Review Article

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The potential of quails as reservoirs for extended-spectrum β-lactamase (ESBL)-producing bacteria: A public health perspective

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ABSTRACT

Quails are included in the group of poultry that are susceptible to various diseases, one of which is colibacillosis. The large and increasing population of quails, if antibiotics are given continuously, will contribute to antibiotic resistance in the livestock sector. extended-spectrum β-lactamase (ESBL) is an enzyme produced in the plasmid of Gram-negative bacteria that have resistance to β-lactam antibiotics. ESBL is produced by nosocomial pathogens such as *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp. The quail farming environment is often a reservoir for ESBL bacteria due to several factors, including intensive use of antibiotics for disease prevention and growth, as well as inadequate sanitation. ESBL-producing bacteria in quails can be transferred to humans through several potential routes. Direct contact with quail or consumption of contaminated processed products can be the main route of transmission of ESBL bacteria to humans. In addition, agricultural environments contaminated with livestock waste are also a source of the spread of resistant bacteria to the environment and ultimately to the human population. Monitoring antimicrobial resistance (AMR) in the poultry sector, especially quail, is essential to prevent the spread of difficult-to-treat infections in humans. This includes improving standards of cage and equipment hygiene, good waste management, and restricting access to the farm area. In addition, antibiotic use must be carried out wisely and based on veterinarian recommendations, to avoid selection of resistant bacteria.

Introduction

Quail is a wild bird with a smaller body compared to other birds. Quail is included in the genus Coturnix and the family Phasianidae (Lokapirnasari *et al.*, 2024). There are 45 species of quail worldwide and two species that are commonly kept and consumed in Indonesia, namely Japanese quail (*Coturnix japonica*) and Bobwhites quail (*Colinus virginianus*) (Morris *et al.*, 2020). The nutritional value of quail is almost the same as broiler chickens, so that quail production continues to increase to meet the demand for animal protein, in addition to being fast to maintain, relatively low feed, and providing high production in the form of meat and eggs (Lokapirnasari *et al.*, 2017). Quail carcasses consist of 76% meat and 10% bones, having the highest proportion of meat and the lowest proportion of bones compared to other poultry species, so quail are preferred by the public (Mohammed and Ejiofor, 2015).

Quail meat is recommended for those who have to follow a low-fat diet because it contains low fat (1.1-1.3g/100g), which accumulates between tissues and cholesterol of 6.8 (Wegner *et al.*, 2024). According to Oke *et al.* (2025) consuming quail products has health benefits, namely being able to strengthen the immune system, support brain development and function, and help regenerate damaged body cells. Quail are able to reproduce with an egg production rate of one egg per day at the age of 45 days (Retes *et al.*, 2022). According to Adom *et al.* (2023) quail workers are the largest contributor of eggs after laying hens. Quail egg production is estimated to reach 250-300 eggs/head/year (Bagh *et al.*, 2016). The population of quail in Indonesia continued to increase in 2016, as many as 3,281,998. In 2017, it increased to 3,684,999, and in 2018, the population increased again to 3,688,687.

Quails are included in the group of poultry that are susceptible to various diseases, one of which is colibacillosis (Kabir, 2010). Colibacillosis is a zoonotic disease caused by the pathogenic *Escherichia coli* bacteria, therefore the usual treatment given is antibiotics (Song *et al.*, 2022; Wibisono *et al.*, 2022). The quail population is large and continues to increase, if antibiotics are given continuously, it will contribute to antibiotic resistance in the livestock sector (Farghaly *et al.*, 2017). The use of antibiotics in livestock farming is a serious contributor to health problems, because the irrational administration of antibiotics and inappropriate doses causes antibiotic resistance (Ghimpețeanu *et al.*, 2022). Antibiotic resistance is a major health issue that causes decreased treatment effectiveness, on the other hand *Enterobacter* such as *Escherichia coli* and *Klebsiella pneumoniae* have β-lactamase enzymes that create resistance to β -lactam antibiotics (Golsha *et al.*, 2021).

Extended-spectrum β-lactamase (ESBL) is an enzyme produced in the plasmid of Gram-negative bacteria that have resistance to β-lactam antibiotics (Akpaka *et al.*, 2021). According to Widodo *et al.* (2020) ESBL is an enzyme produced by bacteria with the ability to break down oxyimino-β-lactam antibiotics, which are currently one of the main therapeutic agents in treating serious infections in humans and animals. According to Giufrè *et al.* (2021) ESBL enzymes found in humans are CTX-M-1, CTX-M-14, CTX-M-15, SHV-12, CMY-2, CTX-M-14 and CTX-M-15. Common ESBL enzymes consist of CTX-M, SHV, and TEM (Tseng *et al.*, 2023). ESBL causes therapeutic failure in severe infections that threaten human life (Palmeira and Ferreira, 2020).

Food that comes from animals has the potential to be a risk factor for the transmission of pathogenic bacterial infections to humans or is zoonotic (Rahman *et al*., 2020). The presence of antibiotic residues in edible tissues can have negative impacts on humans, including triggering allergic reactions, organ damage, changes in microflora balance, and the emergence of resistant bacterial strains (Afnani *et al*., 2022; Muteeb *et al*., 2023). The purpose of this review article is to comprehensively examine the potential of quail as a reservoir of ESBL-producing bacteria and examine its impact on public health.

Understanding extended spectrum β-lactamases

Extended-spectrum β-lactamases (ESBL) are enzymes produced by certain bacteria that can destroy or break down β-lactam antibiotics, which include penicillins, first- to third-generation cephalosporins, carbapenems, and monobactams (Agumah *et al*., 2025; Bush, 2018). ESBLs are produced by nosocomial pathogens such as *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp. (Mulani *et al*., 2019). According to Husna *et al*. (2023) ESBL is a Gram-negative bacteria from the *Enterobacter*iaceae family that carries the ESBL gene on its plasmid or chromosome and produces the β-lactamase enzyme which is capable of hydrolyzing β-lactam antibiotics. ESBL-producing *Enterobacter*iaceae show resistance to penicillin, aztreonam, and first to third generation cephalosporins, but are unable to hydrolyze cephamycin or carbapenems (Kholik *et al*., 2024; Shaikh *et al*., 2015). According to Castanheira *et al*. (2021), ESBL enzymes originally originated from TEM and SHV variants that underwent amino acid substitutions, causing changes in their substrate profile and allowing the enzyme to hydrolyze broad-spectrum cephalosporins.

The genes encoding ESBL enzymes can be grouped into several families, such as *bla*$_{\text{TEM}}$, *bla*$_{\text{SHV,}}$ and *bla*$_{\text{CTX-M}}$ (Husna *et al*., 2023). TEM-1 was the first plasmid carrying a β-lactamase gene transferred via transposon, first identified in the early 1960s from the blood culture of a patient named Temoniera in Greece (Bradford, 2001). This gene has spread widely and is now found in various species in the *Enterobacter*iaceae family, *Pseudomonas aeruginosa*, *Haemophilus influenzae*, and *Neisseria gonorrhoeae* (Rawat and Nair, 2010; Moses *et al*., 2024). The SHV-1 variant is most often found in *Klebsiella* spp. and *Escherichia coli*, while the CTX-M ESBL type is more dominant in *Escherichia coli*, *Klebsiella pneumoniae*, *Salmonella enterica* serovar Typhimurium, and *Shigella* spp. (Bialvaei *et al*., 2016). Plasmid-transferred OXA types and AmpC-type ESBLs were found in *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* isolates, respectively (Zhao *et al*., 2023).

The mechanism of ESBL enzymes is by damaging the β-lactam ring structure in β-lactam antibiotics, which is an important part of the mechanism of action of these antibiotics (Agustin *et al*., 2024). By damaging the β-lactam ring, bacteria become resistant to the effects of antibiotics (Doi *et al*., 2017). ESBLs are formed due to mutations in the β-lactamase gene, which allows bacteria to produce enzymes with a broader spectrum of activity (Mustika *et al*., 2024). This makes bacteria more able to resist previously effective antibiotics (Kaderabkova *et al*., 2022). Increasing antimicrobial resistance, especially from *Enterobacter*iaceae producing ESBL, poses a significant global health challenge because it often causes failure of empirical antibiotic therapy, leading to morbidity and mortality (Husna *et al*., 2023).

ESBL-producing bacteria, such as *Escherichia coli* and *Klebsiella pneumoniae*, have been identified not only in humans but also in various animal species, including small poultry such as quail (Martinez-Laorden *et al*., 2023). The quail farming environment can be an important reservoir for ESBL-producing bacteria due to the uncontrolled use of antibiotics in feed or drinking water, which provides selective pressure for resistant bacteria to survive and proliferate (Bush and Bradford, 2020). Several studies have shown that quail feces contain E. coli isolates carrying ESBL genes, such as *bla*$_{\text{CTX-M}}$ and *bla*$_{\text{TEM}}$, which have the potential to spread to the surrounding environment through soil, water, or human contact contamination (Cormier *et al*., 2019). This raises concerns about the potential for horizontal transfer of resistance genes to human pathogens through the food chain or direct exposure, reinforcing the importance of AMR surveillance in quail as part of the One Health approach.

ESBL-producing bacteria in quail can be transmitted to humans through several potential routes. The first route is through the consumption of quail-derived products, such as eggs and meat, contaminated with resistant bacteria if not cooked properly (Berman *et al*., 2023). The second route is direct contact between humans (farmers, farm workers) with quail or contaminated environments such as cages, feces, and drinking water, which facilitates direct transfer of resistant bacteria or plasmids (Widodo *et al*., 2024). The third route is environmental contamination through improperly managed farm waste disposal, which allows resistant bacteria to persist in groundwater, plants, or other animals in the surrounding area (Li *et al*., 2025; Prayudi *et al*., 2023). Horizontal transfer of resistance genes through plasmids exacerbates this risk, given that ESBL plasmids often carry additional genes that broaden the spectrum of resistance to various antibiotics. Therefore, quail not only act as passive reservoirs, but also as active vectors in the chain of AMR transmission to humans through food, direct contact, and environmental routes.

The role of quail in the transmission of ESBL-producing bacteria

Antibiotic use practices and sanitation measures in quail farming play a crucial role in determining the presence and spread of ESBL-producing bacteria (Agustin *et al*., 2025; Zhang *et al*., 2025). Non-selective administration of broad-spectrum antibiotics, either as mass treatment, prophylaxis, or growth promoter, encourages the selection of resistant bacteria such as *Escherichia coli* carrying the *bla*$_{\text{CTX-M}}$ and *bla*$_{\text{TEM}}$ genes (Founou *et al*., 2016). When antibiotics are used continuously or in subtherapeutic doses, resistant bacteria have a selection advantage to survive and multiply in the quail digestive tract (Manyi-Loh *et al*., 2018).

Poor sanitation practices such as inadequate cage hygiene, indiscriminate fecal management, and contaminated drinking water can accelerate the horizontal spread of ESBL-producing bacteria between individuals (Ziebe *et al*., 2025). Contaminated cage environments serve as reservoirs of resistant pathogens that can persist for long periods and increase the potential for cross-infection (Ansharieta *et al*., 2021; Ndlovu *et al*., 2023). The combination of indiscriminate antibiotic use and poor sanitation standards accelerates the rate of accumulation and distribution of ESBL bacteria not only within the quail population, but also into the external environment and the human food chain (Husna *et al*., 2023).

Quail farming environments are often reservoirs for ESBL bacteria due to several factors, including intensive use of antibiotics for disease prevention and growth, and inadequate sanitation (Hedman *et al*., 2020). A study by Dipineto *et al*. (2014) reported the isolation of ESBL-producing *Escherichia coli* from quail feces and cage environments in several farms. These isolates carried ESBL resistance genes, such as *bla*$_{\text{CTX-M}}$, which is widely known as the dominant ESBL-producing gene (Ariyanti *et al*., 2025). This suggests that the quail farming environment is a reservoir and potential for spreading these resistance genes.

In addition to *Escherichia coli* and *Klebsiella pneumoniae* is also found significantly in quail farming environments. The presence of ESBL-producing *Klebsiella pneumoniae* in the farming environment increases the risk of cross-contamination, especially if biosecurity and hygiene practices are not optimal (Zhang *et al*., 2025). Research by Wareth and Neubauer (2021) revealed that *Klebsiella pneumoniae* ESBL can survive in the farming environment and can even spread to water, soil, and livestock products consumed by humans. This contamination of the farming environment is at high risk of becoming a source of zoonotic infection if the ESBL bacteria are transferred through direct contact, consumption of undercooked animal products, or cross-contamination in the food supply chain. In addition, plasmids carrying ESBL genes can move between bacteria in this environment, accelerating the spread of resistance to other bacteria that may be more pathogenic to humans (Faridah *et al*., 2023; Madec *et al*., 2017). Controlling the presence of *Escherichia coli*, ESBL-producing *Klebsiella pneumoniae* in the quail farming environment should be a priority. Interventions include selective and controlled use of antibiotics, improving cage sanitation standards, routine microbiological surveillance, and educating farmers regarding the risk of AMR (Ramandinianto *et al*., 2020). This approach is important to break the cycle of transmission of ESBL bacteria from animals to humans and the wider environment (Farizqi *et al*., 2023; Matheou *et al*., 2025).

Mechanism of antimicrobial resistance development in quail

Antibiotics are often used in quail farming to prevent disease, treat various bacterial infections, increase growth, and accelerate production (Khairullah *et al*., 2022; Kasimanickam *et al*., 2021). Excessive or inappropriate use, such as giving antibiotics without an accurate diagnosis, using subtherapeutic doses in feed, or using antibiotics for prophylaxis without indications, can encourage the development of AMR (Caneschi *et al*., 2023). Bacteria exposed to antibiotics for a long period of time can experience natural selection, where only resistant strains survive and reproduce (Riwu *et al*., 2022). This condition creates an environment where resistant bacteria, including ESBL-producing *Proteus mirabilis*, can develop in the quail population (Chakkour *et al*., 2024).

ESBL-producing bacteria have been identified in various animal-derived food products (Ribeiro *et al*., 2024; Putri *et al*., 2024). Livestock such as quail act as reservoirs for ESBL-producing *Escherichia coli* bacteria (Mandujano-Hernández *et al*., 2024). The environment can be contaminated with resistant microorganisms through animal feces, allowing them to spread to surrounding areas (Cui *et al*., 2022). Quail also have the potential to be carriers of pathogenic bacteria that can cause zoonotic diseases in humans (Kobuszewska and Wysok, 2024). Several reports have shown cases of ESBL-producing *Escherichia coli* in quail, one of which is from Japan, with a prevalence of 90.9%. The study also revealed the presence of the CTX-M gene at 45.4% and the TEM gene at 68.18% (Arenas *et al*., 1999).

Quail are potential carriers of enteropathogenic bacteria that can spread pathogens to a wide range (Dipineto *et al*., 2014). β-lactam agents, including cephalosporins and carbapenems, and are often associated with resistance to other classes of antimicrobial agents (Watkins *et al*., 2019). According to research conducted by Elshebrawy *et al*. (2021) quails have resistance to penicillin (blaZ). ESBLs provide resistance to antibiotics such as Penicillin, Cephalosporin, and Aztreonam, and are often associated with resistance to other classes of antibiotics outside the penicillin group, including Fluoroquinolones, Aminoglycosides, Trimethoprim-sulfamethoxazole, and combinations of β-lactams with β-lactamase inhibitors (Thenmozhi *et al*., 2014; Riwu *et al*., 2024). ESBL-producing organisms generally exhibit a multidrug resistance phenotype. The ESBL mechanism is located on plasmids, which are extrachromosomal fragments of DNA that are essential for bacterial growth (Fang *et al*., 2024). Plasmids are self-replicating and contain virulence factors (resistance genes) (Rodríguez-Beltrán *et al*., 2021). The spread of resistance genes through plasmids can occur between bacteria of different species.

Food reservoirs include livestock and food products, where various AMR plasmids have been detected (Khairullah *et al*., 2023). Specific combinations of AMR genes and plasmids are more frequently found in food animals and food products (Ribeiro *et al*., 2024). These plasmids act as the main carriers of resistance genes such as ESBL/AmpC, carbapenemases, and colistins, including the IncF, IncI1, IncN, and IncHI1 types. In addition, IncF plasmid subtypes, such as F2:A-:B-, F33:A-:B-, or F31:A4:B-, have been widely detected in samples from food and livestock (Madec and Haenni, 2018).

Public health risks and consequences

ESBL-producing bacteria pose a serious threat to modern healthcare due to their ability to produce enzymes that inactivate most β-lactam antibiotics, especially third-generation cephalosporins (Mancuso *et al*., 2021). The production of ESBL enzymes by Gram-negative bacteria, especially *Escherichia coli* and *Klebsiella pneumoniae*, has led to an increase in cases of difficult-to-treat infections and complicates antibiotic therapy (Nivesvivat *et al*., 2018). Urinary Tract Infection (UTI) is one of the most common manifestations of infection caused by ESBL bacteria. Global data show an increasing prevalence of ESBL isolates from UTI patients, both in hospital and community settings. These infections are at high risk in patients with a history of previous antibiotic use, catheterization, and hospitalization (Balasubramanian *et al*., 2018). UTIs caused by ESBL bacteria tend to be more difficult to treat due to high antibiotic resistance, which contributes to increased treatment duration, complication rates, and costs of care (Flores-Mireles *et al*., 2015).

In addition to UTI, Bloodstream Infections (bacteremia) due to ESBL bacteria show significant mortality rates. Patients with ESBL bacteremia are often immunocompromised or have risk factors such as the use of invasive devices (central venous catheters) and a history of broad-spectrum antibiotic treatment. Delay in effective antibiotic therapy is associated with increased mortality (Tumbarello *et al*., 2007). A retrospective study by Rodríguez-Baño *et al*. (2018) confirmed that bloodstream infections caused by *Klebsiella pneumoniae* and ESBL-producing *Escherichia coli* are closely associated with poor clinical outcomes if initial antibiotic therapy is inappropriate. In addition to these two main types of infections, ESBL bacteria also cause wound, soft tissue, and respiratory tract infections, especially in high-risk patients or in nosocomial settings (Husna *et al*., 2023). Nosocomial infections involving ESBL bacteria are often difficult to treat due to limited therapeutic options due to multidrug resistance (Patel *et al*., 2008).

The main risk factors for ESBL infections include inappropriate use of broad-spectrum antibiotics, prolonged hospitalization, use of invasive devices, and cross-transmission in healthcare facilities (David *et al*., 2019). Therefore, infection control and antibiotic stewardship policies are crucial to suppress the spread of ESBL bacteria. In terms of therapy, carbapenems remain the main choice for treating severe ESBL infections, but the emergence of resistance to carbapenems is increasingly worrying (Tamma and Simner, 2018). New therapeutic alternatives such as new-generation β-lactam/β-lactamase inhibitor combinations, fosfomycin, and aminoglycosides have been used, but the choice of therapy must be based on the results of sensitivity tests and local epidemiology (Zhanel *et al*., 2018). Overall, infections caused by ESBL-producing bacteria, especially urinary tract infections and bloodstream infections, have been an increasing clinical challenge in the last decade. Optimal management requires early detection, strict infection control, and appropriate and responsible antibiotic treatment strategies (Khairullah *et al*., 2019).

Infections caused by ESBL-producing bacteria pose a much greater risk to vulnerable populations, including immunocompromised individuals, children, and the elderly (Theodorakis *et al*., 2024; Ugbo *et al*., 2024). These groups are predisposed to more severe infections, more serious complications, and less than optimal responses to antibiotic therapy. In immunocompromised patients, such as those with HIV/AIDS, transplant patients, or patients undergoing chemotherapy, the risk of ESBL infection is increased because their body's ability to fight pathogens is reduced (Duhaniuc *et al*., 2024). A study by Nguyen *et al*. (2015) showed that immunocompromised patients have a higher incidence of ESBL infections and a poorer prognosis than the general population. Moreover, these infections are often systemic and difficult to treat, which increases mortality and morbidity. Children, especially infants and young children, are also a group that is very susceptible to ESBL infections (Lukac *et al*., 2015). Their immature immune systems, coupled with risk factors such as neonatal hospitalization and inappropriate antibiotic use, increase the likelihood of infection by these multidrug-resistant bacteria (Blaschke *et al.*, 2009).

Research by Agegnehu *et al.* (2020) revealed an increased incidence of urinary tract infections and blood infections by ESBL bacteria in pediatric patients, with a higher rate of therapy failure compared to adult patients. Selective use of antibiotics and strict infection control policies are needed to protect this population. Meanwhile, the elderly are at high risk of being infected by ESBL bacteria due to a number of factors, such as decreased immune function associated with aging (immunosenescence), accompanying comorbidities, and frequent interactions with health facilities (Theodorakis *et al.*, 2024). The elderly who live in nursing homes or who are hospitalized have a greater chance of being exposed to and infected with ESBL bacteria (Blom *et al.*, 2016). Infections in the elderly also have the potential to cause serious complications, including sepsis and organ failure, and have an impact on increasing mortality rates (Patel *et al.*, 2008).

Overall, this vulnerable population faces a greater clinical burden from ESBL infections, requiring a more aggressive and coordinated approach to prevention and treatment (Wibisono *et al.*, 2020). Implementation of antibiotic stewardship programs, increased infection surveillance, and education of healthcare workers and families are essential to reduce the adverse impact of ESBL infections in this group (Tamma and Simner, 2018; Widodo *et al.*, 2023). The spread of ESBL-producing bacteria has reached a global scale, posing a major challenge to health systems in both developed and developing countries (Rawat and Nair, 2010). The widespread distribution of ESBL bacteria is not only through human-to-human transmission in healthcare facilities or communities, but also through zoonotic routes, namely transmission between animals and humans (Ribeiro *et al.*, 2024). Several studies have shown that livestock and wildlife can be reservoirs of ESBL bacteria, including quail, which are a major source of animal protein in some regions (Mandujano-Hernández *et al.*, 2024; Bastidas-Caldes *et al.*, 2022). Quail are often raised in large numbers with the use of antibiotics as a preventive or therapeutic measure, which can trigger the selection of ESBL-producing bacteria in these animal populations (Mo *et al.*, 2016).

A study by Salehi and Ghanbarpour (2010) identified ESBL-producing *Escherichia coli* isolates from quail that had similar resistance genes to human isolates, indicating the potential for cross-transmission between animals and humans. Direct contact with quail or consumption of contaminated processed products can be the main route of transmission of ESBL bacteria to humans (Widodo *et al.*, 2024). In addition, agricultural environments contaminated with livestock waste are also a source of the spread of resistant bacteria into the environment and ultimately to the human population (Manyi-Loh *et al.*, 2018).

This phenomenon reinforces the One Health concept that emphasizes the close relationship between human, animal and environmental health in the context of antimicrobial resistance (AMR) (Velazquez-Meza *et al.*, 2022). The spread of ESBL bacteria from animals to humans through zoonotic pathways significantly contributes to the increasing burden of AMR globally, complicating infection control efforts (Endale *et al.*, 2023). In addition, the spread of ESBL resistance genes through plasmids that are easily transferred between bacteria in various habitats makes this resistance spread rapidly from animal populations to humans and vice versa (Telli *et al.*, 2025). Therefore, monitoring and controlling the use of antibiotics in the livestock sector, including quail, is very important to limit the spread of ESBL bacteria and slow the rate of global AMR (Enshaie *et al.*, 2025).

Quail as livestock that has the potential to be a reservoir of ESBL-producing bacteria must receive attention in AMR control strategies (Ayim-Akonor *et al.*, 2025). Multisectoral interventions involving the human health, veterinary, and environmental sectors are needed to reduce the risk of zoonosis and the widespread spread of antimicrobial resistance (Dafale *et al.*, 2020). In the context of quail farming, *Escherichia coli* and *Klebsiella pneumoniae* are two main bacteria from the *Enterobacter*iaceae family that are often isolated and known to produce ESBL (Ramatla *et al.*, 2023). Both of these bacteria are known as opportunistic pathogens that can infect both humans and animals, and their presence in the farming environment is a major concern due to the potential for cross-species spread of AMR.

Monitoring and control measures

AMR monitoring in the poultry sector, especially quail, is essential to prevent the spread of difficult-to-treat infections in humans (Hedman *et al.*, 2020). Currently, data on the prevalence of ESBL-producing bacteria in quail are still limited. Therefore, an integrated surveillance system is needed to identify and track the presence and spread of these resistant bacteria (Perez and Villegas, 2015). Routine monitoring of pathogenic microorganisms in quail can provide a clearer picture of potential risks to public health and support more effective control policies (Oke *et al.*, 2025; Yunita *et al.*, 2020).

Efforts to prevent the spread of ESBL-producing bacteria in quail farming environments can be done through the implementation of strict biosecurity measures. This includes improving the standards of cage and equipment hygiene, good waste management, and restricting access to the farming area (Becker *et al.*, 2021). In addition, the use of antibiotics must be done wisely and based on veterinarian recommendations, in order to avoid the selection of resistant bacteria (Caneschi *et al.*, 2023). Alternative approaches such as the use of probiotics, vaccination, and improved nutrition can also be considered as more environmentally friendly and sustainable disease control strategies (Hancz, 2022).

Improvements are needed in the national regulatory framework to ensure that the monitoring, control, and prevention of antimicrobial resistance in quail farming are effective (Beber *et al.*, 2025). These regulations should include mandatory reporting of AMR cases, guidelines for the use of antimicrobials in the livestock sector, and sanctions against antibiotic misuse practices (Enshaie *et al.*, 2025). In addition, the integration of cross-sectoral policies through the One Health approach will strengthen coordination between human, animal, and environmental health sectors in addressing the threat of AMR holistically (Velazquez-Meza *et al.*, 2022).

Conclusion

Quails have significant potential as reservoirs of ESBL-producing bacteria, which are one of the main causes of increasing AMR in the livestock sector. Findings from various literatures indicate that quails can carry and spread ESBL-producing bacteria both through direct contact with humans and through environmental contamination, thus posing a serious risk to public health. Given the limited number of studies that specifically examine the dynamics of ESBL transmission in quail farming systems, further research is needed. This research should include microbiological surveillance, tracing the chain of transmission, and evaluating antibiotic use in quail farms. In addition, it is necessary to develop alternative, more sustainable farm management, including the implementation of strict biosecurity and the use of non-antibiotic antimicrobial agents. To overcome the spread of AMR from the livestock sector to the human population, a comprehensive One Health approach needs to be implemented. This includes strengthening antibiotic use policies in the veterinary sector, increasing public and farmer awareness, and implementing evidence-based interventions at the farm level. Without integrated efforts, the existence of quails as vectors of ESBL bacteria can be a real threat to the effectiveness of infection treatment and public health security in the future.

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Conflict of interest

The authors have declared no conflict of interest.

References

Adom, E., Bir, C., Lambert, L.H., 2023. A financial comparison of small-scale quail and laying hen farm enterprises. Poult. Sci. 102, 102507. doi: 10.1016/j.psj.2023.102507.

Afnani, D.A., Fatih, N., Effendi, M.H., Tyasningsih, W., Khairullah, A.R., Kurniawan, S.C., Silaen, O.S.M., Ramandinianto, S.C., Widodo, A., Riwu, K.H.P., 2022. Profile of Multidrug Resistance and Methicillin-Resistant *Staphylococcus aureus* (MRSA) isolated from cats in Surabaya, Indonesia. Biodiversitas 23, 5703–5709. doi: 10.13057/biodiv/d231121.

Agegnehu, A., Worku, M., Nigussie, D., Lulu, B., Tadesse, B.T., 2020. Pediatric Febrile Urinary Tract Infection Caused by ESBL Producing *Enterobacter*iaceae Species. Biomed. Res. Int. 2020, 6679029. doi: 10.1155/2020/6679029.

Agumah, N.B., Effendi, M.H., Tyasningsih, W., Witaningrum, A.M., Ugbo, E.N., Agumah, O.B., Ahmad, R.Z., Nwagwu, C.S., Ugbo, A.I., Khairullah, A.R., Moses, I.B., Yanestria, S.M., Riwu, K.H.P., Wasito, W., 2025. Distribution of cephalosporin-resistant Campylobacter species isolated from meat sold in Abakaliki, Nigeria. Open Vet. J. 15, 1615–1623. doi: 10.5455/OVJ.2025.v15.i4.13.

Agustin, A.L.D., Dameanti, F.N.A.E.P., Effendi, M.H., Tyasningsih, W., Khairullah, A.R., Kurniawan, S.C., Moses, I.B., Hasib, A., Mustika, Y.R. and Kinasih, K.N., 2024. Multidrug resistance to antibiotics in *Escherichia coli* bacteria isolated from bats on Lombok Island, Indonesia. J. Adv. Vet. Res. 14, 683–686.

Agustin, A.L.D., Khairullah, A.R., Effendi, M.H., Tyasningsih, W., Moses, I.B., Budiastuti, B., Plumeriastuti, H., Yanestria, S.M., Riwu, K.H.P., Dameanti, F.N.A.E.P., Wasito, W., Ahmad, R.Z., Widodo, A., Afnani, D.A., 2025. Ecological and public health dimensions of ESBL-producing *Escherichia coli* in bats: A One Health perspective. Vet. World 18, 1199–1213. doi: 10.14202/vetworld.2025.1199-1213.

Akpaka, P.E., Vaillant, A., Wilson, C., Jayaratne, P., 2021. Extended Spectrum Beta-Lactamase (ESBL) Produced by Gram-Negative Bacteria in Trinidad and Tobago. Int. J. Microbiol. 2021, 5582755. doi: 10.1155/2021/5582755.

Ansharieta, R., Effendi, M.H. and Plumeriastuti, H. 2021. Genetic Identification of Shiga Toxin Encoding Gene from Cases of Multidrug Resistance (MDR) *Escherichia coli* Isolated from Raw Milk. Trop. Anim. Sci. J. 44, 10–15. doi: 10.5398/tasj.2021.44.1.10.

Arenas, A., Vicente, S., Luque, I., Gomez-Villamandos, J.C., Astorga, R., Maldonado, A., Tarradas, C., 1999. Outbreak of septicaemic colibacillosis in Japanese quail (*Coturnix coturnix japonica*). Zentralbl. Veterinarmed. B. 46, 399–404. doi: 10.1046/j.1439-0450.1999.00246.x.

Ariyanti, T., Suhaemi, S., Mulyati, S., Sukatma, S., Sumirah, S., Noor, S.M., Rachmawati, F., Widiyanti, P.M., Sukmawinata, E., Andriani, A., Kusumaningtyas, E., Khairullah, A.R., 2025. Dissemination and phenotypic characterization of ESBL-producing *Escherichia coli* in Indonesia. Open Vet. J. 15(3), 1340–1348. doi: 10.5455/OVJ.2025.v15.i3.25.

Ayim-Akonor, M., Larbi, R.O., Owusu-Ntumy, D.D., Sasu, B.K., Asa, H.E.O., Odoom, T., 2025. Antimicrobial Susceptibility Profile and Extended-Spectrum Beta-Lactamase Phenotype of E. coli Isolated From Poultry. Int. J. Microbiol. 2025, 9468425. doi: 10.1155/ijm/9468425.

Bagh, J., Panigrahi, B., Panda, N., Pradhan, C.R., Mallik, B.K., Majhi, B., Rout, S.S., 2016. Body weight, egg production, and egg quality traits of gray, brown, and white varieties of Japanese quail (*Coturnix coturnix japonica*) in coastal climatic condition of Odisha. Vet. World 9, 832–836. doi: 10.14202/vetworld.2016.832-836.

Balasubramanian, S., Kuppuswamy, D., Padmanabhan, S., Chandramohan, V., Amperayani, S., 2018. Extended-spectrum Beta-lactamase-producing Community-acquired Urinary Tract Infections in Children: Chart Review of Risk Factors. J. Glob. Infect. Dis. 10, 222–225. doi: 10.4103/0974-777X.246391.

Bastidas-Caldes, C., Romero-Alvarez, D., Valdez-Vélez, V., Morales, R.D., Montalvo-Hernández, A., Gomes-Dias, C., Calvopiña, M., 2022. Extended-Spectrum Beta-Lactamases Producing *Escherichia coli* in South America: A Systematic Review with a One Health Perspective. Infect. Drug Resist. 15, 5759–5779. doi: 10.2147/IDR.S371845.

Beber, C.L., Aragrande, M., Canali, M., 2025. Policies and strategies to control antimicrobial resistance in livestock production: A comparative analysis of national action plans in European Union Member States. Health Policy 152, 105238. doi: 10.1016/j.healthpol.2024.105238.

Becker, E., Projahn, M., Burow, E., Käsbohrer, A., 2021. Are There Effective Intervention Measures in Broiler Production against the ESBL/AmpC Producer *Escherichia coli*? Pathogens 10, 608. doi: 10.3390/pathogens10050608.

Berman, T.S., Barnett-Itzhaki, Z., Berman, T., Marom, E., 2023. Antimicrobial resistance in food-producing animals: towards implementing a one health based national action plan in Israel. Isr. J. Health Policy Res. 12, 18. doi: 10.1186/s13584-023-00562-z.

Bialvaei, A.Z., Kafil, H.S., Asgharzadeh, M., Aghazadeh, M., Yousefi, M., 2016. CTX-M extended-spectrum β-lactamase-producing *Klebsiella* spp, *Salmonella* spp, *Shigella* spp and *Escherichia coli* isolates in Iranian hospitals. Braz. J. Microbiol. 47, 706–711. doi: 10.1016/j.bjm.2016.04.020.

Blaschke, A.J., Korgenski, E.K., Daly, J.A., LaFleur, B., Pavia, A.T., Byington, C.L., 2009. Extended-spectrum beta-lactamase-producing pathogens in a children's hospital: a 5-year experience. Am. J. Infect. Control 37, 435–441. doi: 10.1016/j.ajic.2008.09.019.

Blom, A., Ahl, J., Månsson, F., Resman, F., Tham, J., 2016. The prevalence of ESBL-producing *Enterobacter*iaceae in a nursing home setting compared with elderly living at home: a cross-sectional comparison. BMC Infect. Dis. 16, 111. doi: 10.1186/s12879-016-1430-5.

Bradford, P.A., 2001. Extended-spectrum beta-lactamases in the 21st century: characterization, epidemiology, and detection of this important resistance threat. Clin. Microbiol. Rev. 14, 933–951. doi: 10.1128/CMR.14.4.933-951.2001.

Bush, K., 2018. Past and Present Perspectives on β-Lactamases. Antimicrob. Agents Chemother. 62, e01076-18. doi: 10.1128/AAC.01076-18.

Bush, K., Bradford, P.A., 2020. Epidemiology of β-Lactamase-Producing Pathogens. Clin. Microbiol. Rev. 33, e00047-19. doi: 10.1128/CMR.00047-19.

Caneschi, A., Bardhi, A., Barbarossa, A., Zaghini, A., 2023. The Use of Antibiotics and Antimicrobial Resistance in Veterinary Medicine, a Complex Phenomenon: A Narrative Review. Antibiotics (Basel) 12, 487. doi: 10.3390/antibiotics12030487.

Castanheira, M., Simner, P.J., Bradford, P.A., 2021. Extended-spectrum β-lactamases: an update on their characteristics, epidemiology and detection. JAC Antimicrob. Resist. 3, dlab092. doi: 10.1093/jacamr/dlab092.

Chakkour, M., Hammoud, Z., Farhat, S., El Roz, A., Ezzeddine, Z., Ghssein, G., 2024. Overview of *Proteus mirabilis* pathogenicity and virulence. Insights into the role of metals. Front. Microbiol. 15, 1383618. doi: 10.3389/fmicb.2024.1383618.

Cormier, A., Zhang, P., Chalmers, G., Weese, J.S., 2019. Diversity of CTX-M-positive *Escherichia coli* recovered from animals across Canada. Vet. Microbiol. 231, 71–77. doi: 10.1016/j.vetmic.2019.02.031.

Cui, L., Zhao, X., Li, R., Han, Y., Hao, G., Wang, G., Sun, S., 2022. Companion Animals as Potential Reservoirs of Antibiotic Resistant Diarrheagenic *Escherichia coli* in Shandong, China. Antibiotics 11, 828. doi: 10.3390/antibiotics11060828.

Dafale, N.A., Srivastava, S., Purohit, H.J., 2020. Zoonosis: An Emerging Link to Antibiotic Resistance Under "One Health Approach". Indian J. Microbiol. 60, 139–152. doi: 10.1007/s12088-020-00860-z.

David, S., Reuter, S., Harris, S.R., Glasner, C., Feltwell, T., Argimon, S., Abudahab, K., Goater, R., Giani, T., Errico, G., Aspbury, M., Sjunnebo, S., EuSCAPE Working Group; ESGEM Study Group, Feil, E.J., Rossolini, G.M., Aanensen, D.M., Grundmann, H., 2019. Epidemic of carbapenem-resistant *Klebsiella pneumoniae* in Europe is driven by nosocomial spread. Nat. Microbiol. 4, 1919–1929. doi: 10.1038/s41564-019-0492-8.

Dipineto, L., Russo, T.P., Gargiulo, A., Borrelli, L., De Luca Bossa, L.M., Santaniello, A., Buonocore, P., Menna, L.F., Fioretti, A., 2014. Prevalence of enteropathogenic bacteria in common quail (*Coturnix coturnix*). Avian Pathol. 43, 498–500. doi: 10.1080/03079457.2014.966055.

Doi, Y., Iovleva, A., Bonomo, R.A., 2017. The ecology of extended-spectrum β-lactamases (ESBLs) in the developed world. J. Travel Med. 24, S44–S51. doi: 10.1093/jtm/taw102.

Duhaniuc, A., Păduraru, D., Nastase, E.V., Trofin, F., Iancu, L.S., Sima, C.M., Dorneanu, O.S., 2024. Multidrug-Resistant Bacteria in Immunocompromised Patients. Pharmaceuticals (Basel) 17, 1151. doi: 10.3390/ph17091151.

Elshebrawy, H.A., Mahros, M.A., Abd-Elghany, S.M., Elgazzar, M.M., Hayashidani, H., Sallam, K.I., 2021. Prevalence and molecular characterization of multidrug-resistant and β-lactamase producing *Salmonella enterica* serovars isolated from duck, pigeon, and quail carcasses in Mansoura, Egypt. LWT 149, 111834. doi: 10.1016/j.lwt.2021.111834.

Endale, H., Mathewos, M., Abdeta, D., 2023. Potential Causes of Spread of Antimicrobial Resistance and Preventive Measures in One Health Perspective-A Review. Infect. Drug Resist. 16, 7515–7545. doi: 10.2147/IDR.S428837.

Enshaie, E., Nigam, S., Patel, S., Rai, V., 2025. Livestock Antibiotics Use and Antimicrobial Resistance. Antibiotics 14, 621. doi: 10.3390/antibiotics14060621.

Fang, L., Chen, R., Li, C., Sun, J., Liu, R., Shen, Y., Guo, X., 2024. The association between the genetic structures of commonly incompatible plasmids in Gram-negative bacteria, their distribution and the resistance genes. Front. Cell. Infect. Microbiol. 14, 1472876. doi: 10.3389/fcimb.2024.1472876.

Farghaly, E.M., Samy, A., Roshdy, H., 2017. Wide Prevalence of Critically Important Antibiotic Resistance in Egyptian Quail Farms With Mixed Infections. Vet. Sci.: Res. Rev. 3, 17–24. doi: 10.17582/journal.vsrr/2017.3.1.17.24.

Faridah, H.D., Wibisono, F.M., Wibisono, F.J., Nisa, N., Fatimah, F., Effendi, M.H., Ugbo, E.N., Khairullah, A.R., Kurniawan, S.C., Silaen, O.S.M., 2023. Prevalence of the *bla*$_{\text{CTX-M}}$ and *bla*$_{\text{TEM}}$ genes among extended-spectrum beta lactamase-producing *Escherichia coli* isolated from broiler chickens in Indonesia. J. Vet. Res. 67, 179–186. doi: 10.2478/jvetres-2023-0025.

Farizqi, M.T.I., Effendi, M.H., Adikara, R.T.S., Yudaniayanti, I.S., Putra, G.D.S., Khairullah, A.R., Kurniawan, S.C., Silaen, O.S.M., Ramadhani, S., Millannia, S.K., Kaben, S.E., Waruwu, Y.K.K., 2023. Detection of extended-spectrum β-lactamase-producing *Escherichia coli* genes isolated from cat rectal swabs at Surabaya Veterinary Hospital, Indonesia. Vet. World 16, 1917–1925. doi: 10.14202/vetworld.2023.1917-1925.

Flores-Mireles, A.L., Walker, J.N., Caparon, M., Hultgren, S.J., 2015. Urinary tract infections: epidemiology, mechanisms of infection and treatment options. Nat. Rev. Microbiol. 13, 269–284. doi: 10.1038/nrmicro3432.

Founou, L.L., Founou, R.C., Essack, S.Y., 2016. Antibiotic Resistance in the Food Chain: A Developing Country-Perspective. Front. Microbiol. 7, 1881. doi: 10.3389/fmicb.2016.01881.

Ghimpețeanu, O.M., Pogurschi, E.N., Popa, D.C., Dragomir, N., Drăgotoiu, T., Mihai, O.D., Petcu, C.D., 2022. Antibiotic Use in Livestock and Residues in Food-A Public Health Threat: A Review. Foods 11, 1430. doi: 10.3390/foods11101430.

Giufrè, M., Mazzolini, E., Cerquetti, M., Brusaferro, S., Marisa Accogli, Fabrizio Agnoletti, Antonella Agodi, Giovanni Loris Alborali, Milena Arghittu, Francesco Auxilia, Martina Barchitta, Natasha Bosco, Alessandro Camporese, Virginia Carfora, Lucia Collini, Pierlanfranco D'Agaro, Rita De Rosa, Nicoletta Formenti, Alessia Franco, Raffaella Koncan, Paolo Lanzafame, Annarita Mazzariol, Chiara Moschioni, Stefania Pane, Lorenza Putignani, Thoma, C., 2021. Extended-spectrum β-lactamase-producing *Escherichia coli* from extraintestinal infections in humans and from food-producing animals in Italy: a 'One Health' study. Int. J. Antimicrob. Agents 58, 106433. doi: 10.1016/j.ijantimicag.2021.106433.

Golsha, R., Montazeri, M., Razaghi, N., Zade, M.E., 2021. Frequency of Beta-Lactamase Antibiotic Resistance Genes in *Escherichia coli* and *Klebsiella pneumoniae*. Ethiop. J. Health Sci. 31, 663–672. doi: 10.4314/ejhs.v31i3.24.

Hancz, C., 2022. Application of Probiotics for Environmentally Friendly and Sustainable Aquaculture: A Review. Sustainability 14, 15479. doi: 10.3390/su142215479.

Hedman, H.D., Vasco, K.A., Zhang, L., 2020. A Review of Antimicrobial Resistance in Poultry Farming within Low-Resource Settings. Animals (Basel) 10, 1264. doi: 10.3390/ani10081264.

Husna, A., Rahman, M.M., Badruzzaman, A.T.M., Sikder, M.H., Islam, M.R., Rahman, M.T., Alam, J., Ashour, H.M., 2023. Extended-Spectrum β-Lactamases (ESBL): Challenges and Opportunities. Biomedicines 11, 2937. doi: 10.3390/biomedicines11112937.

Kabir, S.M.L., 2010. Avian colibacillosis and salmonellosis: a closer look at epidemiology, pathogenesis, diagnosis, control and public health concerns. Int. J. Environ. Res. Public Health 7, 89–114. doi: 10.3390/ijerph7010089.

Kaderabkova, N., Bharathwaj, M., Furniss, R.C.D., Gonzalez, D., Palmer, T., Mavridou, D.A.I., 2022. The biogenesis of β-lactamase enzymes. Microbiology (Reading) 168, 001217. doi: 10.1099/mic.0.001217.

Kasimanickam, V., Kasimanickam, M., Kasimanickam, R., 2021. Antibiotics Use in Food Animal Production: Escalation of Antimicrobial Resistance: Where Are We Now in Combating AMR? Med. Sci. (Basel) 9, 14. doi: 10.3390/medsci9010014.

Khairullah, A.R., Kurniawan, S.C., Silaen, O.S.M., Effendi, M.H., Sudjarwo, S.A., Ramandinianto, S.C., Gelolodo, M.A., Widodo, A., Riwu, K.H.P., Kurniawati, D.A., Rehmank, S., 2023. Methicillin Resistant *Staphylococcus aureus* (MRSA) Isolation and mecA Gene Detection from Milk and Farmer Hand Swab in Tulungagung, Indonesia. Trop. Anim. Sci. J. 46, 231–238. doi: 10.5398/tasj.2023.46.2.231

Khairullah, A.R., Raharjo, D., Rahmahani, J., Suwarno, Tyasningsih, W., Harijani, N., 2019. Antibiotics resistant at *Staphylococcus aureus* and *Streptococcus* sp isolated from bovine mastitis in Karangploso, East Java, Indonesia. Indian J. Forensic Med. Toxicol. 13, 439–444. doi: 10.5958/0973-9130.2019.00329.3.

Khairullah, A.R., Rehman S, Sudjarwo, S.A., Effendi, M.H., Ramandinianto, S.C., Gololodo, M.A., Widodo, A., Riwu, K.H.P., Kurniawati, D.A., 2022. Detection of *mec*A gene and methicillin-resistant *Staphylococcus aureus* (MRSA) isolated from milk and risk factors from farms in Probolinggo, Indonesia. F1000Res. 11, 722. doi: 10.12688/f1000research.122225.3.

Kholik, K., Sukri, A., Riwu, K.H.P., Kurniawan, S.C., Khairullah, A.R., 2024. Detection of the chuA gene encoding the invasive enterohemorrhagic species *Escherichia coli* 0157:H7 using qPCR in horse feces samples on Sumbawa Island, Indonesia. Open Vet. J. 14, 1051–1058. doi: 10.5455/OVJ.2024.v14.i4.12.

Kobuszewska, A., Wysok, B., 2024. Pathogenic Bacteria in Free-Living Birds, and Its Public Health Significance. Animals (Basel) 14, 968. doi: 10.3390/ani14060968.

Li, S., Wang, K., Wang, D., Wang, H., Zhao, H., Pu, J., Wang, K., Li, C., 2025. Distribution and environmental dissemination of antibiotic resistance genes in poultry farms and surrounding ecosystems. Poult. Sci. 104, 104665. doi: 10.1016/j.psj.2024.104665.

Lokapirnasari, W.P., Al-Arif, M.A., Hidayatik, N., Safiranisa, A., Arumdani, D.F., Zahirah, A.I., Yulianto, A.B., Lamid, M., Marbun, T.D., Lisnanti, E.F., Baihaqi, Z.A., Khairullah, A.R., Kurniawan, S.C., Pelawi, E.B.S., Hasib, A., 2024. Effect of probiotics and acidifiers on feed intake, egg mass, production performance, and egg yolk chemical composition in late-laying quails, Vet. World 17, 462–469. doi: 10.14202/vetworld.2024.462-469.

Lokapirnasari, W.P., Dewi, A.R., Fathinah, A., Hidanah, S., Harijani, N., Soeharsono, Karimah, B., Andriani, A.D., 2017. Effect of probiotic supplementation on organic feed to alternative antibiotic growth promoter on production performance and economics analysis of quail. Vet. World 10, 1508–1514. doi: 10.14202/vetworld.2017.1508-1514.

Lukac, P.J., Bonomo, R.A., Logan, L.K., 2015. Extended-spectrum β-lactamase-producing *Enterobacter*iaceae in children: old foe, emerging threat. Clin. Infect. Dis. 60, 1389–1397. doi: 10.1093/cid/civ020.

Madec, J.Y., Haenni, M., 2018. Antimicrobial resistance plasmid reservoir in food and food-producing animals. Plasmid 99, 72–81. doi: 10.1016/j.plasmid.2018.09.001.

Madec, J.Y., Haenni, M., Nordmann, P., Poirel, L., 2017. Extended-spectrum β-lactamase/AmpC- and carbapenemase-producing *Enterobacter*iaceae in animals: a threat for humans? Clin. Microbiol. Infect. 23, 826–833. doi: 10.1016/j.cmi.2017.01.013.

Mancuso, G., Midiri, A., Gerace, E., Biondo, C., 2021. Bacterial Antibiotic Resistance: The Most Critical Pathogens. Pathogens 10, 1310. doi: 10.3390/pathogens10101310.

Mandujano-Hernández, A., Martínez-Vázquez, A.V., Paz-González, A.D., Herrera-Mayorga, V., Sánchez-Sánchez, M., Lara-Ramírez, E.E., Vázquez, K., de Jesús de Luna-Santillana, E., Bocanegra-García, V., Rivera, G., 2024. The Global Rise of ESBL-Producing *Escherichia coli* in the Livestock Sector: A Five-Year Overview. Animals (Basel) 14, 2490. doi: 10.3390/ani14172490.

Manyi-Loh, C., Mamphweli, S., Meyer, E., Okoh, A., 2018. Antibiotic Use in Agriculture and Its Consequential Resistance in Environmental Sources: Potential Public Health Implications. Molecules 23, 795. doi: 10.3390/molecules23040795.

Martinez-Laorden, A., Arraiz-Fernandez, C., Gonzalez-Fandos, E., 2023. Microbiological Quality and Safety of Fresh Quail Meat at the Retail Level. Microorganisms 11, 2213. doi: 10.3390/microorganisms11092213.

Matheou, A., Abousetta, A., Pascoe, A.P., Papakostopoulos, D., Charalambous, L., Panagi, S., Panagiotou, S., Yiallouris, A., Filippou, C., Johnson, E.O., 2025. Antibiotic Use in Livestock Farming: A Driver of Multidrug Resistance? Microorganisms 13, 779. doi: 10.3390/microorganisms13040779.

Mo, S.S., Kristoffersen, A.B., Sunde, M., Nødtvedt, A., Norström, M., 2016. Risk factors for occurrence of cephalosporin-resistant *Escherichia coli* in Norwegian broiler flocks. Prev. Vet. Med. 130, 112–118. doi: 10.1016/j.prevetmed.2016.06.011.

Mohammed, B.R., Ejiofor, C., 2015. The prospects and limitations of Japanese quail (*Coturnix coturnix japonica*) production in Nigeria-A review. Int. J. Multidiscip. Curr. Res. 3, 920–926.

Morris, K.M., Hindle, M.M., Boitard, S., Burt, D.W., Danner, A.F., Eory, L., Forrest, H.L., Gourichon, D., Gros, J., Hillier, L.W., Jaffredo, T., Khoury, H., Lansford, R., Leterrier, C., Loudon, A., Mason, A.S., Meddle, S.L., Minvielle, F., Minx, P., Pitel, F., Seiler, J.P., Shimmura, T., Tomlinson, C., Vignal, A., Webster, R.G., Yoshimura, T., Warren, W.C., Smith, J., 2020. The quail genome: insights into social behaviour, seasonal biology and infectious disease response. BMC Biol. 18, 14. doi: 10.1186/s12915-020-0743-4.

Moses, I.B., Mbam, C.O., Odi, C.O., Effendi, M.H., Khairullah, A.R., Witaningrum, A.M., Oke, B., Ezea, M.C., Rehman, S., 2024. Isolation and Characterization of Multidrug-resistant *Enterobacteri*aceae from Kitchen Sponges: An Under-recognized Public Health Problem. Indian J. Public Health 68, 520–525. doi: 10.4103/ijph.ijph_924_23.

Mulani, M.S., Kamble, E.E., Kumkar, S.N., Tawre, M.S., Pardesi, K.R., 2019. Emerging Strategies to Combat ESKAPE Pathogens in the Era of Antimicrobial Resistance: A Review. Front. Microbiol. 10, 539. doi: 10.3389/fmicb.2019.00539.

Mustika, Y.R., Kinasih, K.N., Effendi, M.H., Puspitasari, Y., Kurniawan, S.C., Khairullah, A.R., Samodra, M.E.E., Hasib, A., Agustin, A.L.D., Moses, I.B., Silaen, O.S.M., 2024. Molecular detection of extended-spectrum β-lactamase-producing *Escherichia coli* from bat caves on Lombok Island. Open Vet. J. 14, 699–706. doi: 10.5455/OVJ.2024.v14.i2.10.

Muteeb, G., Rehman, M.T., Shahwan, M., Aatif, M., 2023. Origin of Antibiotics and Antibiotic Resistance, and Their Impacts on Drug Development: A Narrative Review. Pharmaceuticals (Basel) 16, 1615. doi: 10.3390/ph16111615.

Ndlovu, T., Kgosietsile, L., Motshwarakgole, P., Ndlovu, S.I., 2023. Evaluation of Potential Factors Influencing the Dissemination of Multidrug-Resistant *Klebsiella pneumoniae* and Alternative Treatment Strategies. Trop. Med. Infect. Dis. 8, 381. doi: 10.3390/tropicalmed8080381.

Nguyen, M.L., Toye, B., Kanji, S., Zvonar, R., 2015. Risk Factors for and Outcomes of Bacteremia Caused by Extended-Spectrum ß-Lactamase-Producing *Escherichia coli* and *Klebsiella* Species at a Canadian Tertiary Care Hospital. Can. J. Hosp. Pharm. 68, 136–143. doi: 10.4212/cjhp.v68i2.1439.

Nivesvivat, T., Piyaraj, P., Thunyaharn, S., Watanaveeradej, V., Suwanpakdee, D., 2018. Clinical epidemiology, risk factors and treatment outcomes of extended-spectrum beta-lactamase producing *Enterobacter*iaceae bacteremia among children in a Tertiary Care Hospital, Bangkok, Thailand. BMC Res. Notes 11, 624. doi: 10.1186/s13104-018-3729-3.

Oke, O.E., Oliyide, K.M., Akosile, O.A., Oni, A.I., Adekunle, E.O., Oyebanji, B.O., Aremu, O.P., Adeoba, I.M., Eletu, T.A., Daramola, J.O., 2025. Innovations in Quail Welfare: Integrating Environmental Enrichment, Nutrition and Genetic Advances for Improved Health and Productivity. Vet. Med. Sci. 11, e70424. doi: 10.1002/vms3.70424.

Palmeira, J.D., Ferreira, H.M.N., 2020. Extended-spectrum beta-lactamase (ESBL)-producing *Enterobacter*iaceae in cattle production - a threat around the world. Heliyon 6, e03206. doi: 10.1016/j.heliyon.2020.e03206.

Patel, G., Huprikar, S., Factor, S.H., Jenkins, S.G., Calfee, D.P., 2008. Outcomes of carbapenem-resistant *Klebsiella pneumoniae* infection and the impact of antimicrobial and adjunctive therapies. Infect. Control Hosp. Epidemiol. 29, 1099–1106. doi: 10.1086/592412.

Perez, F., Villegas, M.V., 2015. The role of surveillance systems in confronting the global crisis of antibiotic-resistant bacteria. Curr. Opin. Infect. Dis. 28, 375–383. doi: 10.1097/QCO.0000000000000182.

Prayudi, S.K.A., Effendi, M.H., Lukiswanto, B.S., Az Zah-Ra, R.L., Benjamin, M.I., Kurniawan, S.C., Khairullah, A.R., Silaen, O.S.M., Lisnanti, E.F., Baihaqi, Z.A., Widodo, A., Riwu, K.H. P., 2023. Detection of Genes on *Escherichia coli* Producing Extended Spectrum β-lactamase Isolated from the Small Intestine of Ducks in Traditional Markets Surabaya City, Indonesia. J. Adv. Vet. Res. 13, 1600–1608.

Putri, M.F.R., Khairullah, A.R., Effendi, M.H., Wibisono, F.J., Hasib, A., Moses, I. B., Fauziah, I., Kusala, M.K.J., Raissa, R., Yanestria, S.M., 2024. Detection of the CTX-M Gene Associated with Extended-Spectrum β-Lactamase (ESBL) in Broiler Chickens in Surabaya Traditional Markets. J. Med. Vet. 7, 320–334. doi: 10.20473/jmv.vol7.iss2.2024.320-334.

Rahman, M.T., Sobur, M.A., Islam, M.S., Ievy, S., Hossain, M.J., El Zowalaty, M.E., Rahman, A.T., Ashour, H.M., 2020. Zoonotic Diseases: Etiology, Impact, and Control. Microorganisms 8, 1405. doi: 10.3390/microorganisms8091405.

Ramandinianto, S.C., Khairullah, A.R., Effendi, M.H., Hestiana, E.P., 2020. Profile of multidrug resistance (MDR) and methicillin resistant *Staphylococcus aureus* (MRSA) on dairy farms in east Java province, Indonesia. Indian J. Forensic Med. Toxicol. 14, 3439–3445. doi: 10.37506/ijfmt.v14i4.12157.

Ramatla, T., Mafokwane, T., Lekota, K., Monyama, M., Khasapane, G., Serage, N., Nkhebenyane, J., Bezuidenhout, C., Thekisoe, O., 2023. "One Health" perspective on prevalence of co-existing extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* and *Klebsiella pneumoniae*: a comprehensive systematic review and meta-analysis. Ann. Clin. Microbiol. Antimicrob. 22, 88. doi: 10.1186/s12941-023-00638-3.

Rawat, D., Nair, D., 2010. Extended-spectrum β-lactamases in Gram Negative Bacteria. J. Glob. Infect. Dis. 2, 263–274. doi: 10.4103/0974-777X.68531.

Retes, P.L., Neves, D.G.D., Bernardes, L.F., Alves, V.V., Gonçalves, N.C., Lima, D.R., Alvarenga, R.R., Pereira, B.A., Seidavi, A., Zangeronimo, M.G., 2022. Dietary crude protein levels during growth phase affects reproductive characteristics but not reproductive efficiency of adult male Japanese quails. Anim. Biosci. 35, 385–398. doi: 10.5713/ab.21.0060.

Ribeiro, L.F., Nespolo, N.M., Rossi, G.A.M., Fairbrother, J.M., 2024. Exploring Extended-Spectrum Beta-Lactamase (ESBL)-Producing *Escherichia coli* in Food-Producing Animals and Animal-Derived Foods. Pathogens 13, 346. doi: 10.3390/pathogens13040346.

Riwu, K.H.P., Effendi, M.H., Rantam, F.A., Khairullah, A.R., Kurniawan, S.C., Kurniawan, A., Moses, I.B., Hasib, A., Widodo, A., Yanestria, S.M., Silaen, O.S.M., Shehzad, A., 2024. Molecular detection of *bla*$_{\text{TEM}}$ gene for encoding extended spectrum beta-lactamase (ESBL) on *Escherichia coli* isolated from deer feces in Indonesia. J. Adv. Vet. Res, 14, 722–726.

Riwu, K.H.P., Rantam, F.A., Effendi, M.H., Khairullah, A.R., Widodo, A., Kurniawan, S.C., Ugbo, E.N., 2022. Molecular detection of extended spectrum β-lactamase producing *Klebsiella pneumoniae* from wild deer. Biodiversitas 23, 4256–4262. doi: 10.13057/biodiv/d230849.

Rodríguez-Beltrán, J., DelaFuente, J., León-Sampedro, R., MacLean, R.C., San Millán, Á., 2021. Beyond horizontal gene transfer: the role of plasmids in bacterial evolution. Nat. Rev. Microbiol. 19, 347–359. doi: 10.1038/s41579-020-00497-1.

Rodríguez-Baño, J., Gutiérrez-Gutiérrez, B., Machuca, I., Pascual, A., 2018. Treatment of Infections Caused by Extended-Spectrum-Beta-Lactamase-, AmpC-, and Carbapenemase-Producing *Enterobacter*iaceae. Clin. Microbiol. Rev. 31, e00079-17. doi: 10.1128/CMR.00079-17.

Salehi, M., Ghanbarpour, R., 2010. Phenotypic and genotypic properties of *Escherichia coli* isolated from colisepticemic cases of Japanese quail. Trop. Anim. Health Prod. 42, 1497–504. doi: 10.1007/s11250-010-9583-5.

Shaikh, S., Fatima, J., Shakil, S., Rizvi, S.M., Kamal, M.A., 2015. Antibiotic resistance and extended spectrum beta-lactamases: Types, epidemiology and treatment. Saudi J. Biol. Sci. 22, 90–101. doi: 10.1016/j.sjbs.2014.08.002.

Song, K., Li, J., Tan, Y., Yu, J., Li, M., Shen, S., Peng, L., Yi, P., Fu, B., 2022. Xiaochaihu Decoction Treatment of Chicken Colibacillosis by Improving Pulmonary Inflammation and Systemic Inflammation. Pathogens 12, 30. doi: 10.3390/pathogens12010030.

Tamma, P.D., Simner, P.J., 2018. Phenotypic Detection of Carbapenemase-Producing Organisms from Clinical Isolates. J. Clin. Microbiol. 56, e01140-18. doi: 10.1128/JCM.01140-18.

Telli, N., Telli, A. E., Biçer, Y., Turkal, G., 2025. Extended-Spectrum-Beta-Lactamase (ESBL)-Producing *Escherichia coli* in Laying Hens: Slaughterhouse Prevalence and Antibiotic Resistance Patterns. Antibiotics 14, 351. doi: 10.3390/antibiotics14040351.

Thenmozhi, S., Moorthy, K., Sureshkumar, B.T., Suresh, M., 2014. Antibiotic resistance mechanism of ESBL producing *Enterobacter*iaceae in clinical field: a review. Int. J. Pure Appl. Biosci. 2, 207–226.

Theodorakis, N., Feretzakis, G., Hitas, C., Kreouzi, M., Kalantzi, S., Spyridaki, A., Boufeas, I.Z., Sakagianni, A., Paxinou, E., Verykios, V.S., Nikolaou, M., 2024. Antibiotic Resistance in the Elderly: Mechanisms, Risk Factors, and Solutions. Microorganisms 12, 1978. doi: 10.3390/microorganisms12101978.

Tseng, C.H., Liu, C.W., Liu, P.Y., 2023. Extended-Spectrum β-Lactamases (ESBL) Producing Bacteria in Animals. Antibiotics (Basel) 12, 661. doi: 10.3390/antibiotics12040661.

Tumbarello, M., Sanguinetti, M., Montuori, E., Trecarichi, E.M., Posteraro, B., Fiori, B., Citton, R., D'Inzeo, T., Fadda, G., Cauda, R., Spanu, T., 2007. Predictors of mortality in patients with bloodstream infections caused by extended-spectrum-beta-lactamase-producing *Enterobacter*iaceae: importance of inadequate initial antimicrobial treatment. Antimicrob. Agents Chemother. 51, 1987–1994. doi: 10.1128/AAC.01509-06.

Ugbo, E.N., Ugbo, A.I., Effendi, M.H., Tyasningsih, W., Agumah, B.N., Nwachi, A.C., Khairullah, A.R., Moses, I.B., Raissa, R., Yanestria, S.M., 2024. Prevalence and molecular detection of mecA and lukD genes from livestock-associated methicillin-resistant *Staphylococcus aureus* isolated in raw chicken meats sold in Abakaliki, Nigeria. Open Vet. J. 14, 3327–3335. doi: 10.5455/OVJ.2024.v14.i12.17.

Velazquez-Meza, M.E., Galarde-López, M., Carrillo-Quiróz, B., Alpuche-Aranda, C.M., 2022. Antimicrobial resistance: One Health approach. Vet. World 15, 743–749. doi: 10.14202/vetworld.2022.743-749.

Wareth, G., Neubauer, H., 2021. The Animal-foods-environment interface of *Klebsiella pneumoniae* in Germany: an observational study on pathogenicity, resistance development and the current situation. Vet. Res. 52, 16. doi: 10.1186/s13567-020-00875-w.

Watkins, R.R., Holubar, M., David, M.Z., 2019. Antimicrobial resistance in methicillin-resistant *Staphylococcus aureus* to newer antimicrobial agents. Antimicrob. Agents Chemother. 63, e01216-19. doi: 10.1128/AAC.01216-19.

Wegner, M., Kokoszyński, D., Żochowska-Kujawska, J., Kotowicz, M., Włodarczyk, K., Banaszewska, D., Batkowska, J., 2024. The influence of genotype and sex on carcass composition, meat quality, digestive system morphometry and leg bone dimensions in Japanese quails (*C. coturnix japonica*). Sci. Rep. 14, 19501. doi: 10.1038/s41598-024-70496-2.

Wibisono, F.J., Sumiarto, B., Untari, T., Effendi, M.H., Permatasari, D.A., Witaningrum, A.M., 2020. Short communication: Pattern of antibiotic resistance on extended-spectrum beta-lactamases genes producing *Escherichia coli* on laying hens in Blitar, Indonesia. Biodiversitas 21, 4631–4635. doi: 10.13057/biodiv/d211022.

Wibisono, F.J., Effendi, M.H., Wibisono, F.M., 2022. Occurrence, antimicrobial resistance, and potential zoonosis risk of avian pathogenic *Escherichia coli* in Indonesia: A review. Int. J. One Health 8, 76–85. doi: 10.14202/IJOH.2022.76-85.

Widodo, A., Effendi, M.H., Khairullah, A.R., 2020. Extended-spectrum beta-lactamase (ESBL)-producing *Escherichia coli* from livestock. Sys. Rev. Pharm. 11, 382–392. doi: 10.31838/srp.2020.7.57.

Widodo, A., Khairullah, A.R., Effendi, M.H., Moses, I.B., Agustin, A.L.D., 2024. Extended-spectrum β-lactamase-producing *Escherichia coli* from poultry: A review. Vet. World 17, 2017–2027. doi: 10.14202/vetworld.2024.2017-2027.

Widodo, A., Lamid, M., Effendi, M.H., Khailrullah, A.R., Kurniawan, S.C., Silaen, O.S.M., Riwu, K.H.P., Yustinasari, L.R., Afnani, D.A., Dameanti, F.N.A.E.P., Ramandinianto, S.C., 2023. Antimicrobial resistance characteristics of multidrug resistance and extended-spectrum beta-lactamase producing *Escherichia coli* from several dairy farms in Probolinggo, Indonesia. Biodiversitas 24, 215–221. doi: 10.13057/biodiv/d240126.

Yunita, M.N., Effendi, M.H., Rahmaniar, R.P., Arifah, S., Yanestria, S.M., 2020. Identification of spa gene for strain typing of methicillin resistant *Staphylococcus aureus* (MRSA) isolated from nasal swab of dogs. Biochem. Cell. Arch. 20, 2999–3004. doi: 10.35124/bca.2020.20.S1.2999.

Zhanel, G.G., Lawrence, C.K., Adam, H., Schweizer, F., Zelenitsky, S., Zhanel, M., Lagacé-Wiens, P.R.S., Walkty, A., Denisuik, A., Golden, A., Gin, A.S., Hoban, D.J., Lynch, J.P. 3rd, Karlowsky, J.A., 2018. Imipenem-Relebactam and Meropenem-Vaborbactam: Two Novel Carbapenem-β-Lactamase Inhibitor Combinations. Drugs 78, 65–98. doi: 10.1007/s40265-017-0851-9.

Zhang, S., Yang, J., Abbas, M., Yang, Q., Li, Q., Liu, M., Zhu, D., Wang, M., Tian, B., Cheng, A., 2025. Threats across boundaries: the spread of ESBL-positive *Enterobacter*iaceae bacteria and its challenge to the "one health" concept. Front. Microbiol. 16, 1496716. doi: 10.3389/fmicb.2025.1496716.

Zhao, Q., Sha, L., Wu, Z., Meng, L., Yang, F., Wu, L., Yu, C., Zhang, H., Yu, J., Jin, Z., 2023. Evolution of carbapenem resistance in *Klebsiella pneumoniae* and *Escherichia coli* carrying *bla*$_{\text{NDM-1}}$ gene: imipenem exposure results in sustained resistance memory of strains in vitro. Ann. Clin. Microbiol. Antimicrob. 22, 46. doi: 10.1186/s12941-023-00598-8.

Ziebe, S.D., Ngom, R.V., Akoussa, A.M.M., Bogning, H.P., Zangue, H.A., 2025. Impact of Biosecurity on Production Performance and Antimicrobial Usage in Broiler Farms in Cameroon. Animals 15, 1771. doi: 10.3390/ani15121771.