates recovered from chickens (47.4%) compared to turkeys (16.2%). In Brazil, depending on the study, approximately 18–51.1% of *Salmonella* strains were classified as MDR strains. The majority of MDR strains belonged to the serotypes *S.* Enteritidis, *S.* Typhimurium, *S.* Bredeney, or *S.* Agona (Borges et al., 2019; Moraes et al., 2024). Asia and Africa often report high MDR prevalence linked to intensive antibiotic use and poorer antimicrobial stewardship. The highest MDR rates have been noted in South and Southeast Asia (Starkova et al., 2025). China has reported extensive MDR *Salmonella* circulation, with antimicrobial resistance profiles showing a 61.6% MDR rate in *Salmonella* from broilers (Shu et al., 2023). Similarly, India reports an alarming increase in MDR isolates in 2021–2025, particularly in resistance to commonly used antibiotics such as TET, AMP, and third-generation cephalosporin, and especially in *S.* Typhimurium (Shil et al., 2026). Research conducted in Bangladesh classified 86.1% of isolates as multidrug-resistant (Popy et al., 2025), whereas a 29.1% rate of MDR *Salmonella* was noted in Thailand, and no MDR isolates were identified among Japanese *Salmonella* isolates (Noenchat et al., 2023). In Africa, MDR *Salmonella* isolates have been detected in many studies, with prevalence ranging from 12.1% in Zimbabwe to 100% in Egypt, Ethiopia, Nigeria, Senegal, and South Africa (Salem et al., 2025; Ramtahal et al., 2022). In contrast to broiler chickens and turkeys, MDR prevalence in laying hens is comparatively lower. In Europe, surveillance programmes, vaccination programmes, and stricter antimicrobial regulation have contributed to relatively lower MDR *Salmonella* prevalence (European Food Safety Authority, & European Centre for Disease Prevention and Control 2025c). Similarly, in North America, the prevalence of MDR *Salmonella* in laying hens is generally lower than in broilers and turkeys due to long-term surveillance and control programmes. In Asia and Africa, MDR *Salmonella* isolated from laying hens is reported more frequently than in North America or Europe, but is lower than in chickens. Recent global analyses suggest that the intensification of poultry production, inadequate antimicrobial stewardship, and limited surveillance systems may contribute substantially to the spread of MDR *Salmonella* across continents.

6. Other pathogens

6.1 *Erysipelothrix rhusiopathiae*

Erysipelothrix rhusiopathiae is a gram-positive, facultatively anaerobic bacillus responsible for erysipelas, an infectious disease affecting humans and numerous animal species, including birds. In poultry, erysipelas is most commonly reported in domestic geese, ducks, turkeys, and laying hens. Infection is believed to occur primarily via ingestion of contaminated feed or water, or through damaged skin resulting from feather pecking, scratching, or cannibalism. In laying hens, the poultry red mite, *Dermanyssus gallinae*, has also been suggested as a potential mechanical vector (Jordan & Bisgaard, 2011; Eriksson

et al., 2025). The disease typically manifests as acute septicaemia with sudden mortality, accompanied by splenomegaly, hepatomegaly, renal enlargement, and multifocal haemorrhages. Flock mortality ranges from 1% to as high as 50%, depending largely on how quickly appropriate treatment is implemented (Jordan & Bisgaard, 2011; Bobrek et al., 2016; Nowak et al., 2024). The disease is observed mainly in maturing and adult birds. In commercial goose flocks in Poland, most outbreaks occur in younger birds aged 11–13 weeks, particularly between August and September, indicating a strong seasonal pattern associated with intensive production periods (Jordan & Bisgaard, 2011; Nowak et al., 2024). Importantly, erysipelas is a zoonotic disease, and *E. rhusiopathiae* may be transmitted from infected birds or contaminated biological material to humans, typically through skin injuries. Such infections may result in localized erysipeloid or, less commonly, systemic disease such as septicaemia or endocarditis (Rostamian et al., 2022).

As standard erysipelas treatment involves the administration of antibiotics, continuous monitoring of antimicrobial susceptibility in *E. rhusiopathiae* is essential. In particular, it is important to track the prevalence of resistant strains, identify their resistance mechanisms, and better understand the processes involved in the horizontal transfer of resistance genes. Currently available evidence indicates that poultry-derived *E. rhusiopathiae* isolates retain high susceptibility to β-lactam antibiotics, including PEN, AMP, and AMX, confirming that these agents remain the cornerstone of erysipelas treatment in poultry production (Bobrek & Gaweł, 2023; Dec et al., 2024a; Kerek et al., 2025b). In contrast, *E. rhusiopathiae* strains frequently exhibit high levels of resistance to TETs and fluoroquinolones. In a study by Dec et al. (2024a) involving 60 isolates from geese and ducks in Poland, 85.0% of isolates were resistant to TET and 80.0% to ENR. Similarly, Bobrek & Gaweł (2023) reported that among 47 goose-derived isolates, 76.6% were resistant to ENR, and nearly 64% exhibited resistance to TET. Interestingly, markedly lower resistance rates to these antimicrobials have been reported in poultry isolates from Hungary. According to Kerek et al. (2025b), only 10.5% of isolates were resistant to TET and 2.6% to ENR, indicating substantial geographic differences in resistance patterns, likely reflecting variation in antimicrobial use practices (Table 7). Acquired resistance to other antimicrobial classes, including macrolides (0–7.9%), lincosamides (2.6–16.5%), pleuromutilins (7.9–15%), and phenicols (0–5.3%), remains relatively uncommon in poultry-derived *E. rhusiopathiae* isolates in both Poland and Hungary (Dec et al., 2024a; Bobrek & Gaweł, 2023; Kerek et al., 2025b). However, co-occurrence

Table 7. Summary of antimicrobial resistance characteristics of poultry-derived *E. rhusiopathiae* isolates

Country	Number of isolates	Source of isolation; year of isolate collection	Serotypes – % distribution	Antimicrobial resistance (%)	MDR frequency	Detected resistance genes and MGEs containing resistance genes	Source
Poland	60	Domestic geese (n = 55) and ducks (n = 5); 2019–2021	5–38.3%; 1b – 28.3%; 8–15.0% 2–10% others – 8.3%	TET 85.0%; ENR 80.0%; ERY 3.3%; LIN 16.7%; TIA 15%; PEN, AMP and AMX 0%; FLO 0%; intrinsic resistance to aminoglycosides (GEN, NEO) and STX	16.7% (mainly serotype 8)	*tetM*, *lnuB*, *lsaE*, *ant(6)-Ia*, *spw*, *erm47*; mutated genes *gyrA* and *parB*; Tn916 (18 kb); ICEEr1023 (130 kb); ICEEr1012 (74 kb); GI_Er147 (98 kb), prophage φEr670 (53 kb)	Dec et al. (2024a); Dec et al. (2024b); Dec et al. (2026)
Poland	47	Domestic geese (n = 47); 2008–2018	1b – 55.3%; 2–27.7%; 5–17%	ENR 76.6%; TET – 63.8%; ERY 0%; AMX 0%;	0%	*tetM*, mutated gene *gyrA*;	Bobrek & Gaweł (2023)
Hungary	38	Domestic geese (n = 32), ducks (n = 2) and turkeys (n = 4); 2024	ND	TET 10.5%; ENR 2.6%; LIN 2.6%; TYL 7.9%; TIA 7.9%; FLO 5.3%; PEN and AMX 0%	ND	*tetM*, *tetT*, *erm47*; Tn6009, ISErh6	Kerek et al., 2025

TET – tetracycline; ENR – enrofloxacin; ERY – erythromycin; LIN – lincomycin; TIA – tiamulin; PEN – penicillin; AMP – ampicillin; AMX – amoxicillin; GEN – gentamicin; NEO – neomycin; FLO – florfenicol; STX – trimethoprim/sulfamethoxazole; ND – not determined.

of resistance to these agents alongside resistance to TETs and fluoroquinolones contributes to the emergence and spread of MDR strains. In Polish waterfowl isolates collected between 2019 and 2021, the proportion of MDR strains was estimated at 16.7% (Dec et al., 2024a), highlighting a growing concern for antimicrobial therapy and disease control (Table 7). In addition to acquired antimicrobial resistance mechanisms, *E. rhusiopathiae* exhibits intrinsic resistance to several antimicrobial classes that should be considered when selecting therapeutic agents. Notably, these bacteria are regarded as naturally resistant to aminoglycosides (gentamycin and NEO) and folate pathway inhibitors (STX) (MIC ≥ 512 µg/ml) (Dec et al., 2024a).

Whole-genome sequencing studies have revealed that resistance determinants identified in poultry-derived *E. rhusiopathiae* strains are located within various MGEs, whereas resistance to fluoroquinolones is associated with mutations in the *gyrA* and *parC* genes (Dec et al., 2024a, b; Borek & Gaweł, 2023). Resistance to TET is associated with the presence of the ribosomal protection protein gene *tet(M)*, which in *E. rhusiopathiae* is typically carried on the 18-kb Tn916 transposon. This transposon may occur as an independent MGE or be integrated into larger genomic islands, such as 130-kb ICEEr1023, 74-kb ICEEr1012, and 98-kb GI_Er147. These MGEs may additionally harbour other resistance genes present either individually (*erm(47)*) or in MDR clusters (e.g. *lsa(E)-lnu(B)-ant (6)-Ia-spw*) (Dec et al., 2024b). Furthermore, the lincosamide and pleuromutilin resistance genes *lsa(E)* and *lnu (B)* identified in poultry-derived *E. rhusiopathiae* isolates may also be located within prophage-associated DNA regions, such as the 53-kb φEr670 prophage identified in MDR isolates belonging to serotype 8 (Dec et al., 2026) (Table 7). The presence of transposons, genomic islands, and prophage-associated DNA carrying resistance genes indicates that HGT plays a central role in the dissemination of antimicrobial resistance in *E. rhusiopathiae*.

Taken together, these findings indicate that although β-lactam susceptibility remains well preserved, the progressive emergence of MDR *E. rhusiopathiae* strains in poultry warrants continuous surveillance of antimicrobial susceptibility profiles and prudent antimicrobial stewardship to limit further spread of resistance in this zoonotic pathogen.

6.2 *Riemerella anatipestifera corrig* (*R. anatipestifera*)

Infections caused by *Riemerella anatipestifera corrig* (*R. anatipestifera*), previously called *R. anatipestifer* (https://lpsn.dsmz.de/species/riemerella-anatipestifera), are an important health and economic problem in poultry production, especially duck and goose farming. This bacterium is an etiological agent of disease with a high mortality rate, especially in young birds (Ruiz & Sandhu, 2013). The clinical picture includes sepsis, meningitis, airsacculitis, and fibrinous lesions in internal organs (Hao et al., 2025). The importance of *R. anatipestifera* in veterinary practice results not only from the severe disease course, but also from its high serotype variability, which makes it difficult to develop effective methods of immunoprophylaxis (Yang et al., 2024a). An additional challenge is growing resistance to antimicrobials, which limits therapeutic options and underscores the need for rational use of antibiotics (Hao et al., 2025).

R. anatipestifera shows a high capacity to acquire resistance owing to HGT, supported by an open pan-genome and mechanisms such as natural transformation and outer membrane vesicles (Huang et al., 2021; Wang et al., 2025). Resistance genes can originate in the core genome or be acquired by mobile elements, such as genomic islands. Resistance to fluoroquinolones is mainly due to mutations in the genes *gyr*A, *par*C, and *par*E, while plasmid-mediated mechanisms (plasmid-mediated quinolone resistance) play a smaller role (Pathomchai-Umporn et al., 2025; Zhu et al., 2019). Efflux pumps also play an important role (Li et al., 2016). In the case of aminoglycosides, the dominant mechanisms are modifying enzymes – aminoglycoside phosphotransferases, acetyltransferases, and nucleotidyltransferases – and efflux systems (e.g. RanB and RaeB) (Zhou et al., 2026; Li et al., 2020). TET resistance is associated mainly with the *tet*X gene, efflux pumps, and ribosomal protection proteins (Zhu et al., 2018). Macrolides and lincosamides lose their efficacy mainly through rRNA methylation (*erm* genes) and enzymatic inactivation by the enzyme lincosamide nucleotidyltransferase (*lnu* gene) (Luo et al., 2018; Yang et al., 2024b). Resistance to β-lactams results from the presence of β-lactamases (e.g. RAA-1, RASA-1, or RAD-1) (Luo et al., 2022a, b; Li et al., 2023), while resistance to sulfonamides and trimethoprim is associated with the genes *sul* and *dfr* (Ma et al., 2026; Jiang et al., 2023), and resistance to phenicols is associated with the *cat* and *flo*R genes (Huang et al., 2017). *R. anatipestifera* makes use of numerous, often co-occurring resistance mechanisms, which promotes the rapid spread of MDR strains.

The results of research carried out in 2020–2022 in China provide detailed information on the phenotypic and genotypic resistance of *R. anatipestifera* in ducks. Testing of 74 representative strains showed very high resistance to commonly used drugs. The highest rates of resistance were noted for GEN (77%), ENR (73%), kanamycin (62.2%), and streptomycin (58.1%). All strains were

susceptible to ceftriaxone. Ceftiofur (98.6%) and FLO (64.9%) were also highly effective. As many of 81.1% isolates were resistant to at least three classes of antibiotics. Genes determining resistance to specific groups were very common among the bacteria. The most frequently noted was *tet*X, associated with TET resistance, detected in as many as 95.9% of strains. The *erm*F gene determining resistance to macrolides was present in 77% of strains, half of the strains possessed the *flo*R gene associated with resistance to amphenicols, and bla_{TEM} was detected in 10.8% of strains (Lyu et al., 2023).

Another study (Yan et al., 2026) analysed 88 *R. anatipestifera* strains isolated from ducks in 2023–2024. The highest resistance rates were noted for polymyxin B (97%), amikacin (91%), kanamycin (90%), and fluoroquinolones (about 90%). Resistance to TETs and doxycycline were 80% and 75%, respectively. More than half of strains were resistant to β-lactam antibiotics, including cefotaxime (60%), ceftazidime (55%), and ceftiofur (53%). Susceptibility to rifampicin was relatively high (78%). All strains were classified as MDR. Nearly half of strains (n = 41) were resistant to 6 antimicrobials. Three genes, *tet*X, *flo*R and *erm*F, were detected the most often (90–95%). The presence of *qnr*S in 16% of strains and *rmt*B in 5% of isolates was noted as well (Table 8). However, the other authors (Xihui et al., 2023) in the study on 51 *R. anatipestifera* strains from ducks revealed 100% resistance to most aminoglycosides. A high level of resistance was also shown for amikacin, with only a few strains found to be susceptible. In addition, nearly total resistance to polymyxin B (98%), LIN (94%), and tobramycin (94%) was observed. In the case of azithromycin, resistance was at a level of 88%. Among quinolones, resistance to norfloxacin (55%) and ENR (45%) was highest. The strains largely remained susceptible to β-lactam antibiotics such as cefotaxime or cefepime, as resistance did not exceed 10%. All strains were classified as MDR, among which 88% were resistant to at least five different classes of drugs, and the most resistant strain showed resistance to as many as seven classes. The study identified a number of genes responsible for these phenotypes, which was confirmed by the presence of dominant genes in most strains, including *ran*B (98%), *ran*A (96%), and *aad*S (88%) associated with aminoglycoside resistance, as well as $bla_{\text{OXA-209}}$, *tet*X4, *erm*F, *flo*R, *ere*D, and *tet*Q (Table 8). Another study carried out in China (Dong et al., 2024) on 157 strains of goose- and duck-derived *R. anatipestifera* confirmed previous findings on phenotypic and genotypic antimicrobial resistance. The strains were resistant to kanamycin (98.73%), amikacin (98.09%), GEN (98.09%), and streptomycin (94.91%). The most effective drugs proved to be FLO, ceftriaxone, spectinomycin, sulfafurazole, and cefepime. Each of the 157 strains possessed from 42 to 55 genes determining drug resistance, predominantly TET resistance genes (19), genes encoding efflux pumps (15), glycopeptide resistance genes (11), and macrolide resistance genes (7) (Table 8). The study showed a high level of agreement between the presence of genes and actual resistance for most drugs. For TET and polymyxin B, a 100% correlation was noted for *tet*B(P), *tet*M, *tet*T, and *mcr*-8.1. In the case of macrolides, the *erm*F, *erm*X, and *erm*E genes showed more than 91% correlation for ERY and azithromycin. For aminoglycosides, agreement between genes (*aac(3)*-Ig, *aad*S, and *aac(3)*-Ic) and phenotypic resistance was below 43%, which suggests the presence of as yet undiscovered mechanisms of resistance to these antibiotics in *R. anatipestifera* (Dong et al., 2024).

In another study conducted in Asia, using 69 strains of *R. anatipestifera*, most of the strains were resistant to nalidixic acid (89.9%), streptomycin (75.4%), norfloxacin (72.5%), and kanamycin (65.2%). All isolates were susceptible to AMX + clavulanic acid and imipenem. High susceptibility to piperacillin, cefoperazone, cefepime, cephalexin, FLO, and doxycycline (87–91.3%) was noted as well (Vo et al., 2022). A study carried out in Thailand on 37 strains of *R. anatipestifera* from ducks showed high MIC values for nalidixic acid, ranging from 16 μg/ml to ≥ 128 μg/ml, and low MIC values for ciprofloxacin and ENR, with values of 8 μg/ml and 4 μg/ml, respectively. The main resistance mechanism identified in the study was chromosomal mutations in the gene *gyr*A, where all isolates possessed a single point mutation in codon 83. Neither mutations in the QRDR region of the *par*C gene nor the presence of genes PMQR was noted in any of the strains (Pathomchai-Umporn et al., 2025).

Analysis of the literature reveals that research on resistance in *R. anatipestifera* is mainly concentrated in Asia, whereas other geographic regions remain little studied, which may influence the global assessment of the problem. A study using *R. anatipestifera* strains from Poland (Nowaczek et al., 2023), assessing phenotypic resistance of bacteria by determining MICs, showed very high MIC values for GEN, amikacin, and colistin (≥ 128 μg/ml). Low MICs, indicating that the antibiotics were effective, were obtained for AMX, cefuroxime, cefoperazone, piperacillin, and the STX combination. At least one resistance gene was detected in 72% of isolates; *tet*X and *erm*F were the most frequently identified. The presence of other resistance genes was noted as well: *aph(3')*-VII, *aac(3')*-IV, *cml*A bla_{TEM}, *aad*A, *str*A/*str*B, and *sul*I (Table 8). Another study, conducted in Poland (Tyc et al., 2026) using the disc-diffusion method, showed considerable variation in resistance

Table 8. Antimicrobial resistance in *Riemerella* spp. bacteria isolated from poultry

Type of strains	Type of sample	Number of samples	Country	Most frequently detected resistance genes	Resistance to antibiotics	Most effective antibiotics	References
R. anatipestifera	Duck brain and liver	*n* = 74	China	*tet*X, *erm*F, *flo*R, bla_{TEM}	GEN (77%), ENR (73%), kanamycin (62.2%), streptomycin (58.1%)	Ceftriaxone (100%) ceftiofur (98.6%) FLO (64.9%)	Lyu et al. (2023)
R. anatipestifera	Duck brain, chicken embryos	*n* = 88	China	*tet*X, *flo*R, *erm*F, *qnr*S *rmt*B	Polymyxin B (97%), amikacin (91%), kanamycin (90%), ciprofloxacin (90%), ENR (89%), TET (80%), doxycycline (75%), GEN (74%), cefotaxime (60%), ceftazidime (55%), ceftiofur (53%), chloramphenicol (47%), FLO (55%)	Rifampicin (78%)	Yan et al. (2026)
R. anatipestifera	Duck brain	*n* = 51	China	*ran*A, *ran*B, *aad*S, *erm*F, *flo*R, *tet*X, *tet*X6, *tet*X, *tet*Q, *mef*, *ere*D, $bla_{OXA-209}$	GEN (100%), kanamycin (100%), streptomycin (100%), NEO (100%), LIN (94%), tobramycin (94%), polymyxin B (98%), azithromycin (78%), norfloxacin (55%), ENR (45%), methicillin (88%)	Levofloxacin (90.2%), ciprofloxacin (90.2%), cefotaxime (90%), cefepime (90%)	Xihui et al. (2023)
R. anatipestifera	Geese ducks	*n* = 157	China	*tet*X, *tet*X2, *tet*B(P), *tet*O, *tet*S, *tet*T, *tet*M, *tet*W, *tet*30, *tet*35, *tet*41, *tet*B(46), *tet*A(60), *tet*B(60), *tetA*(58), *tet*X3, *tet*X4, *tet*X5, *tet*X6, *vanH_in_vanA_cl*, *vanH_in_vanF_cl*, *vanZ_in_vanA_cl*, *vanE*, *vanR_in_vanE_cl*, *vanR_in_vanF_cl*, *vanG*, *vanT_in_vanG_cl*, *vanS_in_vanC_cl*, *vanS_in_vanL_cl*, *vanS_in_vanN_cl*, *ermE*, *erm*F, *erm*R, *erm*X, *erm(35)*, *erm(47)*, *ere*D, bla_{GOB-5}, bla_{GOB-12}, $bla_{OXA-209}$, $bla_{OXA-464}$, *vat*B, *vat*E, *vat*F *vat*H, *aac(3)*-Ig, *aac(3)*-Ic, *aad*S, *mcr*-8.1, *bcr*A, *bac*A, *pgp*B, *arr*-1, *dfr*A36, *dfr*A38, *bla*TLA-1, *bla*VEB-10, *flo*R,	AMP (47.77%), kanamycin (98.73%), amikacin (98.09%), GEN (98.09%), streptomycin (94.91%), TET (62.42%), norfloxacin (78.34%), ciprofloxacin (68.15%), lomefloxacin (81.53%), STX (57.33%), trimethoprim (59.87%), polymyxin b (61.78%), clindamycin (82.8%)	Cephalothin (93.63%), ceftriaxone (98.73%), ceftazidime (92.99%), cefepime (95.54%), spectinomycin (95.54%), chloramphenicol (92%), FLO (98.73%), ERY (73.25%), azithromycin (86.62%), sulfafurazole (94.9%), rifampicin (75.16%)	Dong et al. (2024)

Table 8: *Continued*

Type of strains	Type of sample	Number of samples	Country	Most frequently detected resistance genes	Resistance to antibiotics	Most effective antibiotics	References
				*sul*4, *lsa*E, *lsa*C, *lnu*G, *optrA*, *cfrA*, *cfrB, poxtA, sat-4, fos*B2, *sal*A, *cat*B8			
R. anatipestifera	Brain, heart, lungs, liver, blood from ducks	*n* = 69	Vietnam	nd	Nalidixic acid (97.1%), norfloxacin (94.2%), ERY (89.9%), kanamycin (81.1%), streptomycin (78.3%), ciprofloxacin (72.5%), TET (68.1%), NEO (56.5%), STX (53.6%), PEN (50.7%), GEN (49.3%), oxacilin (49.3%), amikacin (30.4%)	AMX/clavulanic acid (100%), imipenem (100%) FLO (91.3%), cefoperazone (89.9%), piperacillin (89.9%), ceftazidime (89.9%), cefepime (87%), cephalecin (87%), doxycycline (87%), cephalothin (78.3%), ceftriaxone (72.5%), ofloxacin (72.5%)	Vo et al. (2022)
R. anatipestifera	Trachea, lungs, brain, infraorbital sinus, hock joint from turkeys, chickens, geese, and ducks	*n* = 24	Poland	nd	Amikacin (100%), streptomycin (100%), spectinomycin (62.5%), clindamycin (91.6%), ERY (95.8%), doxycycline (91.6%), ENR (100%), chloramphenicol (95.7%)	AMP (75%)[b], PEN (66%)[b], cephalexin (95.8%)[b], ceftazidime (95.8%)[b], cefuroxime (95.8%)[b], STX (83.3%)[b]	Tyc et al. (2026)

nd – not detected.

between strains, with the largest inhibition zone diameters noted for cephalexin and ceftazidime. Antibiotics with moderate inhibition zones, measuring 20 mm, included amikacin and chloramphenicol. More than 70% of strains showed no visible growth inhibition zone in response to ENR, clindamycin, ERY, or streptomycin (Tyc et al., 2026).

It can be concluded from the studies cited that *R. anatipestifera* is a significant and growing problem in the context of antimicrobial resistance. Analysis of the results clearly reveals the widespread occurrence of MDR, irrespective of geographic region, although the phenomenon is particularly well documented in Asian countries. The highest level of resistance is shown mainly against aminoglycosides, polymyxins, TETs, and fluoroquinolones. At the same time, some β-lactam antibiotics, FLO, and certain drug combinations (e.g. AMX + clavulanic acid) remain relatively effective, which may be of importance in treating infections. Genotype testing confirms wide dissemination of resistance genes, especially *tet*X, *erm*F, and *flo*R, present in most strains analysed. The high number of resistance genes and their diversity suggest strong selection pressure resulting from the use of antibiotics in poultry farming.

7. Experimental use of bacteriophages to control infections in poultry production

In poultry production, "phage cocktails" are most often used against target bacteria, mainly *Escherichia coli*, *Salmonella* spp., *Campylobacter* spp., and *Listeria* spp. The use of phage cocktails in a titre range from 10^5 to 10^{10} PFU/ml even to 10^{14} PFU/ml (Kuźmińska-Bajor et al, 2023), provides a broad spectrum of antibacterial activity while at the same time enhancing the biocidal effect, thus significantly reducing the concentration of bacteria by 0.4–5.0 $\log_{10}$ CFU/ml in faeces, meat, and the external and internal organs of animals, even up to total elimination (Melaku et al., 2025). In most previous studies, experimental phage preparations have been used in the form of cocktails with lytic titres in a range from 10^5 to 10^{11} PFU/ml (Rahman et al., 2026). Over the last 25 years, the use of phage preparations in animal production, including in poultry, has been the subject of many studies, in which they were mainly used experimentally. Apart from experimental phage therapies, commercial phage preparations are also used in some EU countries, mainly added to feed or water or applied directly to the environment (Wernicki et al., 2017; Dec et al., 2020; Alomari et al., 2021). Bacteriophages specific for *Campylobacter jejuni*, *Salmonella enterica* serovar Enteritidis (*S.* Enteritidis), *Salmonella enterica* serovar Typhimurium (*S.* Typhimurium), *E. coli*, and *Clostridium perfringens* are by far the most commonly used in experimental phage therapies (Muneeb et al., 2025; Melaku et al., 2025), because these bacteria can be transferred via poultry products.

Experimental phage preparations in poultry are usually applied in the form of phage cocktails added to feed or drinking water (Table 9). In some cases, however, preparations containing bacteriophages are administered as injections, e.g. intraperitoneal application of an experimental phage preparation with 10 APEC-specific bacteriophages in 1 day broiler chicks in Kazakhstan (Alexyuk et al., 2024). In that case, the survival rate of chicks exposed to infection was 100%. The efficacy of bacteriophage preparations used in experimental therapy is varied. The concentration of specific pathogens in the gastrointestinal tract and other internal organs usually decreases significantly, as in the case of *Salmonella*, *Campylobacter*, and *E. coli* (Table 9). In the case of *Listeria monocytogenes*, phage preparations are used mainly for control of food products, as *Listeria* spp. bacteria are intracellular pathogens, which precludes phage therapies (Kawacka et al., 2020). Previously published studies have shown a significant effect of phages on bacterial biofilm contaminating food products, including poultry products – mainly broiler chicken carcasses (Efenberger-Szmechtyk & Nowak, 2025).

Recent studies confirm that bacteriophages are beginning to play an important role in food preservation, and their use in poultry products significantly reduces the number of bacteria, leading to their total elimination (Urban-Chmiel et al., 2025). In one study, for example, treatment of poultry with an experimental phage cocktail, e.g. phages specific for strains of *Salmonella* Enteritidis, Typhimurium, Paratyphi A, San Diego, and Typhi (CAU-SEP-1, CAU-SEP-2, CAU-SEP-3, and CAU-SEP-4) at titres of 10^8 PFU/ml, significantly reduced the bacterial count to 3.12 log CFU/ml after 6 h of treatment (Kim et al., 2020). Similar results were observed following the use of experimental phage cocktails against strains of *Shigella* (Shahin & Bouzari, 2018) and *Clostridium perfringens* (Mohammadi et al., 2022). The reduction in the number of bacteria in meat and carcasses ranged from 1.2 to 2.5 log CFU/bird. In the case of pathogenic *E. coli* strains, the use of a cocktail of two phages at a titre of 10^9 PFU/ml reduced bacteria by 1.48 $\log_{10}$ CFU/ml (Berhilevych et al., 2026). For *Campylobacter* spp. strains, the application of a phage cocktail to skin and meat obtained from chicken broilers after

Table 9. Experimental phage therapies in poultry

Poultry species	Country	Type of phage	Host pathogens	Form of application	Scope of use (therapy, prophylaxis, other)	Effect on bacteria	References
Broiler chickens	Thailand	vB_SenS_KP001 vB_SenS_KP005, vB_SenS_WP110	*S.* Anatum, *S.* Kentucky	Phage cocktail, final concentration 7 log PFU/ml, 1 l of 10^{10} PFU/ml added to 1,000 l of drinking water 3 times (4, 13, 16 days of grow-out)	Prophylaxis and other, i.e. elimination of bacteria from digestive tract	From 0 to 17 days of experiment total elimination of *Salmonella* in cloacal samples (0% prevalence)	Pelyuntha et al. (2024)
Broiler chickens	China	vB_SalP_LDW16	*S.* Enteritidis, *S.* Pullorum, *S.* Typhimurium	Application of 100 µl of phage at 10^6 PFU/ml with feed	Prophylaxis and other, i.e. elimination of bacteria from digestive tract	Prevention of *Salmonella* proliferation *in vivo*; survival rate after *S.* Enteritidis challenge was 100% after 1 week; all tissues and organs in the phage treatment group and phage control group could develop normally	Cao et al. (2022)
7-days-old broiler chickens	Poland	vB_SenM-2 vB_Sen-TO17	*S.* Typhimurium	Phage cocktail for 14 days, 1 ml of phage suspension of 2 × 10^9 PFU/ml 1 × 10^9 PFU/ml of each phage *per os*	Therapy against experimental challenge with *S.* Typhimurium	Enrichment of natural intestinal microbiome in birds; early administration of phages (1 day after infection) completely eliminated bacteria, application of phages 2 days after infection only partially eliminated bacteria	Kosznik-Kwaśnicka et al. (2022)
7-dayS-old, *Salmonella*-free ROSS 308 broiler chickens	Poland	UPWr_S1, S2, S4	*S.* Enteritidis A28	Phage cocktail UPWr_S1, UPWr_S3, UPWr_S4, inoculated with a pool of 1 × 10^7 PFU/ml of each phage at 1, 4, 7, 10 and 13 days post-infection	Therapy against experimental challenge with *S.* Enteritidis	Effectively reduced the number of organs infected with *Salmonella* and the pathogen load in internal organs, e.g. spleen, liver, bursa of Fabricius, and caecal tonsils.	Kuźmińska-Bajor et al., 2023

Table 9: *Continued*

Poultry species	Country	Type of phage	Host pathogens	Form of application	Scope of use (therapy, prophylaxis, other)	Effect on bacteria	References
1-day-old female SPF White Leghorn chicks	China	*Salmonella* virulent phage PLL1; nonproductive phage F118P13	*S.* Typhimurium ST149, *S.* Enteritidis SE3377	Phage cocktail 0.5×10^8 PFU/ml applied orally at 8 h, 32 h, 54 h after challenge	Therapeutic effect against *S.* Typhimurium ST149 post-infection	100% survival of chicks after infection; significant decrease in concentration of *S.* Typhimurium strains in spleen and bursa	Hao et al. (2023)
1-day-old chickens	India	vB_EcoS_PJ16	*E. coli* APEC-P02	Application of phage orally at 2, 7, 14 or 2, 3, 4, 5 days of age 1.12×10^{10} PFU/ml	Therapeutic and prophylactic effect against experimental challenge with *E. coli* APEC P02 strain	20% reduction in mortality compared to infected untreated control group; significantly higher weight gain in birds treated with phages	Jhandai et al. (2024
)14-days-old male and female Ross 308 broiler chickens	Poland	UPWr_E1 UPWr_E2 UPWr_E3 UPWr_E4	*E. coli*	Application of 4-phage cocktail 10^8–10^9 PFU/ml to litter for 4 weeks	Preventive effect (*E. coli* elimination); improved production parameters and performance	Significant reduction in total *E. coli* by 3.2 $\log_{10}$ CFU/g in litter, liver, caecal contents, faeces	Kuźmińska-Bajor et al. (2025)
Chicken meat	Germany	vB_Eco_LmqsKl31-21, vB_Eco_LmqsKl33-12, vB_Sty-LmqsSP6	*E. coli* 3981/1/22, *E. coli* 3617/1/22, *Salmonella* LT2	Application of phage cocktail directly to raw chicken fillets	*E. coli* and *Salmonella* food contamination control	Maximum reduction of 1.56 $\log_{10}$ CFU/ml of *Salmonella* BfR 20-SA00418 and 1.48 $\log_{10}$ CFU/ml of *E. coli* 19/302/1/A after 72 h	Berhilevych et al. (2026)
1-day-old chickens (Leghorn)	Kazakhstan	10 lytic *E. coli* bacteriophages belonging to different phylogroups (B1, B2, and D)	*E. coli* APEC	Intraperitoneal injection of cocktail of 10 *E. coli* phages titre 10^8 pfu/ml	Therapeutic effect	100% survival of chickens infected with APEC strains	Alexyuk et al. (2024)
1-day-old Ross 308 broilers	Iraq		*E. coli* strains	Application of *E. coli* bacteriophage titres 3.2×10^8 PFU/g through feeding	Prophylactic effect; improved production parameters	Higher gut *Lactobacillus* and reduced coliform counts; significant ($P < 0.05$) increase in body weight, weight gain, feed consumption, and feed conversion	Aljuhaishi & Albawi (2024)

Table 9: *Continued*

Poultry species	Country	Type of phage	Host pathogens	Form of application	Scope of use (therapy, prophylaxis, other)	Effect on bacteria	References
Broiler chickens 1 week old	Australia	PH5, PH8, PH11, PH13, PH18, and PH19 (Farm B)	*C. jejuni* NCTC 12662, *C. jejuni* NC 3142, *C. coli* NC 2934	3 ml of phage cocktail, final concentration 10^7 PFU/ml by oral gavage in water	Prophylaxis and elimination of bacteria from digestive tract	Decrease in intestinal *Campylobacter* in caecum by 1–3 $\log_{10}$ CFU/g in market-ready chickens	Chinivasagam et al. (2020)
25-dayS-old Ross 308 chickens	Germany	Phage NCTC 12673 phage vB_CcM-LmqsCPL1/1	*C. jejuni* NCTC 12662, *C. coli* NCTC 12667	Phage cocktails via drinking water	Prophylaxis and elimination of bacteria from digestive tract	Significant reductions of *Campylobacter* strains up to 1.1 $\log_{10}$ CFU/ml in faecal samples 1 day after dosing	Bogun et al. (2024)
38-dayS-old broiler chickens	Italy	Phages: Φ7-izsam, Φ16-izsam	*C. jejuni* 252 gM/12 A	Application of phages via oral gavage φ16-izsam (10^7–10^8 PFU/ml)	Preventive effect on *Campylobacter*	Reduction in total bacterial contamination by up to 2 $\log_{10}$	D'Angelantonio et al. (2021)
Meat samples from broiler chickens	China	phage CP6	*C. jejuni, C. coli*	phage suspension (10^7–10^9 PFU/g) dropped onto chicken meat	Prevented *Campylobacter* contamination of chicken breast meat	Reduction in number of live *Campylobacter* bacteria by 1.02–1.23 log after 6 h; inhibition of growth of *C. coli* Cc512 at 4 °C after 24 h	Zhang et al. (2024)
Adult boiler chickens	Netherlands	Phage #7	*C. perfringens* LMG 11264	Phage #7 introduced at 10^4 PFU/mL	Preventive effect – *Clostridium* spp. control	Significant inhibition of growth of *C. perfringens* LMG 11264 *in vitro*	Wiese et al. (2025)
1-day-old Ross 308 broilers	Australia	*Clostridium* spp. phages	*C. perfringens* NE14 NE18 NE21 NE36	Orally gavaged with 1×10^6 units of cocktail of three *C. perfringens* phages	Protective effect against experimental challenge	significantly reduced lesion scores of birds challenged with NE ($P < 0.01$)	Keerqin et al. (2022)
1-day-old male broiler chicks (Ross 308)	South Korea	*C. perfringens* φCJ22 phage	*C. perfringens* wildtype strains	Application of phage titre 10^7 BP PFU/kg to feed for 5 weeks	Protective effect against experimental challenge	Reduction in number of lesions and mortality rates with no changes in performance at the end of experimental period	Bae et al. (2021)

slaughter reduced bacteria to 0.79 $\log_{10}$ CFU/ml (Zampara et al., 2017). The results of experimental phage therapies, presented in Table 9, are indicative of a significant, beneficial effect of bacteriophages in preventing contamination of poultry products.

An interesting solution is the use of bacteriophages to control microbes in the poultry housing environment. An example is our own research (Pyzik et al., 2023) assessing the efficacy of an experimental preparation containing nine phages at titres of 10^9 PFU/ml, isolated from various poultry species and from humans, to support disinfection and improve welfare conditions in poultry housing environments by eliminating pathogenic *E. coli* strains. Sprinkling with the preparation reduced the number of APEC strains in laboratory conditions. The efficacy of the preparation containing bacteriophages isolated from housing environments of broilers, ducks, and chickens was more than 83%. A similar study carried out in Poland by a research centre in Wrocław (Kuźmińska-Bajor et al., 2025), in which a cocktail of four phages specific for *E. coli* strains was applied directly to litter, caused a substantial reduction in the total number of bacteria, by 3.2 $\log_{10}$ CFU/g in both the litter and the internal organs of broiler chickens (Table 9).

Owing to the highly significant beneficial results of the use of bacteriophages to control infections in poultry production, commercial phage preparations have been developed and introduced to the market, especially for food quality control. However, a very important factor significantly hindering the possibility of introducing phages in poultry production in the EU are legislative restrictions, in which phage preparations are treated as VMP requiring a complicated and cost-intensive registration procedure.

8. Commercial phage preparations

There are currently many commercially available phage preparations used to prevent food contamination, mainly by *E. coli*, *Salmonella* spp., *Campylobacter* spp., *L. monocytogenes*, and *Clostridium perfringens* (Urban-Chmiel et al., 2025; de Melo et al., 2018). It should be stressed that many commercial phage preparations have obtained Generally Recognized as Safe (GRAS) certification and U.S. Food and Drug Administration (FDA) approval, authorizing their use in the United States, as well as Food Standards Australia New Zealand (FSANZ) certification.

Some commercial phage preparations have also been approved for use in the EU for food control and as feed additives to control infections caused by *S.* Enteritidis, *S.* Typhimurium, *E. coli*, and *L. monocytogenes*. Examples of such preparations are Listex™ P100, and ListShield™, produced by Intralytix Inc., Baltimore, MD (USA) (Wittebole et al., 2014).

Commercial phage preparations intended for live poultry are also produced in Poland, by Proteon Pharmaceuticals S.A., and are registered for use as feed additives in all species of birds, providing protection against infections caused by APEC strains (BAFACOL™) and *Salmonella* (BAFASAL + G or BAFASAL®) and also improving the microbiome, which translates to improved productivity and performance (Proteon Pharmaceuticals).

A very large number of phage preparations intended for use in live poultry are produced for markets outside of Europe, due to legal restrictions on their use in the EU (Fokas et al., 2026). The most phage preparations by far have been registered in the United States, Canada, and Australia. These preparations predominantly contain bacteriophages that are mainly lytic for *Salmonella* spp. and *E. coli* strains (Table 10). It should be noted that by far the largest group comprises preparations intended for food preservation after slaughter. For poultry, preparations containing phage cocktails are available for preventing contamination with *Salmonella* (SalmoFREE®, SalmoFresh™, SalmoPro®, Salmonelex™, BacWash™, Bafasal®, and Biotector® S), *E. coli* (Ecolicide PX™ and EcoShield™), and *Listeria monocytogenes* (ListShield™ and Listex™ P100) (Table 10). It should also be noted that commercial phage preparations targeting several pathogens at the same time are available as well, e.g. Phagex-ES, containing bacteriophages specific for *Salmonella* and *E. coli* (Vaster Life Sciences, 2025), and Phagovet, which contains phages lytic for *Salmonella*, *E. coli*, *Enterococcus* spp., *Staphylococcus* spp., *Streptococcus* spp., *Pseudomonas*, and *Proteus* (MicroMir, 2022). However, apart from Phagovet, available in Russia, which contains phages specific for *Staphylococcus* spp. strains, and despite the fact that *in vitro* studies have shown high phage specificity for *Staphylococcus* strains, some of the bacteriophages tested contained enterotoxigenic genes, which completely precludes their use in phage therapies (Marek et al., 2019).

At present, there is also no commercial phage preparation for fighting *Campylobacter* spp. infections, due to difficulty in producing safe phage cocktails, associated with optimization of phage multiplication and purification (Żbikowska et al., 2020). According to some studies (Żbikowska et al., 2020; Muneeb et al., 2025), this may be due to the fact that bacteriophages specific for *Campylobacter* have distinct biological properties associated with the occurrence of significant differences between phages, e.g. in terms of host range, lytic activity, and kinetics, as well as the higher prevalence of strains resistant to *Campylobacter* phages (1–14%). Therefore, even despite

Table 10. Examples of commercial phage preparations approved for use in live and post-slaughter poultry to prevent food contamination

Name of phage preparation	Foodborne pathogens	Target food product/poultry species	Company	Certificates/Country of approval for use	Efficacy	Producer website/ References
EcoShield PX™ Phage cocktail	*E. coli* O157:H7 STEC	Poultry and beef products, fish, cheese, vegetables	Intralytix, Inc.	FDA, FCN No. 1018 certified kosher product Generally Recognized as Safe (GRAS Notice No. 528)	Reduction in bacteria (by 3.0 log CFU/g in beef, chicken breast, boiled chicken, salmon, cheese, cantaloupe, and romaine lettuce	Vikram et al. (2022)
Secure Shield E1	Pathogenic *E. coli* strains	Beef meat, turkey products, and other foods	FINK TEC; GmbH (GER)	FDA/GRN 724, USDA, FSIS Directive 7120.1	Significant reduction in bacteria (by 3.2 log CFU/g) in beef. Total elimination of bacteria from products.	Oluwarinde et al. (2023)
FORMIDA®	Pathogenic *E. coli*	Feed additive for poultry	PhageLab Chile, Brazil, Peru, Mexico, Europe, United Kingdom, Argentina, USA	Notified Veterinary Bio-control	Significant reduction in mortality. Supports prevention of colibacillosis. Improves weight gain and rearing performance.	Fokas et al. (2026)
BAFACOL™	APEC	Feed additive for all poultry species, including chickens, turkeys, ducks, and pigeons.	Proteon Pharmaceuticals SA, Poland	EFSA acceptance, registered in Brazil and Poland	Reduces morbidity. Supports prevention of colibacillosis. Significant reduction in mortality. Improves weight gain and rearing performance. Natural alternative to antibiotics without disturbing the microbiome.	Proteonpharma website
BacWash™	*Salmonella* spp.	Applied in the form of washing liquid, mist, or spray directly onto animals before slaughter.	OmniLytics Inc., USA		Effective antimicrobial for surface disinfection and reducing pathogens in animal production – in living animals and post-mortem. Reduces the risk of *Salmonella* in poultry.	Żbikowska et al. (2020); OmniLytics website
Salmonelex™	*Salmonella* spp.	Application to food and water as antimicrobial agent to fight *Salmonella* in doses up to 10^8	Micreos Food Safety BV (the Netherlands)	FDA-approved, GRAS status	Improves growth rates. Reduces *Salmonella* up to total elimination.	Micreos Food Safety BV website; Żbikowska et al. (2020)

Table 10: *Continued*

Name of phage preparation	Foodborne pathogens	Target food product/poultry species	Company	Certificates/Country of approval for use	Efficacy	Producer website/ References
		PFU/g of food Can also be sprayed onto the environment				
PHAGEX-ES	*Salmonella* and *E. coli*	Oral application in water and feed, therapeutic and prophylactic agent against indigenous *Salmonella* and *E. coli*	Vaster Life Sciences, India	India	Effective control of antimicrobial-resistant bacteria strains. Help to control transmission of *Salmonella* and *E. coli* on farm/in hatchery/ indoor spaces. Reduces contamination in hatching rooms and other indoor spaces. Improves feeding efficiency and liver weight, reduces pathogens in broilers. Improves egg production and egg quality in layer hens. Natural, nontoxic, feasible, and inexpensive alternative to antibiotics. Use of bacteriophages as alternative to antibiotics and disinfectants.	Vaster Life Sciences website
BAFASAL + G	*Salmonella* Enteritidis, *Salmonella* Typhimurium and *Salmonella* Gallinarum	All poultry species, including chickens, turkeys, ducks, and pigeons Feed additive to treat the digestive tract of poultry	Proteon Pharmaceuticals SA, Poland	EFSA acceptance, registered in Brazil, Ukraine	Effectively prevents *Salmonella* infections while preserving the natural gut microbiota of birds. Regular use improves production parameters and increases rearing performance	Proteonpharma website
BAFASAL®	*Salmonella* Enteritidis and *Salmonella* Typhimurium		Proteon Pharmaceuticals SA, Poland	EFSA acceptance, Registered in Brazil, Ukraine	Supports prevention of *Salmonella* and loss of	Proteonpharma website

Table 10: *Continued*

Name of phage preparation	Foodborne pathogens	Target food product/poultry species	Company	Certificates/Country of approval for use	Efficacy	Producer website/ References
		All poultry species, including chickens, turkeys, ducks, and pigeons			productivity with no negative effect on the microbiome, thus improving growth, productivity, and performance.	
PhageGuard S™ (previously Salmonelex™)	*Salmonella* sp.	Eggs, chicken, and turkey meat surface of poultry meat products	Phageguard Micreos Food Safety (Wageningen, Netherlands)	Australia/New Zealand. FSANZ processing aid – 2012 USA, FDA GRAS (GRN 468) – 2013 USA, USDA approved processing aid (Directive 7120.1) – 2016 Canada, Health Canada: Processing aid – 2016 India, FSSI: food contact surfaces and processing aid – 2021 Chile, Undersecretary of Public Health (MINSAL) (ORD. B34/ N794) – 2022 Egypt, National Authority of Food Safety Egypt: Approved use in poultry production – 2023 Notified Processing Aid Vietnam, HCMC Food Safety Department – 2025 Dubai, DM Food Safety Department – 2025 Costa Rica, Ministry of Health of the Government of Costa Rica – 2026	Protects against product contamination Reduces or eliminates risk of foodborne salmonellosis. Direct application to poultry	Phageguard website; Vikram et al. (2022); Fokas et al. (2026)
SalmoGuard	*Salmonella* spp. including *S.* Enteritidis, *S.* Typhimurium, *S.*	Poultry feed additives – oral administration	UniFAHS	FDA, Southeast Asian countries		Huang et al. (2022)

Table 10: *Continued*

Name of phage preparation	Foodborne pathogens	Target food product/poultry species	Company	Certificates/Country of approval for use	Efficacy	Producer website/ References
	Gallinarum, *S.* Pullorum, *S.* Hadar, *S.* Infantis *S.* Virchow				Reduces *Salmonella* spp. colonization in broilers and their environment.	
SalmoFREE®	*Salmonella* Enteritidis, *S.* Typhimurium, *S.* Paratyphi B, *S.* Gallinarum	Via drinking water for broilers and laying hens		Latin America	Prevents avian salmonellosis in laying hens wide spectrum of activity against *S.* Gallinarum, S. Pullorum, *S.* Enteritidis, *S.* Typhimurium, *S.* Infantis, and other *Salmonella enterica* serotypes.	Hernández-Villamizar et al. (2025)
SalmoFresh™	*Salmonella enterica* (serotypes Typhimurium, Enteritidis, Heidelberg, Newport, Hadar, Kentucky, Thompson, Georgia, Agona, Grampian, Senftenberg, Alachua, Infantis, Reading, Schwarzengrund)	Poultry, red meat, fish, and shellfish, fresh and processed fruits and vegetables	Intralytix (Columbia, MD, USA)	OMRI GRAS, FDA recognition in 2013 (GRAS Notice No. GRN 000435), Islamic Food and Nutrition Council of America: Halal Certified; Star-K Kosher Certification: Kosher Certified; Health Canada: iLONO; FSIS: Directive 7120.1- USA	Protection against product contamination, Reduces or eliminates risk of foodborne salmonellosis, direct application to poultry	Efenberger-Szmechtyk & Nowak (2025)
Phagelab (CHI)	*Salmonella* spp.	Liquid feed additive	Chile	No available data	Total elimination of *Salmonella* strains from digestive tract of broiler chickens.	Huang et al. (2022)
PhageGuard Listex™ (P100)	*L. monocytogenes L. innocua*	Meat products, including poultry	Micreos Food Safety, Wageningen, Netherlands	GRAS; FDA USA Canada and Switzerland	Degrades bacterial biofilm, eliminates *Listeria* without compromising food quality	Zawiasa et al. (2025)
PhageGuard L.	*L. monocytogenes*	Eggs, chicken, and turkey meat products		OMR from 25.01.2018 USA, FDA GRAS (GRN 218) – 2006 USA, USDA approved processing aid (Directive 7120.1) – 2007	Total elimination of bacterial biofilm from surface of eggs and poultry carcasses.	Phageguard website

Table 10: *Continued*

Name of phage preparation	Foodborne pathogens	Target food product/poultry species	Company	Certificates/Country of approval for use	Efficacy	Producer website/ References
				Canada, Health Canada: Processing aid – 2011 Australia/New Zealand. FSANZ processing aid – 2012 Israel, Food Control Services Ministry of Health: approved processing aid – 2014 Switzerland, Ordinance of the FDHA (SR817.022.42): Approved processing aid for cheese production – 2016 EU, Phageguard L (Listex™) is safe for use (EFSA opinion) – 2016 Chile, Undersecretary of Public Health (MINSAL) (ORD. B34/N794) – 2022 Dubai, DM Food Safety Department – 2025 Costa Rica, Ministry of Health of the Government of Costa Rica – 2026		
istex™	*Listeria monocytogenes*	Meat products		GRAS (GRN No. 198 & No. 218), FDA – USA, Canada, OMRI Listed, FSANZ: Approved as a processing aid by Food Standards Australia New Zealand. Informal clearance in the EU – EFSA evaluation; due to processing-aid interpretation. Kosher & Halal	Significant protection against contamination of meat products obtained from livestock species	Phageguard website; Fokas et al. (2026)

Table 10: *Continued*

Name of phage preparation	Foodborne pathogens	Target food product/poultry species	Company	Certificates/Country of approval for use	Efficacy	Producer website/ References
ListShield™	*L. monocytogenes*	Ready-to-eat meat and poultry, products, smoked salmon, fresh and processed fruits and vegetables, dairy products (including cheese)	Intralytix (Columbia, MD, USA)	Halal; OMRI FDA-cleared phage preparation for food safety Generally Recognized as Safe (GRAS Notice No. 528) USA (FDA 21 CFR § 172.785, FSIS Directive 7120.1, GRAS GRN No. 528), Health Canada (iLONO), National Food Service of Israel (Ref: 70275202)	Eliminates *Listeria monocytogenes* from surfaces of food of animal and plant origin; prevents contamination of equipment that does not have contact with food in processing plants and other food plants.	Vikram et al. (2021); Intralytic website
ShigaShield™	*S. flexneri, S. sonnei, S. dysenteriae*	contamination in foods and food processing facilities; specifically designed for treating ready-to-eat (RTE) meat and poultry, fish (including smoked fish), shellfish, fresh and processed fruits and vegetables, and dairy products, including cheese	Intralytix Inc., USA	GRAS GRN No. 000672, USA Kosher, Halal, and Organic	Reduction and total elimination of contamination in foods and food processing facilities	Połaska & Sokołowska (2019); Fokas et al. (2026)
sPHAGOVET	*E. coli, Salmonella enterica, P. aeruginosa, S. aureus S. epidermidis, S. haemolyticus, Streptococcus pyogenes Enterococcus faecalis, E. faecium, E. hirae, E. durans, Proteus vulgaris*	Application to water for drinking	Microminr Company	GMP certification in 2025, Russian Federation	Prevention and treatment of bacterial infections in poultry, i.e. salmonellosis, colibacillosis, streptococcosis, staphylococcosis, enterococcosis, pseudomonosis, proteus and mixed bacterial infections. Application during viral infections in poultry to prevent secondary bacterial infections	MicroMir company website

significant genetic relatedness, there are many factors making them more difficult to use than other lytic phages, and the process of acquiring them for commercial preparations is more time-consuming and costly (Muneeb et al., 2025). Regarding commercial phage preparations for controlling *Clostridium perfringens* in poultry production, there are virtually no available data confirming their efficacy in commercial conditions, either for prevention or treatment of infections in poultry (Żbikowska et al., 2020).

The growth potential of the commercial phage preparation market in animal production is limited by legislation, in which bacteriophages have been classified as medicinal products in both the United States and the EU since 2011 (Jordá et al., 2023). The bodies responsible for the release of phage preparations for free circulation are the FDA in the American market and the European Medicines Agency (EMA) and the EFSA in the EU. The lack of an established uniform road map for legal regulations guaranteeing the registration of phage products for animals significantly limits the development of commercial bacteriophage products in the European market. Therefore, in some EU countries, including Poland, phage therapies are classified as "experimental," according to the Polish Journal of Laws of 2011, item 1,634, and Article 37 of the Declaration of Helsinki (Naureen et al., 2020). The starting point for initiating a potential solution opening the way to at least temporary acceptance of commercial phage preparations in the EU was Regulation (EU) 2019/6 of the European Parliament and of the Council of 11 December 2018 on VMP, implemented on 28 January 2022. This regulation laid out the criteria that phage preparations must meet to obtain potential acceptance for use. The concept paper (EMA/CVMP/NTWP/32862/2022) published by the EMA in 2023 on the quality, safety, and efficacy of bacteriophages as veterinary medicines was crucial for guidelines regarding the approval of bacteriophage preparations (Jordá et al., 2023). This opened a path for the European Food Safety Authority to recognize the use of phages for combating *Listeria* spp. contamination in food products as safe in the EU (European Food Safety Authority 2016). One example is the positive opinion on the safety and efficacy of the commercial preparation Listex™ P100.

9. Conclusion

To sum up, the problem of drug resistance among bacteria isolated from poultry remains an important factor limiting the possibilities for fighting infections caused by the pathogens most commonly occurring in poultry production, including *Campylobacter* spp., *Salmonella* spp., *E. coli*, *Listeria*, and also ESKAPE pathogens – *Enterococcus* spp. and *Staphylococcus* spp. It is concerning that over the last 5 years, there has been a significant increase in bacterial resistance to the antibiotics most commonly used in poultry production, mainly TETs, fluoroquinolones, beta-lactams, and macrolides, which is indicative of continuing acquisition of resistance by pathogens. Measures undertaken to improve control of infections using bacteriophages as alternatives to antibiotics reveals that the solutions proposed are met with considerable interest. A measurable result is the increase in research in animal production using experimental phage preparations and the development of production of commercial phage preparations. This is particularly important because current trends in European legislation, including the European Commission regulations and guidelines presented in the introduction to this manuscript, continue to classify bacteriophage preparations as VMP. This poses a significant obstacle and, for most preparations, eliminates their use in animal production, including poultry production, on the European countries. However, despite legal restrictions on the use of phages in animal production, research is still underway to develop new commercial phage preparations. The continued growth of public awareness and knowledge about the potential benefits and risks of bacteriophage use will play a significant role in expanding the potential use of bacteriophages in animal production. This may translate into specific legislative actions that will facilitate the registration of commercial phage preparations in the near future, especially on the European market.

Nevertheless, to increase the availability of preparations with bacteriophages, there is a need for further research characterizing bacteriophages and assessing their biosafety and kinetics.

Acknowledgements

The authors would like to express their sincere thanks for the invitation to prepare this manuscript.

Funding information

Authors state no funding involved.

Author contributions

Conceptualization, data curation, formal analysis, R.U.-C.; Investigation, project administration, supervision, writing

(draft/review), M.D.; Data curation, formal analysis, investigation, writing (draft/review), A.M., D.S.-P., A.N., K.H.-O., and M.Z.; Data curation, formal analysis, writing – review & editing, investigation, E.P.

Conflict of interest statement

The authors declare no conflict of interest.

References

Aarestrup, F. M., Seyfarth, A. M., Emborg, H. D., Pedersen, K., Hendriksen, R. S., & Bager, F. (2001). Effect of abolishment of the use of antimicrobial agents for growth promotion on occurrence of antimicrobial resistance in fecal enterococci from food animals in Denmark. *Antimicrobial Agents and Chemotherapy*, *45*(7), 2054–2059. https://doi.org/10.1128/AAC.45.7.2054-2059.2001

Abdalrahman, L. S., Stanley, A., Wells, H., & Fakhr, M. K. (2015). Isolation, virulence, and antimicrobial resistance of methicillin-resistant *Staphylococcus aureus* (MRSA) and methicillin-sensitive *Staphylococcus aureus* (MSSA) strains from Oklahoma retail poultry meats. *International Journal of Environmental Research and Public Health*, *12*, 6148–6161. https://doi.org/10.3390/ijerph120606148

Abdel-Rahman, M. A. A., Hamed, E. A., Abdelaty, M. F., Sorour, H. K., Badr, H., Hassan, W. M., Shalaby, A. G., Mohamed, A. A., Soliman, M. A., & Roshdy, H. (2023). Distribution pattern of antibiotic resistance genes in *Escherichia coli* isolated from colibacillosis cases in broiler farms of Egypt. *Veterinary World*, *16*(1), 1–11. https://doi.org/10.14202/vetworld.2023.1-11

Abou-Jaoudeh, C., Andary, J., & Abou-Khalil, R. (2024). Antibiotic residues in poultry products and bacterial resistance: A review in developing countries. *Journal of Infection and Public Health*, *17*(12), 102592. https://doi.org/10.1016/j.jiph.2024.102592

Abraham, S., Sahibzada, S., Hewson, K., Laird, T., Abraham, R., Pavic, A., Truswell, A., Lee, T., O'Dea, M., & Jordan, D. (2020). Emergence of fluoroquinolone-resistant *Campylobacter jejuni* and *Campylobacter coli* among Australian chickens in the absence of fluoroquinolone use. *Applied and Environmental Microbiology*, *86*, e02765-19. https://doi.org/10.1128/AEM.02765-19

Abunna, F., Adugna, B., Tufa, T., Ayana, D., Gutema, F., Waktole, H., Regassa, F., & Abdi, R. (2022). Detection and antimicrobial resistance of *Staphylococcus* species from chicken, chicken litter, and humans in Addis Ababa, Ethiopia. *Veterinary Medicine International*, *25*, 9084334. https://doi.org/10.1155/2022/9084334

Ahmed, R., Fathy, M., Al-Azeem, M., Elghoneimy, A., & Mohamed, I. (2021). *Staphylococcus aureus* in poultry: Prevalence and antibiogram of methicillin-resistant *Staphylococcus aureus* in avian species in the Southern Provinces of Egypt. *Egyptian Journal of Microbiology*, *56*, 89–98. https://doi.org/10.21608/ejm.2021.65178.1191

Ahmed, W. A., Hotzel, H., Neubauer, H., El-Tawab, A. A. A., Tomaso, H., Sobhy, M. M., & El Hofy, F. I. (2020). Antimicrobial resistance genes associated with enterococci from poultry in Egypt: First reporting of mecA in *Enterococcus* from poultry source. *Advances in Animal and Veterinary Sciences*, *8*(6), 570–581. https://doi.org/10.17582/journal.aavs/2020/8.6.570.581

Aksono, E. B., Riwu, K. H. P., Estoepangestie, A. T. S., & Pertiwi, H. (2020). Phylogenetic analysis and antibiotics resistance of *Listeria monocytogenes* contaminating chicken meat in Surabaya, Indonesia. *Veterinary Medicine International*, *1*, 9761812. https://doi.org/10.1155/2020/9761812

Al Hakeem, W. G., Fathima, S., Shanmugasundaram, R., & Selvaraj, R. K. (2022). *Campylobacter jejuni* in poultry: Pathogenesis and control strategies. *Microorganisms*, *10*, 2134. https://doi.org/10.3390/microorganisms10112134

Alexyuk, M., Alexyuk, P., Moldakhanov, Y., Akanova, K., & Bogoyavlenskiy, A. (2024). Evaluation of phage cocktail efficacy for controlling infections caused by pathogenic *Escherichia coli* in *in vivo* experiments. *BIO Web of Conferences*, *100*, 02004. https://doi.org/10.1051/bioconf/202410002004

Aljuhaishi, D. A., & Albawi, F. H. K. (2024). Using bacteriophage in poultry diet as therapeutics against *Escherichia coli* in broiler chickens. *Journal of Animal Health and Production*, *12*(S1), 23–31. https://doi.org/10.17582/journal.jahp/2024/12.s1.23.31

Alomari, M. M. M., Dec, M., & Urban-Chmiel, R. (2021). Bacteriophages as an alternative method for control of zoonotic and foodborne pathogens. *Viruses*, *13*(12), 2348. https://doi.org/10.3390/v13122348

Amoako, D. G., Somboro, A. M., Abia, A. L. K., Molechan, C., Perrett, K., Bester, L. A., & Essack, S. Y. (2020). Antibiotic resistance in *Staphylococcus aureus* from poultry and poultry products in uMgungundlovu District, South Africa, using the "farm to fork" approach. *Microbial Drug Resistance*, *26*(4), 402–411. https://doi.org/10.1089/mdr.2019.0201

Annex E – EUSR on AMR in zoonotic and indicator bacteria from humans, animals and food 2022/2023. (2025). Annex E – Data reported on MRSA from food-producing animals and derived meat. Zenodo. https://zenodo.org/records/14645440/files/Annex%20E%20MRSA_food_animals_EFSA-ECDC_EUSR_AMR_2022-2023.pdf?download = 1

Antonelli, A., D'Andrea, M. M., Brenciani, A., Galeotti, C. L., Morroni, G., Pollini, S., Varaldo, P. E., & Rossolini, G. M. (2018). Characterization of poxtA, a novel phenicol-oxazolidinone-tetracycline resistance gene from an MRSA of clinical origin. *Journal of Antimicrobial Chemotherapy*, *73*(7), 1763–1769. https://doi.org/10.1093/jac/dky088

Ao, T. T., Feasey, N. A., Gordon, M. A., Keddy, K. H., Angulo, F. J., & Crump, J. A. (2015). Global burden of invasive nontyphoidal *Salmonella* disease, 2010. *Emerging Infectious Diseases*, *21*(6), 941–949. https://doi.org/10.3201/eid2106.140999

Aras, Z., & Ardıç, M. (2015). Occurrence and antibiotic susceptibility of *Listeria* species in Turkey meats. *Korean Journal for Food Science of Animal Resources*, *35*(5), 669–673. https://doi.org/10.5851/kosfa.2015.35.5.669

Arias, C. A., & Murray, B. E. (2012). The rise of the *Enterococcus*: Beyond vancomycin resistance. *Nature Reviews Microbiology*, *10*(4), 266–278. https://doi.org/10.1038/nrmicro2761

Aslantaş, Ö. (2019). Molecular and phenotypic characterization of enterococci isolated from broiler flocks in Turkey. *Tropical Animal Health and Production*, *51*(5), 1073–1082. https://doi.org/://doi.org/10.1007/s11250-018-01784-z

Aziz, S. A. A. A., & Mohamed, M. B. E. D. (2020). Prevalence, virulence genes, and antimicrobial resistance profile of *Listeria monocytogenes* isolated from retail poultry shops in Beni-Suef city, Egypt. *Journal of Advanced Veterinary and Animal Research*, *7*(4), 710–717. https://doi.org/10.5455/javar.2020.g472

Bae, D., Lee, J.-W., Chae, J.-P., Kim, J.-W., Eun, J.-S., Lee, K.-W., & Seo, K.-H. (2021). Characterization of a novel bacteriophage φCJ22 and its prophylactic and inhibitory effects on necrotic enteritis and *Clostridium perfringens* in broilers. *Poultry Science*, *100*, 302–313. https://doi.org/10.1016/j.psj.2020.10.019

Bager, F., Madsen, M., Christensen, J., & Aarestrup, F. M. (1997). Avoparcin used as a growth promoter is associated with the occurrence of vancomycin-resistant *Enterococcus faecium* on Danish poultry and pig farms. *Preventive Veterinary Medicine*, *31*(1–2), 95–112. https://doi.org/10.1016/S0167-5877(96)01119-1

Becker, K., van Alen, S., Idelevich, E. A., Schleimer, N., Seggewiß, J., Mellmann, A., Kaspar, U., & Peters, G. (2018). Plasmid-encoded transferable mecB-mediated methicillin resistance in *Staphylococcus aureus*. *Emerging Infectious Diseases*, *24*(2), 242–248. https://doi.org/10.3201/eid2402.171074

Becker, K., Both, A., Weißelberg, S., Heilmann, C., & Rohde, H. (2020). Emergence of coagulase-negative staphylococci. *Expert Review of Anti-infective Therapy*, *18*(4), 349–366. https://doi.org/10.1080/14787210.2020.1730813

Ben Yahia, H., Trabelsi, I., Arous, F., García-Vela, S., Torres, C., & Ben Slama, K. (2024). Detection of linezolid and vancomycin resistant *Enterococcus* isolates collected from healthy chicken caecum. Journal of Applied Microbiology, 135*(2), lxae027*. https://doi.org/10.1093/jambio/lxae027

Benrabia, I., Hamdi, T., Shehata, A., Neubauer, H., & Wareth, G. (2020). Methicillin-resistant *Staphylococcus aureus* (MRSA) in poultry species in Algeria: Long-term study on prevalence and antimicrobial resistance. *Veterinary Sciences*, *7*(2), 54. https://doi.org/10.3390/vetsci7020054

Berhilevych, O., Peh, E., Vahle, J. C., Plötz, M., & Kittler, S. (2026). Phage-based biocontrol of *Salmonella* and *E. coli* in raw chicken filets: Optimizing phage-based solutions to enhance food safety under cooled storing conditions. *Frontiers in Microbiology*, *16*, 1696826. https://doi.org/10.3389/fmicb.2025.1696826

Bobrek, K., & Gaweł, A. (2023). Antimicrobial resistance of *Erysipelothrix rhusiopathiae* strains isolated from geese to antimicrobials widely used in veterinary medicine. *Antibiotics*, *12*(8), 1339. https://doi.org/10.3390/antibiotics12081339

Bobrek, K., Nowak, M., Borkowska, J., Bobusia, K., & Gaweł, A. (2016). An outbreak of erysipelas in commercial geese. *Pakistan Veterinary Journal*, *36*(3), 372–374.

Bogun, K., Peh, E., Meyer-Kühling, B., Hartmann, J., Hirnet, J., Plötz, M., & Kittler, S. (2024). Investigating bacteriophages as a novel multiple-hurdle measure against *Campylobacter*: Field trials in commercial broiler plants. *Scientific Reports*, *14*(1), 3182. https://doi.org/10.1038/s41598-024-53365-w

Borges, K. A., Furian, T. Q., Souza, S. N., Salle, C. T. P., Moraes, H. L. S., & Nascimento, V. P. (2019). Antimicrobial resistance and molecular characterization of *Salmonella enterica* serotypes isolated from poultry sources in Brazil. *Brazilian Journal of Poultry Science*, *21*(1), 1–8. https://doi.org/10.1590/1806-9061-2018-0827

Bortolaia, V., Mander, M., Jensen, L. B., Olsen, J. E., & Guardabassi, L. (2015). Persistence of vancomycin resistance in multiple clones of *Enterococcus faecium* isolated from Danish broilers 15 years after the ban of avoparcin. *Antimicrobial Agents and Chemotherapy*, *59*(5), 2926–2929. https://doi.org/10.1128/AAC.05072-14

Boulbair, I., Hu, J., Hammoudi, A., Zhang, B., Aissat, S., Wang, X., Foudil, M., & Wang, S. (2025). Molecular characterization and antibiotic resistance of avian pathogenic *Escherichia coli* (APEC) isolates from broiler chickens in Algeria. *Animals*, *15*, 3324. https://doi.org/10.3390/ani15223324

Bzdil, J., Sladecek, V., Senk, D., Stolar, P., Waicova, Z., Kollertova, N., Zouharova, M., Matiaskova, K., Linhart, P., & Nedbalcova, K. (2023). Enterococci isolated from one-day-old chickens and their phenotypic susceptibility to antimicrobials in the Czech Republic. *Antibiotics*, *12*(10), 1487. https://doi.org/10.3390/antibiotics12101487

Cao, S., Yang, W., Zhu, X., Liu, C., Lu, J., Si, Z., Pei, L., Zhang, L., Hu, W., Li, Y., Wang, Z., Pang, Z., Xue, X., & Li, Y. (2022). Isolation and identification of the broad-spectrum high-efficiency phage vB_SalP_LDW16 and its therapeutic application in chickens. *BMC Veterinary Research*, *18*(1), 386. https://doi.org/10.1186/s12917-022-03490-3

Casalino, G., Bozzo, G., Dinardo, F. R., D'Amico, F., Dimuccio, M. M., Camarda, A., Ceci, E., Romito, D., & Circella, E. (2022). Prevalence and antimicrobial resistance *of Campylobacter jejuni* and *Campylobacter coli* from laying hens housed in different rearing systems. *Animals*, *12*, 2978. https://doi.org/10.3390/ani12212978

Cason, E. E., Carlson, A. V., Siemens, A. L., & Shariat, N. W. (2024). High-resolution serotyping reveals *Salmonella* surveillance challenges in the turkey industry. *Journal of Food Protection*, *87*(10), 100319. https://doi.org/10.1016/j.jfp.2024.100319

Charpentier, E., & Courvalin, P. (1999). Antibiotic resistance in *Listeria* spp. *Antimicrobial Agents and Chemotherapy*, *43*(9), 2103–2108. https://doi.org/10.1128/AAC.43.9.2103

Chen, C., & Wu, F. (2021). Livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) colonisation and infection among livestock workers and veterinarians: A systematic review and meta-analysis. *Occupational and Environmental Medicine*, *78*(1), 530–540. https://doi.org/10.1136/oemed-2020-106418

Chen, P., Cheng, F., Huang, Q., Dong, Y., Sun, P., & Peng, Q. (2024). Distribution and antimicrobial resistance characterization of *Listeria monocytogenes* in poultry meat in Jiading District, Shanghai. *Journal of Food Protection*, *87*(3), 100234. https://doi.org/10.1016/j.jfp.2024.100234

Chinivasagam, H. N., Estella, W., Maddock, L., Mayer, D. G., Weyand, C., Connerton, P. L., & Connerton, I. F. (2020). Bacteriophages to control *Campylobacter* in commercially farmed broiler chickens, in Australia. *Frontiers in Microbiology*, *11*, 632. https://doi.org/10.3389/fmicb.2020.00632

Chu, Y., Wang, D., Hao, W., Sun, R., Sun, J., Liu, Y., & Liao, X. (2024). Prevalence, antibiotic resistance, virulence genes and molecular characteristics of *Salmonella* isolated from ducks and wild geese in China. *Food Microbiology*, *118*, 104423. https://doi.org/10.1016/j.fm.2023.104423

Clewell, D. B., Weaver, K. E., Dunny, G. M., Coque, T. M., Francia, M. V., & Hayes, F. (2014). Extrachromosomal and mobile elements in enterococci: Transmission, maintenance, and epidemiology. In M. S. Gilmore et al. (Eds.) *Enterococci: From Commensals to Leading Causes of Drug Resistant Infection*. Massachusetts Eye and Ear Infirmary.

Concha-Toloza, M., Lopez-Cantillo, M., Molina-Mora, J. A., & Collado, L. (2023). Genomic characterization of antibiotic-resistant *Campylobacterales* isolated from Chilean poultry meat. *Antibiotics*, *12*, 917. https://doi.org/10.3390/antibiotics12050917

Council of the European Union (2023). Council Recommendation of 13 June 2023 on stepping up EU actions to combat antimicrobial resistance in a One Health approach. *Official Journal of the European Union*, *C 220*, 1–20.

D'Angelantonio, D., Scattolini, S., Boni, A., Neri, D., Di Serafino, G., Connerton, P., Connerton, I., Pomilio, F., Di Giannatale, E., Migliorati, G., & Aprea, G. (2021). Bacteriophage therapy to reduce colonization of *Campylobacter jejuni* in broiler chickens before slaughter. *Viruses*, *13*(8), 1428. https://doi.org/10.3390/v13081428

da Silva, A. C., Rodrigues, M. X., & Silva, N. C. C. (2020). Methicillin-resistant *Staphylococcus aureus* in food and the prevalence in Brazil: A review. *Brazilian Journal of Microbiology*, *51*(1), 347–356. https://doi.org/10.1007/s42770-019-00168-1

da Silva, Ó., De Sá Barreto Maia Leite, D., Barbosa, I., Silva, V., De Oliveira Silva, M., Da Silva, A., Moreira, M., De Moura, A., Barros, M., & Mota, R. (2025). Phenotypic and genotypic resistance of *Staphylococcus aureus* in fresh meats marketed in

Pernambuco, Brazil. *Food Science and Technology*, *45*, e00462. https://doi.org/10.5327/fst.00462

Davam, H., Jansson, D. S., Nord, E., Rydén, J., & Hansson, I. (2026). Antibiotic susceptibility and resistance genes in *Escherichia coli* from broilers reared in a low-antibiotic-use production system. *Poultry Science*, *105*, 106764. https://doi.org/10.1016/j.psj.2026.106764

de Melo, A. G., Levesque, S., & Moineau, S. (2018). Phages as friends and enemies in food processing. *Current Opinion in Biotechnology*, *49*, 185–190. https://doi.org/10.1016/j.copbio.2017.09.004

Dec, M., Wernicki, A., & Urban-Chmiel, R. (2020). Efficacy of experimental phage therapies in livestock. *Animal Health Research Reviews*, *21*, 69–83. https://doi.org/10.1017/S1466252319000161

Dec, M., Nowak, T., Webster, J., & Wódz, K. (2024a). Serotypes, antimicrobial susceptibility, and potential mechanisms of resistance gene transfer in *Erysipelothrix rhusiopathiae* strains from waterfowl in Poland. *International Journal of Molecular Sciences*, *25*, 12192. https://doi.org/10.3390/ijms252212192

Dec, M., Zomer, A., Webster, J., Nowak, T., Stępień-Pyśniak, D., & Urban-Chmiel, R. (2024b). Integrative and conjugative elements and prophage DNA as carriers of resistance genes in *Erysipelothrix rhusiopathiae* strains from domestic geese in Poland. *International Journal of Molecular Sciences*, *25*(9), 4638. https://doi.org/10.3390/ijms25094638

Dec, M., Zomer, A. L., Broekhuizen-Stins, M. J., & Urban-Chmiel, R. (2026). Prophage φEr670 and genomic island GI_Er147 as carriers of resistance genes in *Erysipelothrix rhusiopathiae* strains. *International Journal of Molecular Sciences*, *27*(1), 250. https://doi.org/10.3390/ijms27010250

Delahoy, M. J., Shah, H. J., Weller, D. L., Ray, L. C., Smith, K., McGuire, S., Trevejo, R. T., Scallan Walter, E., Wymore, K., Rissman, T., McMillian, M., Lathrop, S., LaClair, B., Boyle, M. M., Harris, S., Zablotsky-Kufel, J., Houck, K., Devine, C. J., Lau, C. E., Tauxe, R. V., Bruce, B. B., Griffin, P. M., & Payne, D. C. (2023). Preliminary incidence and trends of infections caused by pathogens transmitted commonly through food – Foodborne Diseases Active Surveillance Network, 10 U.S. sites, 2022. *MMWR Morbidity and Mortality Weekly Report*, *72*, 701–706. https://doi.org/10.15585/mmwr.mm7226a1

Di Taranto, P., Petruzzi, F., Normanno, G., Pedarra, C., Occhiochiuso, G., Faleo, S., Didonna, A., Galante, D., Pace, L., Rondinone, V., Trisolini, C., Del Sambro, L., Beverelli, M., Catanzariti, R., Caruso, M., Palazzo, L., Di Castri, A., & Parisi, A. (2025). Prevalence and antimicrobial resistance of *Salmonella* strains isolated from chicken samples in Southern Italy. *Microorganisms*, *13*(2), 270. https://doi.org/10.3390/microorganisms13020270

Dlamini, S. B., Mlambo, V., Mnisi, C. M., & Ateba, C. N. (2024). Virulence, multiple drug resistance, and biofilm-formation in *Salmonella* species isolated from layer, broiler, and dual-purpose indigenous chickens. *PLoS One*, *19*(10), e0310010. https://doi.org/10.1371/journal.pone.0310010

Dong, H., Zhu, S., Sun, F., Feng, Q., Guo, C., Wu, Z., Wu, S., Wang, A., & Yu, S. (2024). Comparative analysis of antimicrobial resistance phenotype and genotype of *Riemerella anatipestifer*. *Veterinary Microbiology*, *292*, 110047. https://doi.org/10.1016/j.vetmic.2024.110047

Efenberger-Szmechtyk, M., & Nowak, A. (2025). Bacteriophage power: Next-gen biocontrol strategies for safer meat. *Molecules*, *30*, 3641. https://doi.org/10.3390/molecules30173641

EFSA Panel on Biological Hazards (BIOHAZ), Koutsoumanis, K., Allende, A., Álvarez-Ordóñez, A., Bolton, D., Bover-Cid, S., Chemaly, M., Davies, R., De Cesare, A., Herman, L., Hilbert, F., Lindqvist, R., Nauta, M., Ru, G., Simmons, M., Skandamis, P., Suffredini, E., Argüello, H., Berendonk, T., Cavaco, L. M., Gaze, W., Schmitt, H., Topp, E., Guerra, B., Liébana, E., Stella, P., & Peixe, L. (2021). Role played by the environment in the emergence and spread of antimicrobial resistance (AMR) through the food chain. *EFSA Journal*, *19*(6), e06651. https://doi.org/10.2903/j.efsa.2021.6651

Elghaieb, H., Freitas, A. R., Abbassi, M. S., Novais, C., Zouari, M., Hassen, A., & Peixe, L. (2019). Dispersal of linezolid-resistant enterococci carrying poxtA or optrA in retail meat and food-producing animals from Tunisia. *Journal of Antimicrobial Chemotherapy*, *74*(10), 2865–2869. https://doi.org/10.1093/jac/dkz263

Elsayed, M. M., El-Basrey, Y. F. H., El-Baz, A. H., Dowidar, H. A., Shami, A., Al-Saeed, F. A., Alsamghan, A., Salem, H. M., Alhazmi, W. A., El-Tarabily, K. A., & Khedr, M. H. E. (2024). Ecological prevalence, genetic diversity, and multidrug resistance of *Salmonella enteritidis* recovered from broiler and layer chicken farms. *Poultry Science*, *103*(2), 103320. https://doi.org/10.1016/j.psj.2023.103320

Endersen, L., & Coffey, A. (2020). The use of bacteriophages for food safety. *Current Opinion in Food Science*, *36*, 1–8. https://doi.org/10.1016/j.cofs.2020.10.006

Eriksson, H., Wattrang, E., Söderlund, R., & Jansson, D. S. (2025). Erysipelas – A review of an emerging disease

in layers. *Avian Diseases*, *68*(S1), 506–520. https://doi.org/10.1637/aviandiseases-D-24-00076

European Centre for Disease Prevention and Control, European Food Safety Authority, & European Medicines Agency (2024). Antimicrobial consumption and resistance in bacteria from humans and food-producing animals. *EFSA Journal*, *22*(2), e8589. https://doi.org/10.2903/j.efsa.2024.8589

European Food Safety Authority (2016). Evaluation of the safety and efficacy of Listex™ P100 for reduction of pathogens on different ready-to-eat (RTE) food products. *EFSA Journal*, *14*, e04565. https://doi.org/10.2903/j.efsa.2016.4565

European Food Safety Authority, & European Centre for Disease Prevention and Control (2023a). The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2020/2021. *EFSA Journal*, *European Food Safety Authority*, *21*(3), e07867. https://doi.org/10.2903/j.efsa.2023.7867

European Food Safety Authority, & European Centre for Disease Prevention and Control (2023b). The European Union One Health 2022 Zoonoses Report. *EFSA Journal*, *21*(12), e8442. https://doi.org/10.2903/j.efsa.2023.8442

European Food Safety Authority, & European Centre for Disease Prevention and Control (2024a). The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2021–2022. *EFSA Journal*, *22*, e8583. https://doi.org/10.2903/j.efsa.2024.8583

European Food Safety Authority, & European Centre for Disease Prevention and Control (2024b). The European Union One Health 2023 Zoonoses report. *EFSA Journal*, *22*(12), e9106. https://doi.org/10.2903/j.efsa.2024.9106

European Food Safety Authority, & European Centre for Disease Prevention and Control (2025a). The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2022–2023. *EFSA Journal*. https://doi.org/10.2903/j.efsa.2025.9237

European Food Safety Authority, & European Centre for Disease Prevention and Control (2025b). The European Union One Health 2024 Zoonoses Report. *EFSA Journal*, *23*(12), e9759. https://doi.org/10.2903/j.efsa.2025.9759

European Food Safety Authority, & European Centre for Disease Prevention and Control (2025c). The European Union summary report on antimicrobial resistance in zoonotic and indicator bacteria from humans, animals and food in 2023–2024. *EFSA Journal*. https://doi.org/10.2903/j.efsa.2026.9887

European Medicines Agency (2021). Sales of veterinary antimicrobial agents in 31 European countries in 2021: Trends from 2010 to 2021 – Twelfth ESVAC report. https://www.ema.europa.eu/en/documents/report/sales-veterinary-antimicrobial-agents-31-european-countries-2021-trends-2010-2021-twelfth-esvac-report_en.pdf

European Medicines Agency (2022a). Sales of veterinary antimicrobial agents in 31 European countries in 2019 and 2020: Trends from 2010 to 2020 – Eleventh ESVAC report. https://www.ema.europa.eu/en/documents/report/sales-veterinary-antimicrobial-agents-31-european-countries-2019-and-2020-trends-2010-2020-eleventh-esvac-report_en.pdf

European Medicines Agency (2022b). Sales of veterinary antimicrobial agents in 31 European countries in 2022: Trends from 2010 to 2022 – Thirteenth ESVAC report. https://www.ema.europa.eu/en/documents/report/sales-veterinary-antimicrobial-agents-31-european-countries-2022-trends-2010-2022-thirteenth-esvac-report_en.pdf

European Sales and Use of Antimicrobials for Veterinary Medicine (ESUAvet). (2023). Annual surveillance report for 2023 (EMA/CVMP/ESUAVET/80289/2025)

European Sales and Use of Antimicrobials for Veterinary Medicine (ESUAvet). (2024). Annual surveillance report for 2024 (EMA/CVMP/ESUAVET/376993/2025)

Eurostat (2025). Poultry statistics. European Union. https://ec.europa.eu/eurostat/statistics-explained/index.php?title = Poultry_statistics

Fatoba, D. O., Amoako, D. G., Akebe, A. L. K., Ismail, A., & Essack, S. Y. (2022). Genomic analysis of antibiotic-resistant *Enterococcus* spp. reveals novel enterococci strains and the spread of plasmid-borne Tet(M), Tet(L) and Erm(B) genes from chicken litter to agricultural soil in South Africa. *Journal of Environmental Management*, *302(Pt B)*, 114101. https://doi.org/10.1016/j.jenvman.2021.114101

Fernandes, C. J., Fernandes, L. A., & Collignon, P. (2005). Australian Group on Antimicrobial Resistance: Cefoxitin resistance as a surrogate marker for the detection of methicillin-resistant *Staphylococcus aureus*. *Journal of Antimicrobial Chemotherapy*, *55*(4), 506–510. https://doi.org/10.1093/jac/dki052

Fokas, R., Kalatzis, P. G., & Vantarakis, A. (2026). Bacteriophages as food biocontrol agents: A One Health framework for manufacturing quality, regulatory governance, and ethical stewardship – A

narrative review. *Viruses*, *18*(3), 368. https://doi.org/10.3390/v18030368

Food and Drug Administration. (2026). NARMS interim data updates. https://www.fda.gov/animal-veterinary/national-antimicrobial-resistance-monitoring-system/narms-interim-data-updates

Franjus, C., Cavaiuolo, M., Nicolas, A., Nia, Y., & Guédon, E. (2026). Staphylococcal enterotoxins and food poisoning: New players in the game. *Current Opinion in Food Science*, *69*, Article 101396. https://doi.org/10.1016/j.cofs.2026.101396

Friese, A., Schulz, J., Zimmermann, K., Tenhagen, B. A., Fetsch, A., Hartung, J., & Rösler, U. (2013). Occurrence of livestock-associated methicillin-resistant *Staphylococcus aureus* in turkey and broiler barns and contamination of air and soil surfaces in their vicinity. *Applied and Environmental Microbiology*, *79*(8), 2759–2766. https://doi.org/10.1128/AEM.03939-12

Garcia-Llorens, J., Monroy, I., Torres-Boncompte, J., Soriano, J. M., Catalá-Gregori, P., & Sevilla-Navarro, S. (2024). Tracking the prevalence of antibiotic resistance in *Enterococcus* within the Spanish poultry industry: Insights from a One Health approach. *Antibiotics*, *14*(1), 16. https://doi.org/10.3390/antibiotics14010016

García-Solache, M., & Rice, L. B. (2019). The *Enterococcus*: A model of adaptability to its environment. *Clinical Microbiology Reviews*, *32*(2), e00058-18. https://doi.org/10.1128/CMR.00058-18

Ghaffar, A., Liljebjelke, K., Checkley, S., Van Der Meer, F., Farooq, M., Mudiyanselage, H., & Abdul-Careem, M. (2025). Whole genome sequencing of non-aureus *Staphylococcus* species from poultry barn bioaerosols across Alberta reveals circulation of isolates with multiple antibiotic-resistant genes and disinfectant resistant genes. *Journal of Global Antimicrobial Resistance*, *43*, 18–26. https://doi.org/10.1016/j.jgar.2025.03.014

Ghorbani, A., Khoshbakht, R., Kaboosi, H., Shirzad-Aski, H., & Peyravii Ghadikolaii, F. (2022). Study on antibiotic resistance and phylogenetic comparison of avian-pathogenic *Escherichia coli* (APEC) and uropathogenic *Escherichia coli* (UPEC) isolates. *Veterinary Research Forum*, *13*(4), 569–576. https://doi.org/10.30466/vrf.2021.527563.3160

Gómez-Sanz, E., Kadlec, K., Feßler, A. T., Zarazaga, M., Torres, C., & Schwarz, S. (2013). Novel *erm*(T)-carrying multiresistance plasmids from porcine and human isolates of methicillin-resistant *Staphylococcus aureus* ST398 that also harbor cadmium and copper resistance determinants. *Antimicrobial Agents and Chemotherapy*, *57*, 3275–3282. https://doi.org/10.1128/AAC.00171-13

Götz, F., Bannerman, T., & Schleifer, K. H. (2006). The genera *Staphylococcus* and *Macrococcus*. In M. Dworkin, S. Falkow, E. Rosenberg, K. H. Schleifer, & E. Stackebrandt (Eds.), *The prokaryotes* (pp. 5–75). Springer. https://doi.org/10.1007/0-387-30744-3_1

Grimont, P. A. D., & Weill, F.-X. (2007). Antigénic formulae of the Salmonella serovars (9th ed.). WHO Collaborating Centre for Reference and Research on Salmonella, Institut Pasteur. https://www.pasteur.fr/sites/default/files/veng_0.pdf

Hado, H., & Assafi, M. (2021). Molecular fingerprinting of methicillin-resistant *Staphylococcus aureus* strains isolated from human and poultry in Duhok, Iraq. *Iraqi Journal of Veterinary Sciences*, *35*(1), 99–103. https://doi.org/10.33899/ijvs.2020.126375.1310

Hailu, W., Helmy, Y. A., Carney-Knisely, G., Kauffman, M., Fraga, D., & Rajashekara, G. (2021). Prevalence and antimicrobial resistance profiles of foodborne pathogens isolated from dairy cattle and poultry manure amended farms in Northeastern Ohio, the United States. *Antibiotics*, *10*(12), 1450. https://doi.org/10.3390/antibiotics10121450

Hammerum, A. M. (2012). Enterococci of animal origin and their significance for public health. *Clinical Microbiology and Infection*, *18*(7), 619–625. https://doi.org/10.1111/j.1469-0691.2012.03829.x

Hamza, D. A., Abd-Elsalam, R. M., Nader, S. M., Elhariri, M., Elhelw, R., & El-Mahallawy, H. S. (2020). Pathways of methicillin-resistant *Staphylococcus aureus* in animal model: New insights regarding public health. *Infection and Drug Resistance*, *13*, 1593–1600. https://doi.org/10.2147/IDR.S252332

Hao, G., Li, P., Huang, J., Cui, K., Liang, L., Lin, F., Lu, Z., & Sun, S. (2023). Research note: Therapeutic effect of a Salmonella phage combination on chicks infected with *Salmonella* Typhimurium. *Poultry Science*, *102*, 102715. https://doi.org/10.1016/j.psj.2023.102715

Hao, J., Zhang, J., He, X., Wang, Y., Su, J., Long, J., Zhang, L., Guo, Z., Zheng, Y., Wang, M., & Sun, Y. (2025). Unveiling the silent threat: A comprehensive review of *Riemerella anatipestifer* – From pathogenesis to drug resistance. *Poultry Science*, *104*(4), 104915. https://doi.org/10.1016/j.psj.2025.104915

Hao, R., Shoaib, M., Tang, M., Cao, Z., Liu, G., Zhang, Y., Wang, S., Shang, R., Zhang, H., & Pu, W. (2024). Genomic insights into resistome, virulome, and mobilome as organic contaminants of ESKAPE pathogens and *E. coli* recovered from milk, farm workers, and environmental settings in Hainan, China. *Emerging*

Contaminants, *10*(4), 100385. https://doi.org/10.1016/j.emcon.2024.100385

Hernández-Villamizar, S., Bonilla, J. A., García-Vega, A. S., Arevalo-Mayorga, S., Castrillo, D., Medina, V. A., Triviño-García, E. S., Romero, N., Piñeros, R., Fonseca, L., Donado, P., Vives, M. J., Barato, P., & Clavijo, V. (2025). Improving health and productivity in laying hens with the phage cocktail SalmoFree®. *Poultry Science*, *104*(11), 105638. https://doi.org/10.1016/j.psj.2025.105638

Hollenbeck, B. L., & Rice, L. B. (2012). Intrinsic and acquired resistance mechanisms in enterococcus. *Virulence*, *3*(5), 421–433. https://doi.org/10.4161/viru.21282

Hryniewicz, M. M., & Garbacz, K. (2017). Borderline oxacillin-resistant *Staphylococcus aureus* (BORSA) – a more common problem than expected?. *Journal of Medical Microbiology*, *66*(10), 1367–1373. https://doi.org/10.1099/jmm.0.000585

Huang, L., Yuan, H., Liu, M. F., Zhao, X. X., Wang, M. S., Jia, R. Y., Chen, S., Sun, K. F., Yang, Q., Wu, Y., Chen, X. Y., Cheng, A. C., & Zhu, D. K. (2017). Type B chloramphenicol acetyltransferases are responsible for chloramphenicol resistance in *Riemerella anatipestifer*, China. *Frontiers in Microbiology*, *8*, 297. https://doi.org/10.3389/fmicb.2017.00297

Huang, L., Liu, M., Ammanath, A. V., Zhu, D., Jia, R., Chen, S., Zhao, X., Yang, Q., Wu, Y., Zhang, S., Huang, J., Ou, X., Mao, S., Gao, Q., Sun, D., Tian, B., Götz, F., Wang, M., & Cheng, A. (2021). Identification of the natural transformation genes in *Riemerella anatipestifer* by random transposon mutagenesis. *Frontiers in Microbiology*, *12*, 712198. https://doi.org/10.3389/fmicb.2021.712198

Huang, Y., Wang, W., Zhang, Z., Gu, Y., Huang, A., Wang, J., & Hao, H. (2022). Phage products for fighting antimicrobial resistance. *Microorganisms*, *10*(7), 1324. https://doi.org/10.3390/microorganisms10071324

Igbinosa, E. O., Beshiru, A., Igbinosa, I. H., Ogofure, A. G., Ekundayo, T. C., & Okoh, A. I. (2023). Prevalence, multiple antibiotic resistance and virulence profile of methicillin-resistant *Staphylococcus aureus* (MRSA) in retail poultry meat from Edo, Nigeria. *Frontiers in cellular and infection microbiology*, *13*, 1122059. https://doi.org/10.3389/fcimb.2023.1122059

Intralytix. Food safety. https://www.intralytix.com/food-safety

Jesumirhewe, C., Odufuye, T. O., Ariri, J. U., Adebiyi, A. A., Sanusi, A. T., Stöger, A., Daza-Prieto, B., Allerberger, F., Cabal-Rosel, A., & Ruppitsch, W. (2024). Genetic characterization of antibiotic-resistant *Staphylococcus* spp. and *Mammaliicoccus sciuri* from healthy humans and poultry in Nigeria. *Antibiotics (Basel, Switzerland)*, *13*(8), 733. https://doi.org/10.3390/antibiotics13080733

Jhandai, P., Mittal, D., Gupta, R., Kumar, M., & Khurana, R. (2024). Therapeutics and prophylactic efficacy of novel lytic *Escherichia* phage vB_EcoS_PJ16 against multidrug-resistant avian pathogenic *E. coli* using in vivo study. *International microbiology: the official journal of the Spanish Society for Microbiology*, *27*(3), 673–687. https://doi.org/10.1007/s10123-023-00420-7

Jiang, Y., Peng, K., Wang, Q., Wang, M., Li, R., & Wang, Z. (2023). Novel Trimethoprim Resistance Gene *dfrA49* Identified in *Riemerella anatipestifer* from China. *Microbiology spectrum*, *11*(2), e0474722. https://doi.org/10.1128/spectrum.04747-22

Jordá, J., Lorenzo-Rebenaque, L., Montoro-Dasi, L., Marco-Fuertes, A., Vega, S., & Marin, C. (2023). Phage-based biosanitation strategies for minimizing persistent *Salmonella* and *Campylobacter* bacteria in poultry. *Animals: an open access journal from MDPI*, *13*(24), 3826. https://doi.org/10.3390/ani13243826

Jordan, F. T. W., & Bisgaard, M. (2011). *Erysipelothrix rhusiopathiae* – różyca. W M. Pattison, P. F. McMullin, J. M. Bradbury, & D. J. Alexander (red.), *Choroby drobiu* (wyd. 1, s. 257–261). Edra Urban & Partner. (Polish edition; in Polish)

Joseph, J., Jennings, M., Barbieri, N., Zhang, L., Adhikari, P., & Ramachandran, R. (2023). Characterization of avian pathogenic *Escherichia coli* isolated from broiler breeders with colibacillosis in Mississippi. *Poultry*, *2*(1), 24–39. https://doi.org/10.3390/poultry2010004

Kasimoglu-Dogru, A., Gencay, Y. E., & Ayaz, N. D. (2010). Prevalence and antibiotic resistance profiles of *Enterococcus* species in chicken at slaughter level; absence of *vanA* and *vanB* genes in *E. faecalis* and *E. faecium*. *Research in veterinary science*, *89*(2), 153–158. https://doi.org/10.1016/j.rvsc.2010.02.005

Katayama, Y., Ito, T., & Hiramatsu, K. (2000). A new class of genetic element, staphylococcus cassette chromosome *mec*, encodes methicillin resistance in *Staphylococcus aureus*. *Antimicrobial agents and chemotherapy*, *44*(6), 1549–1555. https://doi.org/10.1128/AAC.44.6.1549-1555.2000

Katkowska, M., Kosecka-Strojek, M., Wolska-Gębarzewska, M., Kwapisz, E., Wierzbowska, M., Międzobrodzki, J., & Garbacz, K. (2025). Emerging challenges in methicillin resistance of coagulase-negative staphylococci. *Antibiotics*, *14*(1), 37. https://doi.org/10.3390/antibiotics14010037

Kawacka, I., Olejnik-Schmidt, A., Schmidt, M., & Sip, A. (2020). Effectiveness of phage-based inhibition of

Listeria monocytogenes in food products and food processing environments. *Microorganisms*, *8*(11), 1764. https://doi.org/10.3390/microorganisms8111764

Keerqin, C., McGlashan, K., Van, T. T. H., Chinivasagam, H. N., Moore, R. J., Choct, M., & Wu, S. B. (2022). A lytic bacteriophage isolate reduced *Clostridium perfringens* induced lesions in necrotic enteritis challenged broilers. *Frontiers in Veterinary Science*, *9*, 1058115. https://doi.org/10.3389/fvets.2022.1058115

Keithlin, J., Sargeant, J., Thomas, M. K., & Fazil, A. (2014). Systematic review and meta-analysis of the proportion of *Campylobacter* cases that develop chronic sequelae. *BMC public health*, *14*, 1203. https://doi.org/10.1186/1471-2458-14-1203

Kerek, Á., Szabó, Á., & Jerzsele, Á. (2024). Antimicrobial susceptibility profiles of commensal *Enterococcus* spp. isolates from chickens in Hungarian poultry farms between 2022 and 2023. *Antibiotics (Basel, Switzerland)*, *13*(12), 1194. https://doi.org/10.3390/antibiotics13121194

Kerek, Á., Szabó, Á., Barnácz, F., Csirmaz, B., Kovács, L., & Jerzsele, Á. (2025a). Antimicrobial susceptibility profiles of commensal *Enterococcus* spp. isolates from turkeys in Hungarian poultry farms between 2022 and 2023. *Antibiotics (Basel, Switzerland)*, *14*(4), 331. https://doi.org/10.3390/antibiotics14040331

Kerek, Á., Tornyos, G., Kaszab, E., Fehér, E., & Jerzsele, Á. (2025b). Comparative phenotypic and genotypic analysis of *Erysipelothrix rhusiopathiae* strains isolated from poultry. *Antibiotics (Basel, Switzerland)*, *15*(1), 11. https://doi.org/10.3390/antibiotics15010011

Kim, J. H., Kim, H. J., Jung, S. J., Mizan, M. F. R., Park, S. H., & Ha, S. D. (2020). Characterization of *Salmonella* spp.-specific bacteriophages and their biocontrol application in chicken breast meat. *Journal of Food Science*, *85*(3), 526–534. https://doi.org/10.1111/1750-3841.15042

Kosznik-Kwaśnicka, K., Podlacha, M., Grabowski, Ł., Stasiłojć, M., Nowak-Zaleska, A., Ciemińska, K., Cyske, Z., Dydecka, A., Gaffke, L., Mantej, J., Myślińska, D., Necel, A., Pierzynowska, K., Piotrowska, E., Radzanowska-Alenowicz, E., Rintz, E., Sitko, K., Topka-Bielecka, G., Węgrzyn, G., & Węgrzyn, A. (2022). Biological aspects of phage therapy versus antibiotics against Salmonella enterica serovar Typhimurium infection of chickens. *Frontiers in Cellular and Infection Microbiology*, *12*, 941867. https://doi.org/10.3389/fcimb.2022.941867

Kovács, L., Szabó, Á., Barnácz, F., Csirmaz, B., Jerzsele, Á., & Kerek, Á. (2025). Antimicrobial susceptibility profiles of commensal *Staphylococcus* spp. isolates from turkeys in Hungarian poultry farms between 2022 and 2023. *Antibiotics (Basel, Switzerland)*, *14*(2), 200. https://doi.org/10.3390/antibiotics14020200

Krupa, P., Bystroń, J., Podkowik, M., Empel, J., Mroczkowska, A., & Bania, J. (2015). Population structure and oxacillin resistance of *Staphylococcus aureus* from pigs and pork meat in south-west of Poland. *BioMed Research International*, *2015*, 141475. https://doi.org/10.1155/2015/141475

Kuźmińska-Bajor, M., Śliwka, P., Korzeniowski, P., Kuczkowski, M., Moreno, D. S., Woźniak-Biel, A., Śliwińska, E., & Grzymajło, K. (2023). Effective reduction of *Salmonella* Enteritidis in broiler chickens using the UPWr_S134 phage cocktail. *Frontiers in Microbiology*, *14*, 1136261. https://doi.org/10.3389/fmicb.2023.1136261

Kuźmińska-Bajor, M., Kuczkowski, M., Konkol, D., Korczyński, M., Rakicka-Pustułka, M., Kozioł, S., Tomaszewska-Hetman, L., & Rywińska, A. (2025). Environmental application of a bacteriophage cocktail reduces antibiotic-resistant *Escherichia coli* in poultry litter without disrupting gut microbiota. *Animals: an Open Access Journal from MDPI*, *15*(17), 2525. https://doi.org/10.3390/ani15172525

Lakhundi, S., & Zhang, K. (2018). Methicillin-resistant *Staphylococcus aureus*: Molecular characterization, evolution, and epidemiology. *Clinical Microbiology Reviews*, *31*(4), e00020-18. https://doi.org/10.1128/CMR.00020-18

Lebreton, F., Willems, R. J. L., & Gilmore, M. S. (2014). *Enterococcus* diversity, origins in nature, and gut colonization. In M. S. Gilmore, D. B. Clewell, Y. Ike, & N. Shankar (Eds.), *Enterococci: From Commensals to Leading Causes of Drug Resistant Infection*. Massachusetts Eye and Ear Infirmary. https://www.ncbi.nlm.nih.gov/books/NBK190427/

Li, P., Gao, M., Feng, C., Yan, T., Sheng, Z., Shi, W., Liu, S., Zhang, L., Li, A., Lu, J., Lin, X., Li, K., Xu, T., Bao, Q., & Sun, C. (2022). Molecular characterization of florfenicol and oxazolidinone resistance in *Enterococcus* isolates from animals in China. *Frontiers in Microbiology*, *13*, 811692. https://doi.org/10.3389/fmicb.2022.811692

Li, P., Yang, Z., Lei, T., Dai, Y., Zhou, Y., Zhu, D., & Luo, H. (2023). Identification of a novel carbapenem-hydrolysing class D β-lactamase RAD-1 in *Riemerella anatipestifer*. *Journal of Antimicrobial Chemotherapy*, *78*, 1117–1124. https://doi.org/10.1093/jac/dkad058

Li, S., Chen, Q., Gong, X., Liu, Y., & Zheng, F. (2020). RanB, a putative ABC-type multidrug efflux transporter contributes to aminoglycosides resistance and organic solvents tolerance in Riemerella anatipestifer.

Veterinary Microbiology, *243*, Article 108641. https://doi.org/10.1016/j.vetmic.2020.108641

Li, Y. F., Jiang, H. X., Xiang, R., Sun, N., Zhang, Y. N., Zhao, L. Q., Gu, P., Wang, L. Q., & Zeng, Z. L. (2016). Effects of two efflux pump inhibitors on the drug susceptibility of *Riemerella anatipestifer* isolates from China. *Journal of Integrative Agriculture*, *15*(4), 929–933. https://doi.org/10.1016/S2095-3119(15)61031-0

Lika, E., Puvača, N., Jeremić, D., Stanojević, S., Shtylla Kika, T., Cocoli, S., & de Llanos Frutos, R. (2021). Antibiotic susceptibility of *Staphylococcus* species isolated in raw chicken meat from retail stores. *Antibiotics (Basel, Switzerland)*, *10*(8), 904. https://doi.org/10.3390/antibiotics10080904

Liu, X., Li, X., Liu, J., Chen, R., Liu, R., Zhao, R., Zhao, J., Hao, J., Yang, S., Luo, A., & Chen, A. (2025a). Antimicrobial resistance of *Escherichia coli* from broilers in large-scale poultry farms in Shandong Province. *Frontiers in Microbiology*, *16*, 1685522. https://doi.org/10.3389/fmicb.2025.1685522

Liu, Y., Wang, L., Wang, J., Lu, M., Liu, N., Zhao, J., Hu, F., Han, K., Liu, J., Wang, J., & Qu, Z. (2025b). Epidemic trend of *Salmonella* from swines and broilers in China from 2014 to 2023 and genetic evolution analysis of ESBLs-producing strains. *Frontiers in Microbiology*, *16*, 1510751. https://doi.org/10.3389/fmicb.2025.1510751

López, M., Sáenz, Y., Alvarez-Martínez, M. J., Marco, F., Robredo, B., Rojo-Bezares, B., Ruiz-Larrea, F., Zarazaga, M., & Torres, C. (2010). Tn*1546* structures and multilocus sequence typing of *vanA*-containing enterococci of animal, human and food origin. *The Journal of Antimicrobial Chemotherapy*, *65*(8), 1570–1575. https://doi.org/10.1093/jac/dkq192

Lory, S. (2014). The family *Staphylococcaceae*. In E. Rosenberg, E. F. DeLong, S. Lory, E. Stackebrandt, & F. Thompson (Eds.), *The Prokaryotes: Firmicutes and Tenericutes* (4th ed., p. 573). Springer. https://doi.org/10.1007/978-3-642-30120-9

Lúcio, C. J., Hansen, P. H. C., Griebeler, J., Kipper, D., & Lunge, V. R. (2025). Virulence and antimicrobial resistance of avian pathogenic *Escherichia coli* (APEC) isolates from poultry in Brazil. Poultry, *4*(1), Article 10. https://doi.org/10.3390/poultry4010010

Luo, H. Y., Liu, M. F., Wang, M. S., Zhao, X. X., Jia, R. Y., Chen, S., Sun, K. F., Yang, Q., Wu, Y., Chen, X. Y., Biville, F., Zou, Y. F., Jing, B., Cheng, A. C., & Zhu, D. K. (2018). A novel resistance gene, *lnu*(H), conferring resistance to lincosamides in *Riemerella anatipestifer* CH-2. *International Journal of Antimicrobial Agents*, *51*(1), 136–139. https://doi.org/10.1016/j.ijantimicag.2017.08.022

Luo, H., Zhu, D., Li, M., Tang, Y., Zhang, W., Wang, H., & Li, P. (2022a). RAA enzyme is a new family of class A extended-spectrum β-lactamase from *Riemerella anatipestifer* strain RCAD0122. *Antimicrobial Agents and Chemotherapy*, *66*(3), e0175721. https://doi.org/10.1128/AAC.01757-21

Luo, H., Li, M., Yang, Z., Zhu, D., & Li, P. (2022b). Characterization of RASA-1, a novel class A extended-spectrum beta-lactamase from *Riemerella anatipestifer*. *Veterinary Microbiology*, *270*, 109456. https://doi.org/10.1016/j.vetmic.2022.109456

Łusiak-Szelachowska, M., Żaczek, M., Weber-Dąbrowska, B., Międzybrodzki, R., Letkiewicz, S., Fortuna, W., Rogóż, P., Szufnarowski, K., Jończyk-Matysiak, E., Olchawa, E., Walaszek, K. M., & Górski, A. (2017). Antiphage activity of sera during phage therapy in relation to its outcome. *Future Microbiology*, *12*, 109–117. https://doi.org/10.2217/fmb-2016-0156

Lyu, Z., Han, S., Li, J., Guo, Z., Geng, N., Lyu, C., Qin, L., & Li, N. (2023). Epidemiological investigation and drug resistance characteristics of *Riemerella anatipestifer* strains from large-scale duck farms in Shandong Province, China from March 2020 to March 2022. *Poultry Science*, *102*(7), 102759. https://doi.org/10.1016/j.psj.2023.102759

Ma, H., Zhang, L., Wang, L., Yang, Z., Liu, J., Sun, H., Ge, S., & Quan, C. (2026). Antibiotic mechanisms and resistance: Molecular insights and therapeutic strategies. *Antibiotics (Basel, Switzerland)*, *15*(4), 351. https://doi.org/10.3390/antibiotics15040351

Madhaiyan, M., Wirth, J. S., & Saravanan, V. S. (2020). Phylogenomic analyses of the *Staphylococcaceae* family suggest the reclassification of five species within the genus *Staphylococcus* as heterotypic synonyms, the promotion of five subspecies to novel species, the taxonomic reassignment of five *Staphylococcus* species to *Mammaliicoccus* gen. nov., and the formal assignment of *Nosocomiicoccus* to the family *Staphylococcaceae*. *International Journal of Systematic and Evolutionary Microbiology*, *70*(11), 5926–5936. https://doi.org/10.1099/ijsem.0.004498

Majewski, M., Józefiak, A., Kimsa-Furdzik, M., Dziubdziela, L., Hudak-Nowak, M., Wilczyński, J., & Anusz, K. (2021). Antimicrobial resistance of *Escherichia coli* and *Klebsiella* spp. conventionally sampled from factory-farmed chickens – clinical submissions. *Annals of agricultural and environmental medicine: AAEM*, *28*(2), 271–276. https://doi.org/10.26444/aaem/120927

Majowicz, S. E., Musto, J., Scallan, E., Angulo, F. J., Kirk, M., O'Brien, S. J., Jones, T. F., Fazil, A., Hoekstra, R. M., &

International Collaboration on Enteric Disease 'Burden of Illness' Studies (2010). The global burden of nontyphoidal *Salmonella* gastroenteritis. *Clinical infectious diseases: an official publication of the Infectious Diseases Society of America*, *50*(6), 882–889. https://doi.org/10.1086/650733

Marek, A., Pyzik, E., Stępień-Pyśniak, D., Urban-Chmiel, R., & Nowaczek, A. (2019). Characterization of bacteriophages and their carriage in *Staphylococcus aureus* isolated from broilers in Poland. *British Poultry Science*, *60*(4), 373–380. https://doi.org/10.1080/00071668.2018.1426831

Martinez-Laorden, A., Arraiz-Fernandez, C., Cantalejo, M. J., & Gonzalez-Fandos, E. (2024). Prevalence, identification and antimicrobial resistance of *Listeria monocytogenes* and *Listeria* spp. isolated from poultry and pork meat. *International Journal of Food Science & Technology*, *59*(5), 2667–2675. https://doi.org/10.1111/ijfs.17013

Mehrotra, M., Wang, G., & Johnson, W. M. (2000). Multiplex PCR for detection of genes for *Staphylococcus aureus* enterotoxins, exfoliative toxins, toxic shock syndrome toxin 1, and methicillin resistance. *Journal of Clinical Microbiology*, *38*(3), 1032–1035. https://doi.org/10.1128/JCM.38.3.1032-1035.2000

Melaku, M., Wang, J., Xie, Y., Ali, A., Yi, B., Ma, T., Zhong, R., Chen, L., & Zhang, H. (2025). Reviving hope: Phage therapy application for antimicrobial resistance in farm animal production over the past decade. *Animal Feed Science and Technology*, *324*, 116333. https://doi.org/10.1016/j.anifeedsci.2025.116333

Meng, F., Zhou, D., Li, R., Lang, F., Xiang, B., Yang, L., & Cheng, Z. (2025). Emergence of linezolid-resistant *Enterococcus cecorum* clade F harboring *optrA/fexA* causing enterococcal spondylitis in commercial broilers in China. *BMC Microbiology*, *25*(1), 313. https://doi.org/10.1186/s12866-025-04045-w

Meyer, M., Bobeck, E., Sato, Y., & El-Gazzar, M. (2021). Comparison of naturally occurring versus experimental infection of *Staphylococcus aureus* septicemia in laying hens in two different age groups. *Avian Diseases*, *65*(2), 310–320. https://doi.org/10.1637/0005-2086-65.2.310

Micreos Food Safety BV. Salmonelex™. U.S. Food and Drug Administration.https://www.fda.gov/media/98485/download

MicroMir (2022). Micromir drugs. https://micromircorp.ru/en/products/fagovet

Mohammadi, N. T., Shen, C., Li, Y., Zayda, M. G., Sato, J., Masuda, Y., Honjoh, K. I., & Miyamoto, T. (2022). Characterization of *Clostridium perfringens* bacteriophages and their application in chicken meat and milk. *International Journal of Food Microbiology*, *361*, 109446. https://doi.org/10.1016/j.ijfoodmicro.2021.109446

Mohibbullah, M., Hasibul, H., Rahman, S., Rafia, R., Harunur, R., Akter, R., & Afroz, F. (2022). Identification of bacteria associated with chicken omphalitis and their antibiotic profiles. *Cohesive Journal of Microbiology & Infectious Disease*, *6*(1), 000627. https://doi.org/10.31031/CJMI.2022.06.000627

Molechan, C., Amoako, D. G., Abia, A. L. K., Somboro, A. M., Bester, L. A., & Essack, S. Y. (2019). Molecular epidemiology of antibiotic-resistant *Enterococcus* spp. from the farm-to-fork continuum in intensive poultry production in KwaZulu-Natal, South Africa. *The Science of the Total Environment*, *692*, 868–878. https://doi.org/10.1016/j.scitotenv.2019.07.324

Monroy, I., Catalá-Gregori, P., & Sevilla-Navarro, S. (2025). Assessment of antibiotic resistance and virulence in *Escherichia coli* strains isolated from poultry in Spain. *Poultry Science*, *104*(2), 104838. https://doi.org/10.1016/j.psj.2025.104838

Moraes, D. M. C., Almeida, A. M. S., Andrade, M. A., Nascente, E. P., Duarte, S. C., Nunes, I. A., Jayme, V. S., & Minafra, C. (2024). Antibiotic resistance profile of *Salmonella* sp. isolates from commercial laying hen farms in Central-Western Brazil. *Microorganisms*, *12*(4), 669. https://doi.org/10.3390/microorganisms12040669

Seyedeh Mozhgan, M. B., Ebrahim, R., Hashemi, S. M., & Noosha, Z. J. (2025). Investigating the Prevalence of Enterotoxin and Antibiotic Resistance in Methicillin-Resistant Staphylococcus aureus (MRSA) Isolated from Meat and Edible Viscera of Broiler Chickens. *Veterinary medicine and science*, *11*(4), e70413. https://doi.org/10.1002/vms3.70413

Mpundu, P., Muma, J. B., Mukubesa, A. N., Kainga, H., Mudenda, S., Bumbangi, F. N., Muleya, W., Katemangwe, P., & Munyeme, M. (2022). Antibiotic resistance patterns of *Listeria* species isolated from broiler abattoirs in Lusaka, Zambia. *Antibiotics (Basel, Switzerland)*, *11*(5), 591. https://doi.org/10.3390/antibiotics11050591

Muneeb, M., Ullah Khan, E., Ahmad, S., Hussain, I., Batool, S., Fatima, A., Soumeh, E. A., Al Sulaiman, A. R., & Abudabos, A. E. (2025). A comprehensive review of the application of bacteriophages against enteric bacterial infection in poultry: Current status, challenges, and future prospects. *Antibiotics (Basel, Switzerland)*, *14*(12), 1207. https://doi.org/10.3390/antibiotics14121207

Mwambene, S. J., Mtenga, A. B., Chengula, A. A., & Hoza, A. S. (2025). Detection and antibiotic resistance of Salmonella isolates from selected poultry farms in Dar es Salaam, Tanzania. *Access Microbiology*, *7*(5), 000879.v5. https://doi.org/10.1099/acmi.0.000879.v5

Mwikuma, G., Kainga, H., Kallu, S. A., Nakajima, C., Suzuki, Y., & Hang'ombe, B. M. (2023). Determination of the prevalence and antimicrobial resistance of *Enterococcus faecalis* and *Enterococcus faecium* associated with poultry in four districts in Zambia. *Antibiotics (Basel, Switzerland)*, *12*(4), 657. https://doi.org/10.3390/antibiotics12040657

Naureen, Z., Dautaj, A., Anpilogov, K., Camilleri, G., Dhuli, K., Tanzi, B., Maltese, P. E., Cristofoli, F., De Antoni, L., Beccari, T., Dundar, M., & Bertelli, M. (2020). Bacteriophages presence in nature and their role in the natural selection of bacterial populations. *Acta Bio-Medica: Atenei Parmensis*, *91*(13-S), e2020024. https://doi.org/10.23750/abm.v91i13-S.10819

Nechypurenko, O., Avdeeva, L., Dreval, D., & Sobko, I. (2024). Avian pathogenic *Escherichia coli* and its antibiotic resistance. *Mikrobiolohichnyi Zhurnal*, *86*(5), 61–74. https://doi.org/10.15407/microbiolj86.05.061

Noenchat, P., Direksin, K., & Sornplang, P. (2023). The phenotypic and genotypic antimicrobial resistance patterns of *Salmonella* isolated from chickens and meat at poultry slaughterhouses in Japan and Thailand. *Veterinary World*, *16*(7), 1527–1533. https://doi.org/10.14202/vetworld.2023.1527-1533

Nowaczek, A., Dec, M., Stępień-Pyśniak, D., Urban-Chmiel, R., Marek, A., & Różański, P. (2021). Antibiotic resistance and virulence profiles of *Escherichia coli* strains isolated from wild birds in Poland. *Pathogens (Basel, Switzerland)*, *10*(8), 1059. https://doi.org/10.3390/pathogens10081059

Nowaczek, A., Dec, M., Stępień-Pyśniak, D., Wilczyński, J., & Urban-Chmiel, R. (2023). Characterization of *Riemerella anatipestifer* strains isolated from various poultry species in Poland. *Antibiotics (Basel, Switzerland)*, *12*(12), 1648. https://doi.org/10.3390/antibiotics12121648

Nowak, T., Wódz, K., Kwieciński, P., Kwieciński, A., & Dec, M. (2024). Incidence of erysipelas in waterfowl in Poland – clinical and pathological investigations. *British Poultry Science*, *65*(6), 762–768. https://doi.org/10.1080/00071668.2024.2406331

Nunes, A., Oleastro, M., Alves, F., Liassine, N., Lowe, D. M., Benejat, L., Ducounau, A., Jehanne, Q., Borges, V., Gomes, J. P., Godbole, G., & Philippe, L. (2023). Recurrent *Campylobacter jejuni* infections with *in vivo* selection of resistance to macrolides and carbapenems: Molecular characterization of resistance determinants. *Microbiology Spectrum*, *11*(4), e0107023. https://doi.org/10.1128/spectrum.01070-23

Obe, T., Siceloff, A. T., Crowe, M. G., Scott, H. M., & Shariat, N. W. (2023). Combined quantification and deep serotyping for *Salmonella* risk profiling in broiler flocks. *Applied and Environmental Microbiology*, *89*(4), e0203522. https://doi.org/10.1128/aem.02035-22

Oliveira, J. M., Cardoso, M. F., Moreira, F. A., & Müller, A. (2022). Phenotypic antimicrobial resistance (AMR) of avian pathogenic *Escherichia coli* (APEC) from broiler breeder flocks between 2009 and 2018. *Avian Pathology: Journal of the W.V.P.A*, *51*(4), 388–394. https://doi.org/10.1080/03079457.2022.2074816

Oluwarinde, B. O., Ajose, D. J., Abolarinwa, T. O., Montso, P. K., Du Preez, I., Njom, H. A., & Ateba, C. N. (2023). Safety properties of *Escherichia coli* O157:H7 specific bacteriophages: Recent advances for food safety. *Foods (Basel, Switzerland)*, *12*(21), 3989. https://doi.org/10.3390/foods12213989

OmniLytics (2026). Food safety. https://omnilytics.com/food-water/

Palmer, K. L., & Gilmore, M. S. (2010). Multidrug-resistant enterococci lack CRISPR-cas. *mBio*, *1*(4), Article e00227-10. https://doi.org/10.1128/mBio.00227-10

Panera-Martínez, S., Rodríguez-Melcón, C., Serrano-Galán, V., Alonso-Calleja, C., & Capita, R. (2022). Prevalence, quantification and antibiotic resistance of *Listeria monocytogenes* in poultry preparations. *Food Control*, *135*, 108609. https://doi.org/10.1016/j.foodcont.2021.108608

Paravisi, M., Laviniki, V., Bassani, J., Kunert Filho, H. C., Carvalho, D., Wilsmann, D. E., Borges, K. A., Furian, T. Q., Salle, C. T. P., Moraes, H. L. S., & Nascimento, V. P. (2020). Antimicrobial resistance in *Campylobacter jejuni* isolated from Brazilian poultry slaughterhouses. *Brazilian Journal of Poultry Science*, *22*, 1–8. https://doi.org/10.1590/1806-9061-2020-1262

Partridge, S. R., Kwong, S. M., Firth, N., & Jensen, S. O. (2018). Mobile genetic elements associated with antimicrobial resistance. *Clinical Microbiology Reviews*, *31*(4), e00088-17. https://doi.org/10.1128/CMR.00088-17

Patel, S. S., Patel, A. C., Mohapatra, S. K., Chauhan, H. C., Sharma, K. K., Shrimali, M. D., Raval, S. H., & Prajapati, B. I. (2024). Antibiotic resistance and virulence gene patterns associated with multi drug resistant avian pathogenic *Escherichia coli* (APEC) isolated from broiler chickens in India. *Indian Journal of Microbiology*, *64*(3), 917–926. https://doi.org/10.1007/s12088-023-01132-2

Pathomchai-Umporn, C., Laopiem, S., Witoonsatian, K., Kulprasetsri, S., Panomwan, P., Songserm, T., & Sinwat, N. (2025). Quinolone resistance in *Riemerella anatipestifer* from Thai ducks: Mutation analysis of *gyrA, parC*, and *plasmid-mediated quinolone resistance* genes. *Veterinary World*, *18*(7), 1891–1898. https://doi.org/10.14202/vetworld.2025.1891-1898

Pelyuntha, W., Ngasaman, R., Yingkajorn, M., Chukiatsiri, K., Guyonnet, V., & Vongkamjan, K. (2024). Phage cocktail administration to reduce *Salmonella* load in broilers. *Research in Veterinary Science*, *169*, 105163. https://doi.org/10.1016/j.rvsc.2024.105163

Phageguard. (2026). Applied phage technology to eliminate food pathogens. https://www.phageguard.com/

Połaska, M., & Sokołowska, B. (2019). Bacteriophages – a new hope or a huge problem in the food industry. *AIMS Microbiology*, *5*(4), 324–346. https://doi.org/10.3934/microbiol.2019.4.324

Popy, N. N., Khan, M. F. R., Islam, M. S., Biswas, L., Yasmin, L., Siddique, M. P., Rahman, M., & Rahman, M. B. (2025). Serovar-specific antimicrobial resistance and virulence profiles of *Salmonella enterica* from poultry in Bangladesh. *MicrobiologyOpen*, *14*(5), e70091. https://doi.org/10.1002/mbo3.70091

Poudel, S., Li, T., Chen, S., Zhang, X., Cheng, W. H., Sukumaran, A. T., Kiess, A. S., & Zhang, L. (2022). Prevalence, antimicrobial resistance, and molecular characterization of *Campylobacter* isolated from broilers and broiler meat raised without antibiotics. *Microbiology Spectrum*, *10*(3), e0025122. https://doi.org/10.1128/spectrum.00251-22

Proteonpharma webside: https://proteonpharma.com/pl

Pyzik, E., Nowaczek, A., Urban-Chmiel, R., Korona-Głowniak, I., Dec, M., Herman, K., Stępień-Pyśniak, D., Marek, A., & Nowak, T. (2023). Efektywność eksperymentalnego preparatu bakteriofagowego do wspomagania dezynfekcji i poprawy dobrostanu środowisk utrzymania drobiu w zakresie eliminacji patogennych szczepów Escherichia coli in vitro. In K. Śmietanka (Ed.), Choroby związane z układem rozrodczym ptaków. Materiały konferencyjne, Puławy, 6-7.10.2023 (pp. 67–70). Państwowy Instytut Weterynaryjny – Państwowy Instytut Badawczy

Pyzik, E., Urban-Chmiel, R., Herman, K., & Nowaczek, A. (2024). Solutions limiting the use of antibiotics in poultry production in Poland and other European Union countries. *Animal Science and Genetics*, *20*(2), 41–53. https://doi.org/10.5604/01.3001.0054.6542

Racewicz, P., Majewski, M., Biesiada, H., Nowaczewski, S., Wilczyński, J., Wystalska, D., Kubiak, M., Pszczoła, M., & Madeja, Z. E. (2022). Prevalence and characterisation of antimicrobial resistance genes and class 1 and 2 integrons in multiresistant *Escherichia coli* isolated from poultry production. *Scientific Reports*, *12*(1), 6062. https://doi.org/10.1038/s41598-022-09996-y

Rahman, M. A., Abraham, R., Abraham, S., Hampson, D. J., & Uddin, J. M. (2026). Application of bacteriophages to control bacterial infections of food animals in the era of antimicrobial resistance: An overview. *Veterinary Microbiology*, *316*, 110988. https://doi.org/10.1016/j.vetmic.2026.110988

Ramtahal, M. A., Amoako, D. G., Akebe, A. L. K., Somboro, A. M., Bester, L. A., & Essack, S. Y. (2022). A public health insight into *Salmonella* in poultry in Africa: A review of the past decade: 2010–2020. *Microbial Drug Resistance (Larchmont, N.Y.)*, *28*(6), 710–733. https://doi.org/10.1089/mdr.2021.0384

Ranabhat, G., Subedi, D., Karki, J., Paudel, R., Luitel, H., & Bhattarai, R. K. (2024). Molecular detection of avian pathogenic *Escherichia coli* (APEC) in broiler meat from retail meat shop. *Heliyon*, *10*(15), e35661. https://doi.org/10.1016/j.heliyon.2024.e35661

Rau, R. B., Ribeiro, A. R., dos Santos, A., & Barth, A. L. (2021). Antimicrobial resistance of *Salmonella* from poultry meat in Brazil: results of a nationwide survey. *Epidemiology and Infection*, *149*, e228. https://doi.org/10.1017/S0950268821002156

Rehman, M. A., Yin, X., Zaheer, R., Goji, N., Amoako, K. K., McAllister, T., Pritchard, J., Topp, E., & Diarra, M. S. (2018). Genotypes and phenotypes of enterococci isolated from broiler chickens. *Frontiers in Sustainable Food Systems*, *2*, 83. https://doi.org/10.3389/fsufs.2018.00083

Romero-Barrios, P., Deckert, A., Parmley, E. J., & Leclair, D. (2020). Antimicrobial resistance profiles of *Escherichia coli* and *Salmonella* isolates in Canadian broiler chickens and their products. *Foodborne Pathogens and Disease*, *17*(11), 672–678. https://doi.org/10.1089/fpd.2019.2776

Rostamian, M., Rahmati, D., & Akya, A. (2022). Clinical manifestations, associated diseases, diagnosis, and treatment of human infections caused by *Erysipelothrix rhusiopathiae*: A systematic review. *Germs*, *12*(1), 16–31. https://doi.org/10.18683/germs.2022.1303

Ruiz, J. A., & Sandhu, T. S. (2013). *Riemerella anatipestifer* infection. In D. E. Swayne, J. R. Glisson, L. R. McDougald, V. Nolan, D. L. Suarez, & V. L. Nair (Ed.), Diseases of poultry, 13 ed. (pp. 823–828). Wiley-Blackwell.

Salem, M., Ghabbour, R., Mostafa, N. F., Awad, A., & Younis, G. (2025). Molecular characterization

of *Salmonella* isolates from poultry in Egypt: Detection of virulence, ESBLs genes and antimicrobial resistance profiling. *Veterinary Research Communications*, *50*(1), Article 44. https://doi.org/10.1007/s11259-025-10936-0

Schwarz, S., Kehrenberg, C., Doublet, B., & Cloeckaert, A. (2004). Molecular basis of bacterial resistance to chloramphenicol and florfenicol. *FEMS Microbiology Reviews*, *28*(5), 519–542. https://doi.org/10.1016/j.femsre.2004.04.001

Seiler, C., & Berendonk, T. U. (2012). Heavy metal driven co-selection of antibiotic resistance in soil and water bodies impacted by agriculture and aquaculture. *Frontiers in Microbiology*, *3*, Article 399. https://doi.org/10.3389/fmicb.2012.00399

Sgariglia, E., Aconiti Mandolini, N., Napoleoni, M., Medici, L., Fraticelli, R., Conquista, M., Gianfelici, P., Staffolani, M., Fisichella, S., Capuccella, M., Sargenti, M., & Perugini, G. (2019). Antibiotic resistance pattern and virulence genes in avian pathogenic *Escherichia coli* (APEC) from different breeding systems. *Veterinaria Italiana*, *55*(1), 26–33. https://doi.org/10.12834/VetIt.1617.8701.1

Shahin, K., & Bouzari, M. (2018). Bacteriophage application for biocontrolling *Shigella flexneri* in contaminated foods. *Journal of Food Science and Technology*, *55*(2), 550–559. https://doi.org/10.1007/s13197-017-2964-2

Shakir, Z. M., Alhatami, A. O., Ismail Khudhair, Y., & Muhsen Abdulwahab, H. (2021). Antibiotic resistance profile and multiple antibiotic resistance index of *Campylobacter* species isolated from poultry. *Archives of Razi Institute*, *76*(6), 1677–1686. https://doi.org/10.22092/ari.2021.356400.1837

Shchur, N., Chechet, O., Mazur, T., Martyniuk, O., Gorbatiuk, O., Buchkovska, H., Musiets, I., Ordynska, D., Finkova, O., Moskalenko, L., Ponomaryova-Gerasimyuk, T., Lusta, M., & Nedosekov, V. (2023). Prevalence and antimicrobial resistance of *Campylobacter* isolated from animals and poultry in Ukraine. *Advances in Animal and Veterinary Sciences*, *11*(5), 852–863. https://doi.org/10.17582/journal.aavs/2023/11.5.852.863

Shil, S., Haldar, S., Arora, S. S., Pan, D., Koley, H., Chowdhury, J., Maity, A., & Debnath, A. (2026). Antimicrobial resistance in *Salmonella* from Indian poultry: Trends, challenges, and One Health perspectives. *Journal of Pure and Applied Microbiology*, *20*(1), 1–32. https://doi.org/10.22207/JPAM.20.1.31

Shore, A. C., & Coleman, D. C. (2013). Staphylococcal cassette chromosome *mec*: Recent advances and new insights. *International Journal of Medical Microbiology*, *303*(6–7), 350–359. https://doi.org/10.1016/j.ijmm.2013.02.002

Shu, G., Qiu, J., Zheng, Y., Chang, L., Li, H., Xu, F., Zhang, W., Yin, L., Fu, H., Yan, Q., Gan, T., & Lin, J. (2023). Association between phenotypes of antimicrobial resistance, ESBL resistance genes, and virulence genes of *Salmonella* isolated from chickens in Sichuan, China. *Animals: an open access journal from MDPI*, *13*(17), 2770. https://doi.org/10.3390/ani13172770

Silva, V., Caniça, M., Ferreira, E., Vieira-Pinto, M., Saraiva, C., Pereira, J. E., Capelo, J. L., Igrejas, G., & Poeta, P. (2022). Multidrug-resistant methicillin-resistant coagulase-negative staphylococci in healthy poultry slaughtered for human consumption. *Antibiotics (Basel, Switzerland)*, *11*(3), 365. https://doi.org/10.3390/antibiotics11030365

Singh, S., Kriti, M., Anamika, K. S., Sharma, P., Pal, N., Sarma, D. K., Tiwari, R., & Kumar, M. (2025). A One Health approach addressing poultry-associated antimicrobial resistance: Human, animal and environmental perspectives. *The Microbe*, *7*, Article 100309. https://doi.org/10.1016/j.microb.2025.100309

Skowron, K., Wałecka-Zacharska, E., Wiktorczyk-Kapischke, N., Skowron, K. J., Grudlewska-Buda, K., Bauza-Kaszewska, J., Bernaciak, Z., Borkowski, M., & Gospodarek-Komkowska, E. (2020). Assessment of the prevalence and drug susceptibility of *Listeria monocytogenes* strains isolated from various types of meat. *Foods (Basel, Switzerland)*, *9*(9), 1293. https://doi.org/10.3390/foods9091293

Song, F., Li, W., Zhao, X., Hou, S., Wang, Y., Wang, S., Gao, J., Chen, X., Li, J., Zhang, R., Jiang, S., & Zhu, Y. (2024). Epidemiological and molecular investigations of *Salmonella* isolated from duck farms in southwest and around area of Shandong, China. *Microbial Pathogenesis*, *195*, 106816. https://doi.org/10.1016/j.micpath.2024.106816

Ssemakadde, T., Pauline Petra, N., Busingye, J. C., Bazira, J., & Taseera, K. (2025). Prevalence and antimicrobial resistance of *Salmonella* and pathogenic *E. coli* in broiler farms, Wakiso district, Uganda. *PLoS One*, *20*(7), e0309599. https://doi.org/10.1371/journal.pone.0309599

Starkova, D., Egorova, S., Suzhaeva, L., Nguyen, T. Q., Kaftyreva, L., Makarova, M., Zhamborova, S., Polev, D., Saitova, A., Nguyen, V. H., Vo, T. K., & Nguyen, L. T. (2025). Antimicrobial resistance and phylogenetic analysis of multidrug-resistant non-typhoidal *Salmonella* isolates from different sources in Southern Vietnam. *Antibiotics (Basel, Switzerland)*, *14*(5), 489. https://doi.org/10.3390/antibiotics14050489

Stępień-Pyśniak, D., Marek, A., Banach, T., Adaszek, Ł., Pyzik, E., Wilczyński, J., & Winiarczyk, S. (2016). Prevalence and antibiotic resistance of *Enterococcus* strains isolated from poultry. *Acta Veterinaria Hungarica*, *64*(2), 148–163. https://doi.org/10.1556/004.2016.016

Stępień-Pyśniak, D., Hauschild, T., Dec, M., Marek, A., Brzeski, M., & Kosikowska, U. (2021). Antimicrobial resistance and genetic diversity of *Enterococcus faecalis* from yolk sac infections in broiler chicks. *Poultry Science*, *100*(12), 101491. https://doi.org/10.1016/j.psj.2021.101491

Stępień-Pyśniak, D., Hauschild, T., Łopucki, R., Kosikowska, U., Wilczyński, J., Brzeski, M., Matusevičius, P., & Christensen, H. (2025). Differences in tests of phenotypic colistin resistance in clinical *Escherichia coli* isolates from poultry and their genetic diversity. *Veterinary Microbiology*, *307*, 110581. https://doi.org/10.1016/j.vetmic.2025.110581

Syed, M. A., Ullah, H., Tabassum, S., Fatima, B., Woodley, T. A., Ramadan, H., & Jackson, C. R. (2020). Staphylococci in poultry intestines: a comparison between farmed and household chickens. *Poultry Science*, *99*(9), 4549–4557. https://doi.org/10.1016/j.psj.2020.05.051

Szabó, Á., Jerzsele, Á., Kovács, L., & Kerek, Á. (2025). Antimicrobial susceptibility profiles of commensal *Staphylococcus* spp. isolates from chickens in Hungarian poultry farms between 2022 and 2023. *Antibiotics (Basel, Switzerland)*, *14*(1), 103. https://doi.org/10.3390/antibiotics14010103

Tang, B., Zou, C., Schwarz, S., Xu, C., Hao, W., Yan, X. M., Huang, Y., Ni, J., Yang, H., Du, X. D., & Shan, X. (2023). Linezolid-resistant *Enterococcus faecalis* of chicken origin harbored chromosome-borne *optrA* and plasmid-borne *cfr*, *cfr*(D), and *poxtA2* genes. *Microbiology Spectrum*, *11*(3), e0274122. https://doi.org/10.1128/spectrum.02741-22

Tang, M., Zhou, Q., Zhang, X., Zhou, S., Zhang, J., Tang, X., Lu, J., & Gao, Y. (2020). Antibiotic resistance profiles and molecular mechanisms of *Campylobacter* from chicken and pig in China. *Frontiers in Microbiology*, *11*, 592496. https://doi.org/10.3389/fmicb.2020.592496

Tegegne, H. A., Koláčková, I., Florianová, M., Gelbíčová, T., Madec, J. Y., Haenni, M., & Karpíšková, R. (2021). Detection and molecular characterisation of methicillin-resistant *Staphylococcus aureus* isolated from raw meat in the retail market. *Journal of Global Antimicrobial Resistance*, *26*, 233–238. https://doi.org/10.1016/j.jgar.2021.06.012

Thomrongsuwannakij, T., Blackall, P. J., Djordjevic, S. P., Cummins, M. L., & Chansiripornchai, N. (2020). A comparison of virulence genes, antimicrobial resistance profiles and genetic diversity of avian pathogenic *Escherichia coli* (APEC) isolates from broilers and broiler breeders in Thailand and Australia. *Avian Pathology: Journal of the W.V.P.A*, *49*(5), 457–466. https://doi.org/10.1080/03079457.2020.1764493

Tian, T., Bao, Y., Hui, J., Gao, Y., Wang, L., Zhao, J., Hao, X., Song, C., Wang, J., & Zhao, G. (2025). Analysis of avian pathogenic *Escherichia coli* (APEC) and its antimicrobial resistance risk characteristics and critical control points in laying hens. *Poultry Science*, *104*(12), 106049. https://doi.org/10.1016/j.psj.2025.106049

Timur, N. P. V. T., Kristianingrum, Y. P., Suardana, I. W., & Wibowo, M. H. (2025). Phenotypic and resistance patterns of avian pathogenic *Escherichia coli* isolated from commercial poultry farm. *Tropical Animal Science Journal*, *49*(1), 79–87. https://doi.org/10.5398/tasj.2026.49.1.79

Tiseo, K., Huber, L., Gilbert, M., Robinson, T. P., & Van Boeckel, T. P. (2020). Global trends in antimicrobial use in food animals from 2017 to 2030. *Antibiotics (Basel, Switzerland)*, *9*(12), 918. https://doi.org/10.3390/antibiotics9120918

Tuominen, K. S., Sternberg Lewerin, S., Jacobson, M., & Rosendal, T. (2022). Modelling environmentally mediated spread of livestock-associated methicillin-resistant *Staphylococcus aureus* in a pig herd. *Animal: an International Journal of Animal Bioscience*, *16*(2), 100450. https://doi.org/10.1016/j.animal.2021.100450

Tyc, J., Kalwasińska, A., Olszewska-Tomczyk, M., & Woźniakowski, G. (2026). Phylogenetic analysis and susceptibility to antibiotics and phytogenics of *Riemerella anatipestifer* strains isolated in Poland. *Journal of Veterinary Research*, *70*(1), 33–42. https://doi.org/10.2478/jvetres-2026-0019

Tyson, G. H., Sabo, J. L., Rice-Trujillo, C., Hernandez, J., & McDermott, P. F. (2018). Whole-genome sequencing based characterization of antimicrobial resistance in *Enterococcus*. *Pathogens and Disease*, *76*(2), 10.1093/femspd/fty018. https://doi.org/10.1093/femspd/fty018

Ünal, N., Bal, E., Karagöz, A., Altun, B., & Koçak, N. (2020). Detection of vancomycin-resistant enterococci in samples from broiler flocks and houses in Turkey. *Acta Veterinaria Hungarica*, *68*(2), 117–122. https://doi.org/10.1556/004.2020.00024

Urban-Chmiel, R., & Pyzik, E. (2025). Selected mechanisms of action of bacteriophages in bacterial infections in animals. *Viruses*, *17*(1), 101. https://doi.org/10.3390/v17010101

Urban-Chmiel, R., Marek, A., Stępień-Pyśniak, D., Wieczorek, K., Dec, M., Nowaczek, A., & Osek, J.

(2022). Antibiotic resistance in bacteria – A review. *Antibiotics (Basel, Switzerland), 11*(8), 1079. https://doi.org/10.3390/antibiotics11081079

Urban-Chmiel, R., Osek, J., & Wieczorek, K. (2025). Methods of controlling microbial contamination of food. *Pathogens (Basel, Switzerland)*, *14*(5), 492. https://doi.org/10.3390/pathogens14050492

USDA Report (2024). Poultry and products annual (Report No. E42024-0027). U.S. Department of Agriculture, Foreign Agricultural Service. https://apps.fas.usda.gov/newgainapi/api/Report/DownloadReportByFileName?fileName = Poultry%20and%20Products%20Annual_Paris_European%20Union_E42024-0027

Van Cuong, N., Kiet, B. T., Phu, D. H., Van, N. T. B., Hien, V. B., Thwaites, G., Carrique-Mas, J., & Choisy, M. (2021). Effects of prophylactic and therapeutic antimicrobial uses in small-scale chicken flocks. *Zoonoses and Public Health*, *68*(5), 483–492. https://doi.org/10.1111/zph.12839

Vaster Life Sciences. (2025). Phagex-ES: Unique cocktail of bacteriophages for poultry. https://www.vasterlifesciences.com/phagex-es.php

Velhner, M., Prunić, B., Aleksić, N., Todorović, D., Knežević, S., & Ljubojević Pelić, D. (2024). Antimicrobial resistance of *Enterococcus* isolates from poultry farms in the Republic of Serbia (Autonomous Province of Vojvodina). *Microorganisms*, *12*(7), 1483. https://doi.org/10.3390/microorganisms12071483

Vikram, A., Woolston, J., & Sulakvelidze, A. (2021). Phage biocontrol applications in food production and processing. *Current Issues in Molecular Biology*, *40*, 267–302. https://doi.org/10.21775/cimb.040.267

Vikram, A., Callahan, M. T., Woolston, J. W., Sharma, M., & Sulakvelidze, A. (2022). Phage biocontrol for reducing bacterial foodborne pathogens in produce and other foods. *Current Opinion in Biotechnology*, *78*, 102805. https://doi.org/10.1016/j.copbio.2022.102805

Vo, T. T., Dang, V. T., Le, D. H., & Nguyen, T. H. (2022). Identification, serotyping, and antimicrobial susceptibility of *Riemerella anatipestifer* isolated from ducks in Vietnam. *Open Veterinary Journal*, *12*(3), 391–398. https://doi.org/10.5455/OVJ.2022.v12.i3.13

Wang, C., Wang, X., Hao, J., Kong, H., Zhao, L., Li, M., Zou, M., & Liu, G. (2024). Serotype distribution and antimicrobial resistance of *Salmonella* isolates from poultry sources in China. *Antibiotics (Basel, Switzerland)*, *13*(10), 959. https://doi.org/10.3390/antibiotics13100959

Wang, M., Yao, Y., Yang, Y., Zhu, D., Wang, M., Jia, R., Chen, S., Zhao, X., Yang, Q., Wu, Y., Zhang, S., Huang, J., Ou, X., Tian, B., Sun, D., Zhang, L., Yu, Y., He, Y., Wu, Z., Cheng, A., Liu, M. (2025). The characterization of outer membrane vesicles (OMVs) and their role in mediating antibiotic-resistance gene transfer through natural transformation in *Riemerella anatipestifer*. *Poultry Science*, *104*(2), 104730. https://doi.org/10.1016/j.psj.2024.104730

Wernicki, A., Nowaczek, A., & Urban-Chmiel, R. (2017). Bacteriophage therapy to combat bacterial infections in poultry. *Virology Journal*, *14*(1), 179. https://doi.org/10.1186/s12985-017-0849-7

Wessels, K., Rip, D., & Gouws, P. (2021). *Salmonella* in chicken meat: Consumption, outbreaks, characteristics, current control methods and the potential of bacteriophage use. *Foods (Basel, Switzerland)*, *10*(8), 1742. https://doi.org/10.3390/foods10081742

Wieczorek, K., Bocian, Ł., & Osek, J. (2020). Prevalence and antimicrobial resistance of *Campylobacte*r isolated from carcasses of chickens slaughtered in Poland – a retrospective study. *Food Control*, *112*, 107159. https://doi.org/10.1016/j.foodcont.2020.107159

Wieczorek, K., Bocian, Ł., & Osek, J. (2021). Bovine and pig carcasses as a source of *Campylobacter* in Poland: A reservoir for antimicrobial-resistant *Campylobacter coli*. *Foodborne Pathogens and Disease*, *18*(7), 462–468. https://doi.org/10.1089/fpd.2020.2914

Wiese, M., Klaassens, E. S., Hatt, V., Kreikamp, A., Baak, M. L., Heerikhuisen, M., & Van Der Vossen, J. M. B. M. (2025). Demonstration of phage inhibitory action against *Clostridium perfringens* LMG 11264 within a complex chicken cecal microbiota *in vitro*. *Frontiers in Antibiotics*, *4*, 1599939. https://doi.org/10.3389/frabi.2025.1599939

Wigmore, S. M., Greenhill, A. R., & Bean, D. C. (2024). Isolation and characterization of enterococci from poultry reveals high incidence of *Enterococcus thailandicus* in Victoria, Australia. Journal of Applied Microbiology, 135*(8), lxae194*. https://doi.org/10.1093/jambio/lxae194

Wittebole, X., De Roock, S., & Opal, S. M. (2014). A historical overview of bacteriophage therapy as an alternative to antibiotics for the treatment of bacterial pathogens. *Virulence*, *5*(1), 226–235. https://doi.org/10.4161/viru.25991

World Health Organization (2024). WHO bacterial priority pathogens list, 2024: Bacterial pathogens of public health importance to guide research, development and strategies to prevent and control antimicrobial resistance.

World Organisation for Animal Health (2024). Annual report on antimicrobial agents intended for use in animals: 8th report. https://www.woah.org/app/uploads/2024/05/woah-amu-report-2024-final.pdf

Woźniak-Biel, A., Bugla-Płoskońska, G., Burdzy, J., Korzekwa, K., Ploch, S., & Wieliczko, A. (2019).

Antimicrobial resistance and biofilm formation in *Enterococcus* spp. isolated from humans and turkeys in Poland. *Microbial Drug Resistance (Larchmont, N.Y.)*, *25*(2), 277–286. https://doi.org/10.1089/mdr.2018.0221

Xihui, Z., Yanlan, L., Zhiwei, W., Zheyu, P., Zhenshu, S., Cheng, L., Jianbiao, L., Shengliang, C., Lanying, P., & Yubao, L. (2023). Antibiotic resistance of *Riemerella anatipestifer* and comparative analysis of antibiotic-resistance gene detection methods. *Poultry Science*, *102*(3), 102405. https://doi.org/10.1016/j.psj.2022.102405

Yan, M., Song, X., Chen, H., Zhang, H., Li, Y., Liu, D., Liu, B., & Zou, M. (2026). Study on antimicrobial resistance and molecular characteristics of *Riemerella anatipestifer*. *Animals: an Open Access Journal from MDPI*, *16*(3), 442. https://doi.org/10.3390/ani16030442

Yang, Z., Lan, T., Luo, H., Li, P., Wang, M., Jia, R., Chen, S., Liu, M., Zhao, X., Yang, Q., Wu, Y., Zhang, S., Huang, J., Ou, X., Mao, S., Gao, Q., Sun, D., Tian, B., Cheng, A., & Zhu, D. (2024a). Emergence and mobilization of a novel lincosamide resistance gene lnu(I): From environmental reservoirs to pathogenic bacteria. *The Science of the Total Environment*, *906*, 167400. https://doi.org/10.1016/j.scitotenv.2023.167400

Yang, Z., Yang, X., Wang, M., Jia, R., Chen, S., Liu, M., Zhao, X., Yang, Q., Wu, Y., Zhang, S., Huang, J., Ou, X., Mao, S., Gao, Q., Sun, D., Tian, B., Zhu, D., & Cheng, A. (2024b). Genome-wide association study reveals serovar-associated genetic loci in *Riemerella anatipestifer*. *BMC Genomics*, *25*(1), 57. https://doi.org/10.1186/s12864-024-09988-4

Yuki N. (2001). Infectious origins of, and molecular mimicry in, Guillain-Barré and Fisher syndromes. *The Lancet. Infectious Diseases*, *1*(1), 29–37. https://doi.org/10.1016/S1473-3099(01)00019-6

Zampara, A., Martine, C., Holst-Sørensen, M. C., Elsser-Gravesen, A. A., & Brøndsted, L. (2017). Significance of phage-host interactions for biocontrol of *Campylobacter jejuni* in food. *Food Control*, *73*, 1169–1175. https://doi.org/10.1016/j.foodcont.2016.10.033

Zawiasa, A., Schmidt, M., & Olejnik-Schmidt, A. (2025). Phage-based control of *Listeria innocua* in the food industry: A strategy for preventing *Listeria monocytogenes* persistence in biofilms. *Viruses*, *17*(4), 482. https://doi.org/10.3390/v17040482

Żbikowska, K., Michalczuk, M., & Dolka, B. (2020). The use of bacteriophages in the poultry industry. *Animals: an Open Access Journal from MDPI*, *10*(5), 872. https://doi.org/10.3390/ani10050872

Zhang, X., Tang, M., Zhou, Q., Lu, J., Zhang, H., Tang, X., Ma, L., Zhang, J., Chen, D., & Gao, Y. (2024). A broad host phage, CP6, for combating multidrug-resistant *Campylobacter* prevalent in poultry meat. *Poultry Science*, *103*(4), 103548. https://doi.org/10.1016/j.psj.2024.103548

Zhou, M., Yang, Z., Wang, M., Jia, R., Chen, S., Liu, M., Zhao, X., Yang, Q., Wu, Y., Zhang, S., Huang, J., Ou, X., Sun, D., Tian, B., He, Y., Wu, Z., Cheng, A., & Zhu, D. (2026). Identification and characteristics of a novel acquired aminoglycoside phosphotransferase, APH(3')-IVb, from *Riemerella anatipestifer*. *Antimicrobial Agents and Chemotherapy*, *70*(5), e0163125. https://doi.org/10.1128/aac.01631-25

Zhou, Y., Wu, K., Lin, H., Hu, Y. L., Xu, W., Zhang, J., Zhou, S., Yu, K., Liu, C. G., Wang, H. N., & Lei, C. W. (2025). Whole genome sequencing of *Salmonella* in poultry from China reveals the presence of bla_{NDM-5} in different serotypes. *Poultry Science*, *104*(11), 105647. https://doi.org/10.1016/j.psj.2025.105647

Zhu, D. K., Luo, H. Y., Liu, M. F., Zhao, X. X., Jia, R. Y., Chen, S., Sun, K. F., Yang, Q., Wu, Y., Chen, X. Y., Cheng, A. C., & Wang, M. S. (2018). Various profiles of *tet* genes addition to *tet*(X) in *Riemerella anatipestifer* isolates from ducks in China. *Frontiers in Microbiology*, *9*, 585. https://doi.org/10.3389/fmicb.2018.00585

Zhu, D., Zheng, M., Xu, J., Wang, M., Jia, R., Chen, S., Liu, M., Zhao, X., Yang, Q., Wu, Y., Zhang, S., Huang, J., Liu, Y., Zhang, L., Yu, Y., Pan, L., Chen, X., & Cheng, A. (2019). Prevalence of fluoroquinolone resistance and mutations in the *gyrA*, *parC* and *parE* genes of *Riemerella anatipestifer* isolated from ducks in China. *BMC Microbiology*, *19*(1), 271. https://doi.org/10.1186/s12866-019-1659-4