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The role of dogs and cats as reservoirs of antimicrobial resistance: A molecular and epidemiological review with focus on Southeast Asian context

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ABSTRACT

Antimicrobial resistance (AMR) is an increasingly complex global threat that transcends the boundaries of the human health sector. Within the One Health framework, companion animals such as dogs and cats are receiving increased attention due to their close proximity to humans and their potential role as reservoirs of resistant bacteria. Intense interactions in domestic environments, antibiotic exposure in veterinary clinical practice, and linkages with environmental factors make companion animals an integral part of the AMR epidemiological network. This review aimed to comprehensively examine the role of dogs and cats as reservoirs of antimicrobial resistance, with emphasis on molecular characterization of resistance genes and identification of environmental risk factors that contribute to their dissemination. This article discusses key findings related to the most frequently reported resistance genes in commensal and pathogenic bacteria from companion animals, including genes associated with resistance to β-lactams, tetracyclines, aminoglycosides, and fluoroquinolones. Furthermore, molecular mechanisms such as the involvement of mobile genetic elements and phylogenetic relatedness among isolates from animals and humans are analysed to assess the potential for cross-host transmission. Environmental risk factors, including antibiotic use practices, household sanitation, animal population density, and intensity of human-animal contact, are discussed as important determinants in maintaining and spreading antimicrobial resistance. These findings indicate that dogs and cats not only serve as passive hosts, but also as active components in the ecology of AMR. Overall, this review affirms the need to integrate companion animals into One Health-based surveillance strategies, control measures, and antimicrobial resistance policies to sustainably reduce public health risks.

Introduction

Antimicrobial resistance (AMR) has evolved into one of the most serious global health challenges of the 21st century (Coque *et al*., 2023). This phenomenon threatens the effectiveness of antibiotics that have served as the foundation for infectious disease control in humans and animals for several decades (Muteeb *et al*., 2025). From a One Health perspective, AMR is understood as a cross-sectoral problem involving close interconnections among human health, animal health, and the environment (Al-Khalaifah *et al*., 2025). The widespread and often irrational use of antimicrobials across various sectors has created selection pressure that drives the emergence and spread of resistant bacteria, making AMR a complex and dynamic microbial ecology issue (Ahmed *et al*., 2024).

Within the One Health ecosystem, attention to the role of animals is not limited only to production livestock, but is increasingly directed toward companion animals, particularly dogs and cats (Overgaauw *et al*., 2020). The increasing population of companion animals in urban areas, accompanied by high-intensity interactions between animals and humans, makes dogs and cats important components in the AMR epidemiological network (Marco-Fuertes *et al*., 2022). Companion animals live in the same environments as humans, share domestic spaces, and are frequently exposed to antibiotics either through clinical therapy or indirect contact with contaminated environments (Vercelli *et al*., 2025). These conditions create opportunities for colonization by resistant bacteria and cross-host exchange of resistance genes (Monteiro *et al*., 2025).

Numerous reports indicate an increase in resistant bacterial isolates identified in dogs and cats, both in animals with clinical symptoms and in apparently healthy animals (Khairullah *et al*., 2023; Yildiz and Demirbilek, 2024). Enteric bacteria such as *Escherichia coli* and *Enterococcus* spp., as well as opportunistic pathogens such as Staphylococcus and *Klebsiella*, have been reported to carry resistance genes against various clinically important antibiotic classes (Afnani *et al*., 2025; Frenzer *et al*., 2024; Moon *et al*., 2023; Ojasanya *et al*., 2025). These findings confirm that companion animals not only serve as temporary hosts but also have the potential to become stable reservoirs for resistant bacteria and their genetic determinants. The presence of resistant bacteria in healthy animals demonstrates that AMR can persist outside the context of active infection and potentially spread undetected (Cave *et al*., 2021).

Although epidemiological evidence regarding AMR in companion animals continues to accumulate, understanding of the molecular characterization of resistance genes and the underlying environmental risk factors remains incomplete (Zelaya *et al*., 2025). Many studies focus on phenotypic detection of resistance, while information regarding resistance gene types, mobile genetic elements, and phylogenetic relationships among isolates remains limited, especially in developing countries (Partridge *et al*., 2018). Furthermore, environmental factors such as antibiotic use practices in veterinary clinics, domestic environmental sanitation, animal population density, and closeness of human-animal contact are often not analysed in an integrated manner (Graham *et al*., 2019). This knowledge gap hinders accurate risk assessment and the formulation of evidence-based AMR control strategies (Ahmad *et al*., 2023).

Based on this background, this review aimed to systematically examine the role of dogs and cats as reservoirs of antimicrobial resistance, with emphasis on molecular characterization of resistance genes and analysis of environmental risk factors that contribute to their dissemination. The scope of the review includes identification of major resistance genes reported in bacteria from companion animals, molecular mechanisms that support resistance spread, and environmental factors and human practices that influence AMR dynamics. With a One Health-based approach, this review is expected to provide a more complete conceptual framework

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for understanding the contribution of companion animals to AMR epidemiology and support the development of integrated and sustainable control strategies.

Antimicrobial resistance concepts in a one health perspective

Antimicrobial resistance represents a biological phenomenon that develops through complex interactions among microorganisms, antibiotic selective pressure, and the interconnections of humans, animals, and the environment within a unified health ecosystem.

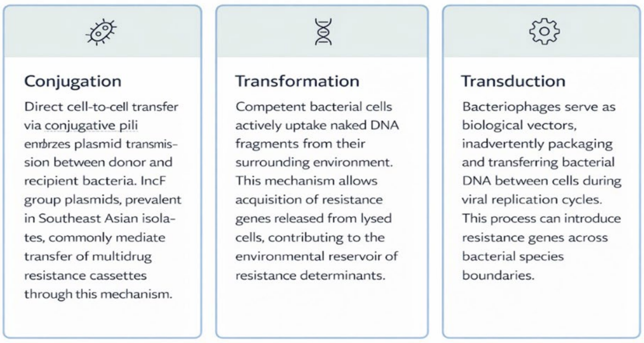
Definition and basic mechanisms of AMR

Antimicrobial resistance results from bacteria's adaptive capacity to reduce or eliminate antimicrobial activity through specific biological mechanisms (Reygaert, 2018). This phenomenon develops as a response to selective pressure imposed by antibiotic exposure and directly contributes to therapeutic failure in bacterial infections affecting both humans and animals (Salam *et al*., 2023).

Mechanistically, AMR can be classified into intrinsic and acquired resistance. Intrinsic resistance is an inherent trait of certain bacterial species, independent of prior antibiotic exposure, relating to fundamental cellular characteristics such as cell wall structure, membrane permeability, or absence of antibiotic molecular targets (Belay *et al*., 2024). For instance, Gram-negative bacteria possess intrinsic resistance to vancomycin due to the antibiotic's inability to penetrate the outer membrane (Maher and Hassan, 2023).

Acquired resistance emerges from genetic changes enabling sensitive bacteria to become resistant through two primary routes: chromosomal mutations or acquisition of resistance genes from external sources (Galgano *et al*., 2025). Chromosomal mutations typically affect genes involved in antibiotic binding, essential metabolic pathways, or protein expression regulation (Lin *et al*., 2025). For example, fluoroquinolone resistance frequently develops through point mutations in *gyr*A and *par*C genes encoding DNA *gyr*ase and topoisomerase IV (Kivata *et al*., 2019).

The mechanism with the broadest epidemiological impact is horizontal gene transfer (HGT), enabling genetic material transfer among bacteria lacking direct lineage relationships (Nielsen *et al*., 2014). Through conjugation, transformation, or transduction, bacteria acquire resistance genes located on mobile genetic elements including plasmids, transposons, and integrons (Tao *et al*., 2022) (Figure 1). A landmark study by Liu *et al*. demonstrated that the plasmid-mediated colistin resistance gene *mcr*-1 spread across multiple bacterial species and geographic regions within months of its discovery, exemplifying HGT's role in rapid resistance dissemination (Lin *et al*., 2022).



Conjugation

Direct cell-to-cell transfer via conjugative pili enrbrzes plasmid transmission between donor and recipient bacteria. IncF group plasmids, prevalent in Southeast Asian isolates, commonly mediate transfer of multidrug resistance cassettes through this mechanism.

Transformation

Competent bacterial cells actively uptake naked DNA fragments from their surrounding environment. This mechanism allows acquisition of resistance genes released from lysed cells, contributing to the environmental reservoir of resistance determinants.

Transduction

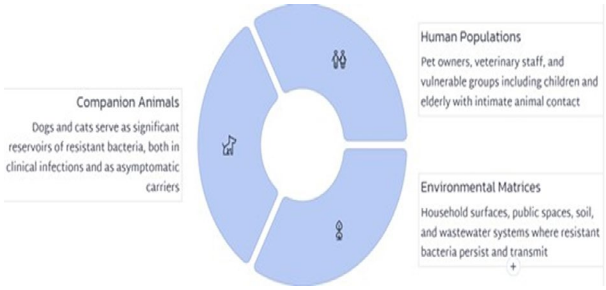
Bacteriophages serve as biological vectors, inadvertently packaging and transferring bacterial DNA between cells during viral replication cycles. This process can introduce resistance genes across bacterial species boundaries.

Figure 1. Molecular mechanisms of horizontal gene transfer in antimicrobial resistance dissemination.

In the context of companion animals, the presence of commensal and pathogenic bacteria carrying both intrinsic and acquired resistance mechanisms positions dogs and cats as significant AMR reservoirs (Monteiro *et al*., 2025). Intensive interactions with humans and domestic environments create optimal conditions for resistance selection and horizontal transfer of resistance determinants, reinforcing the relevance of these mechanisms within the One Health framework (McEwen and Collignon, 2018).

One Health and human–animal–environment interconnections

AMR transmission within the One Health framework occurs through complex interactions among dogs, cats, humans, and interconnected environments (Figure 2). Companion animals experience multidirectional exposure to resistant bacteria through contact with humans, contaminated surfaces, and public environments including parks, veterinary facilities, and commercial pet establishments (Jin *et al*., 2023).



Companion Animals

Dogs and cats serve as significant reservoirs of resistant bacteria, both in clinical infections and as asymptomatic carriers

Human Populations

Pet owners, veterinary staff, and vulnerable groups including children and elderly with intimate animal contact

Environmental Matrices

Household surfaces, public spaces, soil, and wastewater systems where resistant bacteria persist and transmit

Figure 2. One Health framework for AMR dynamics in companion animal-human-environment interface.

The environment serves as a critical intermediary compartment enabling bacterial persistence and redistribution (Bengtsson-Palme *et al*., 2018). Companion animal faeces, inadequately managed household waste, and environmental antibiotic residues create contamination networks facilitating resistance gene dissemination (Zalewska *et al*., 2021). A study in Surabaya revealed that 38.7% of soil samples from areas frequented by companion animals tested positive for ESBL-producing bacteria, with resistance gene profiles matching those in local animal and human populations (Kristianingtyas *et al*., 2021).

Importantly, AMR transmission frequently occurs through asymptomatic colonization rather than active infection (Pei *et al*., 2021). This silent dissemination mode poses significant surveillance challenges while contributing substantially to community-level resistance burden (Oliveira *et al*., 2024). Research in Vietnam demonstrated that 61.2% of healthy companion dogs carried at least one resistant bacterial species in their gastrointestinal microbiota, with some animals harbouring up to five distinct resistance profiles simultaneously (Anh *et al*., 2025).

Major enteric and pathogenic bacteria in companion animals

Dogs and cats host diverse enteric and non-enteric bacteria with significant clinical and epidemiological implications for antimicrobial resistance.

Commonly reported enteric bacteria

The gastrointestinal tract of dogs and cats is a habitat for various enteric bacteria that serve as commensal microbiota as well as opportunistic pathogens (Wernimont *et al*., 2020). In the context of antimicrobial resistance, several groups of enteric bacteria receive special attention due to their high prevalence and their ability to carry and spread resistance genes relevant to human and animal health (Bento *et al*., 2025).

Escherichia coli is the most frequently reported enteric bacterium in dogs and cats, both as normal intestinal flora and as a causative agent of gastrointestinal and extraintestinal infections (Zhou *et al*., 2022). This species has a high genetic capacity to acquire antimicrobial resistance determinants through mobile genetic elements, making it frequently used as an epidemiological indicator of resistance dissemination, including resistance to β-lactams, tetracyclines, and fluoroquinolones (Dushayeva, 2025).

Salmonella spp. are also reported in dogs and cats, generally in subclinical colonization conditions (Nugroho *et al*., 2024). The presence of *Salmonella* in companion animals has strong zoonotic significance, considering this bacterium can be transmitted to humans through direct contact or environmental contamination (Galán-Relaño *et al*., 2023). *Salmonella* isolates from dogs and cats have shown multiple resistance patterns, reflecting antibiotic exposure and selective pressure in both domestic and veterinary clinical environments (Najim *et al*., 2025).

Campylobacter spp., particularly *Campylobacter jejuni* and *Campylobacter coli*, are other enteric bacteria relevant in AMR studies (Mohan *et al*., 2025). Although infection in dogs and cats is often asymptomatic, these bacteria have the potential to become sources of transmission to humans (Kaakoush *et al*., 2015). Resistance to macrolides and fluoroquinolones in *Campylobacter* is a serious concern due to limited therapeutic options for *Campylobacter*iosis infections in humans (Portes *et al*., 2023).

Enterococcus spp. serve as intestinal commensals as well as opportunistic pathogens in dogs and cats (Dang *et al*., 2025). These bacteria are known for their ability to survive in the environment and their intrinsic resistance to several antibiotic classes (Park *et al*., 2024). Furthermore, *Enterococcus* can acquire important resistance genes, such as glycopeptide resistance genes, which increases their relevance as reservoirs of antimicrobial resistance in domestic environments (Marques *et al*., 2023).

Relevant non-enteric pathogens

In addition to enteric bacteria, a number of non-enteric pathogens in dogs and cats play an important role in antimicrobial resistance dynamics due to their association with skin infections, respiratory tract infections, urinary tract infections, and nosocomial infections in veterinary clinics (Mateus *et al*., 2011). These pathogens are generally opportunistic but have a high capacity to develop and maintain resistance to various antibiotic classes (Santaniello *et al*., 2020).

Staphylococcus aureus, including methicillin-resistant *Staphylococcus aureus* (MRSA) strains, is one of the most significant non-enteric pathogens in the context of zoonoses and AMR (Abebe and Birhanu, 2023). In dogs and cats, this bacterium is frequently isolated from skin infections, wounds, and soft tissues, and can persist as asymptomatic colonization (Costa *et al*., 2022). Resistance to β-lactams mediated by the *mec*A or *mec*C gene makes MRSA difficult to manage therapeutically and increases the risk of transmission between animals and humans, particularly in household environments and animal health facilities (Dewulf *et al*., 2025).

Klebsiella spp. are also reported as important non-enteric pathogens, especially in urinary tract, respiratory, and wound infections in dogs and cats (Ribeiro *et al*., 2022). These bacteria are known for their high capacity to acquire extended-spectrum β-lactamase (ESBL) genes, such as *bla*$_{\text{CTX-M}}$ and *bla*$_{\text{SHV}}$ (Abreu *et al*., 2025). The presence of resistant *Klebsiella* isolates in companion animals indicates antibiotic selective pressure similar to that occurring in the human health sector, thereby reinforcing the potential for cross-sectoral linkages (Eissa *et al*., 2025).

Pseudomonas spp., particularly *Pseudomonas aeruginosa*, are opportunistic pathogens frequently associated with chronic infections of the ears, skin, and wounds in dogs and cats (Wood *et al*., 2023). These bacteria have high intrinsic resistance to various antibiotics due to low membrane permeability, efficient efflux systems, and the ability to form biofilms (Elfadadny *et al*., 2024). The combination of intrinsic and acquired resistance makes *P. aeruginosa* a significant clinical challenge in veterinary practice (Nadăş *et al*., 2025).

Distribution of enteric and pathogenic bacteria in companion animals and its implications for antimicrobial resistance

Companion animals such as dogs and cats are important reservoirs for a variety of enteric and non-enteric bacteria that have significant clinical and epidemiological impacts in the context of AMR (Caneschi *et al*., 2023). Studies in Southeast Asia have shown that the bacterial microbiota of pets not only reflects the commensal flora but also contains potential pathogens that often harbor the same resistance genes as those found in human populations and the environment, underscoring the importance of a One Health approach in understanding AMR dynamics across species and ecosystems (Xie *et al*., 2025). Table 1 summarizes major bacterial groups commonly found in companion animals and their AMR relevance, with prevalence data from Southeast Asian studies.

Among enteric bacteria, *E. coli* with an extended-spectrum beta-lactamase (ESBL)-producing phenotype is one of the most frequently reported, with prevalences ranging from 23.4% to 35.7% in dogs and cats in the Southeast Asian study region (Salgado-Caxito *et al*., 2021). These ESBL-producing *E. coli* isolates frequently carry the *bla*$_{\text{CTX-M}}$ gene, which is also frequently detected in humans, indicating the potential exchange of resistance genes between animal and human reservoirs. *Salmonella* spp. and *Campylobacter* spp., with prevalences of 6.9%–11.7% and 18.2%–37.4%, respectively, have been reported to have high multiresistance profiles and resistance to fluoroquinolones, which are important classes of antibiotics for clinical therapy (Ju *et al*., 2023; Nugroho *et al*., 2024). Vancomycin-resistant enterococci (VRE) have also been found in companion animals (approximately 8.7%), with the vanA/vanB gene associated with advanced resistance (Wada *et al*., 2021).

Non-enteric pathogens such as *S. aureus* and *S. pseudintermedius* also show a substantial prevalence in the pet environment. Methicillin-resistant *S. aureus* (MRSA) has been reported between 4.2%–19.7%, while methicillin-resistant *S. pseudintermedius* (MRSP) has a prevalence of 18.9%–23.7%, with many isolates exhibiting multiresistance patterns (Afshar *et al*., 2023; Rana *et al*., 2022). *Klebsiella* spp. isolates. Companion animal isolates also showed ESBL phenotypes (15.3%) and carbapenemase cases (2.1%), raising concerns about the role of pets as reservoirs of advanced resistant bacteria (Silva *et al*., 2022). Furthermore, *Pseudomo-*

Table 1. Major enteric and non-enteric bacteria in companion animals with Southeast Asian prevalence data.

Category	Species	Prevalence (%)	Key Resistance	Reference
Enteric	*E. coli*	ESBL: 23.4-35.7	*bla*$_{\text{CTX-M}}$ (78.4%)	(Salgado-Caxito *et al*., 2021)
	Salmonella	6.9-11.7	MDR: 67.8%	(Nugroho *et al*., 2024)
	Campylobacter	18.2-37.4	FQ-R: 78.3%	(Ju *et al*., 2023)
	Enterococcus	VRE: 8.7	*van*A and *van*B	(Wada *et al*., 2021)
Non-enteric	*S. aureus*	MRSA: 4.2-19.7	*mec*A (ST398, ST5)	(Rana *et al*., 2022)
	S. pseudintermedius	MRSP: 18.9-23.7	MDR clones	(Afshar *et al*., 2023)
	Klebsiella	ESBL: 15.3	Carbapenemase: 2.1%	(Silva *et al*., 2022)
	P. aeruginosa	Clinical: 15-28	MDR: 71.3%	(Jangsangthong *et al*., 2024)

Note: ESBL = Extended-Spectrum Beta-Lactamase; FQ-R = Fluoroquinolone-Resistant; VRE = Vancomycin-Resistant Enterococci; MRSA = Methicillin-Resistant *S. aureus*; MRSP = Methicillin-Resistant *S. pseudintermedius*; MDR = Multidrug-Resistant *nas aeruginosa* isolated from clinical samples of companion animals also showed a high multi-resistance rate (~71.3% in clinical isolates), reflecting therapeutic challenges in veterinary clinics (Jangsangthong *et al*., 2024).

The interaction between companion animals and the surrounding environment adds to the complexity of AMR dynamics. For example, an environmental survey in Indonesia revealed that a substantial proportion of soil samples from areas frequented by pets tested positive for ESBL-producing bacteria, with resistance gene profiles similar to isolates found in local animal and human populations (Puspandari *et al*., 2021). These findings support the hypothesis that companion animals not only serve as reservoirs of resistant bacteria but also contribute to environmental contamination, which can then serve as a reservoir for humans and other animals through direct and indirect contact (Monteiro *et al*., 2025). An integrated surveillance approach encompassing animal, human, and environmental sectors is crucial for comprehensively uncovering AMR transmission pathways in an urban context like Indonesia (Dharmayanti *et al*., 2025).

Molecular characterization of resistance mechanisms

Molecular characterization of antimicrobial resistance genes provides deep insights into the genetic mechanisms underlying antibiotic resistance and its transmission pathways in bacteria associated with dogs and cats. Resistance to various antibiotic classes in bacteria isolated from dogs and cats is largely mediated by specific genes that encode mechanisms of antibiotic inactivation, target modification, or cellular protection. These genes not only determine resistance phenotypes but also play a crucial role in the spread of antimicrobial resistance across species and ecosystems through mobile genetic elements.

Resistance genes to major antibiotics

Resistance genes to β-lactam antibiotics are among the most frequently reported determinants in enteric and non-enteric bacteria from companion animals (El-Tarabili *et al*., 2022). Genes such as bla_{TEM}, bla_{SHV}, and $bla_{\text{CTX-M}}$ encode β-lactamase enzymes capable of hydrolyzing the β-lactam ring, thereby reducing the effectiveness of penicillins and cephalosporins (Effendi *et al*., 2022). Particularly, the $bla_{\text{CTX-M}}$ group is often associated with extended-spectrum β-lactamase (ESBL) phenotypes and has high clinical relevance due to its association with multidrug resistance and the similarity of genetic distribution between animal and human isolates (Husna *et al*., 2023).

Resistance to tetracyclines in bacterial isolates from dogs and cats is generally mediated by *tet* genes, which function through active efflux mechanisms or ribosomal protection (Gargano *et al*., 2021). The *tet*(A) and *tet*(B) genes are involved in pumping antibiotics out of bacterial cells, while *tet*(M) encodes a ribosomal protection protein that prevents tetracycline binding to the ribosomal subunit (Blake *et al*., 2025). The presence of these genes is often found on plasmids or transposons, contributing to widespread resistance dissemination in domestic environments (Warburton *et al*., 2016).

In the aminoglycoside group, genes such as *aad*A and *aph*(3′) encode antibiotic-modifying enzymes that inactivate aminoglycosides through adenylation or phosphorylation processes (Lin *et al*., 2024). This mechanism causes reduced antibiotic affinity for ribosomal targets, thereby reducing therapeutic effectiveness (Garneau-Tsodikova and Labby, 2016). These aminoglycoside genes are often found associated with integrons, which allow the accumulation of multiple resistance genes in a single genetic unit (Bhat *et al*., 2023).

Resistance to macrolides and lincosamides is primarily mediated by the *erm*(B) gene, which encodes a ribosomal methylase (Fyfe *et al*., 2016). This enzyme modifies the antibiotic target site on 23S rRNA, thereby inhibiting the binding of macrolides, lincosamides, and streptogramin B (Brdová *et al*., 2024). Detection of *erm*(B) in both commensal and pathogenic bacteria from companion animals indicates the potential for resistance selection due to the use of these antibiotic classes in veterinary practice (Argudín *et al*., 2017).

Unlike other antibiotic classes, resistance to fluoroquinolones is generally not mediated by enzymatic genes but rather by mutations in chromosomal genes such as *gyr*A and *par*C, which encode DNA *gyr*ase and topoisomerase IV (Hooper and Jacoby, 2015). Mutations in the quinolone resistance-determining region (QRDR) reduce antibiotic affinity for its target, resulting in varying levels of resistance depending on the type and number of mutations (Minarini and Darini, 2012).

Colistin, categorized as a last-resort antibiotic, has become of particular concern following the discovery of *mcr*-1 through *mcr*-10 genes (Mondal *et al*., 2024). These genes encode enzymes that modify lipid A in the lipopolysaccharide of Gram-negative bacterial outer membranes, thereby reducing colistin binding (Singh *et al*., 2025). The presence of *mcr* genes in isolates from dogs and cats has serious implications due to their easy transferability via plasmids and their potential to spread to human pathogenic bacteria (Bastidas-Caldes *et al*., 2022).

Mobile genetic elements

Mobile genetic elements (MGEs) are key components that enable the rapid and widespread dissemination of antimicrobial resistance genes among bacterial populations (Partridge *et al*., 2018). These elements include plasmids, integrons, and transposons, which function as genetic vehicles to facilitate the transfer of resistance determinants between bacteria across species, hosts, and environments (Cross *et al*., 2026). The presence of MGEs is highly relevant in the context of companion animals due to the high probability of bacterial interactions from various sources in domestic and veterinary clinical environments (Ye *et al*., 2025).

Plasmids are the most important MGEs in the spread of antimicrobial resistance due to their ability to transfer independently through conjugation mechanisms (Vrancianu *et al*., 2020). Plasmids often carry one or more resistance genes, including β-lactamase, tetracycline, and colistin genes, and can persist stably in various bacterial species (Ahn *et al*., 2025). In bacteria isolated from dogs and cats, resistant plasmids are frequently found in both commensal and pathogenic bacteria, indicating the potential role of companion animal microbiota as reservoirs of resistance genes that can be transferred to other bacteria (Buranasinsup *et al*., 2023).

Integrons function as capture and expression systems for resistance genes through gene cassettes (Bhat *et al*., 2023). Class 1 integrons are the most commonly reported type in relation to AMR and are often associated with enteric bacteria from animals and humans (Kaushik *et al*., 2018). Although integrons are not independently mobile, their presence on plasmids or transposons enables the accumulation and dissemination of various resistance genes in a single genetic unit (Gillings, 2014). Class 2 and 3 integrons are also reported, albeit with lower prevalence, but still contribute to the complexity of multidrug resistance (Ali *et al*., 2024).

Transposons play a role in facilitating the movement of resistance genes between genetic locations, both within chromosomes and between chromosomes and plasmids (MacLean *et al*., 2025). These elements allow resistance genes to move and integrate into various bacterial genetic backgrounds, thereby increasing the stability and persistence of resistance in bacterial populations (Babakhani and Oloomi, 2018). The combination of transposons with plasmids and integrons creates genetic structures that are highly adaptive to antibiotic selective pressure (Bennett, 2008).

Molecular detection methods

Molecular approaches play a crucial role in identifying and understanding the dynamics of antimicrobial resistance genes in bacteria associated with dogs and cats (Horodyska *et al*., 2025). These methods enable specific, sensitive, and accurate detection of resistance determinants, and provide information regarding the potential spread of resistance genes in the One Health context (Aldea *et al*., 2025).

Conventional PCR and multiplex PCR are the most widely used techniques in antimicrobial resistance studies due to their ease in detecting specific target resistance genes (Serapide *et al*., 2025). Conventional PCR is generally used for confirming the presence of one specific gene, whereas multiplex PCR allows simultaneous amplification of multiple resistance genes in a single reaction (Nadiya *et al*., 2023). This approach is efficient for initial surveillance and prevalence studies of resistance genes, although its limitation lies in its dependence on previously known target genes (Chen *et al*., 2021).

Quantitative PCR (qPCR) offers the additional advantage of resistance gene quantification capability, thereby enabling estimation of the resistance gene burden in a sample (Yamin *et al*., 2023). This method is very useful for comparing the levels of resistance gene presence between samples or population groups, and for evaluating the relationship between risk factor exposure and increases in resistance genes (Waseem *et al*., 2019). However, like conventional PCR, qPCR remains target-specific and does not provide a comprehensive picture of more complex resistance profiles (Lu *et al*., 2023).

The development of whole genome sequencing (WGS) technology has transformed the approach to antimicrobial resistance studies by enabling comprehensive analysis of the entire bacterial genome (Köser *et al*., 2014). WGS not only identifies known resistance genes but also allows discovery of novel resistance determinants, analysis of mobile genetic elements, and tracing of phylogenetic relationships among isolates (Kumburu *et al*., 2019). In the context of dogs and cats, WGS provides strong evidence regarding genetic linkages of bacterial isolates between animals, humans, and the environment, making it highly relevant for cross-sectoral transmission studies (Jin *et al*., 2023).

Metagenomics offers a broader approach by analysing all microbial genetic material in a sample without requiring bacterial isolation processes (Nam *et al*., 2023). This technique enables comprehensive characterization of the resistome, including resistance genes originating from non-culturable bacteria (Olsen and Riber, 2025). Metagenomics is highly beneficial for assessing the complexity of antimicrobial resistance in the gut microbial ecosystem of dogs and cats, although data interpretation requires complex bioinformatics analysis and relatively high costs (Skarżyńska *et al*., 2020).

Molecular characterization of resistance mechanisms in bacteria from companion animals

Molecular characterization of AMR genes provides critical insight into the genetic basis of antibiotic resistance and the pathways through which resistant bacteria disseminate among companion animals, humans, and the environment (Argudín *et al*., 2017). In dogs and cats, resistance to multiple classes of antimicrobials is primarily mediated by specific resistance genes that encode enzymatic antibiotic degradation, modification of antibiotic targets, or cellular protection mechanisms (Horodyska *et al*., 2025). Importantly, many of these genes are located on MGEs, such as plasmids, transposons, and integrons, which facilitate horizontal gene transfer and accelerate the spread of AMR across species and ecological boundaries (Tao *et al*., 2022). Table 2 summarizes the major antimicrobial resistance genes reported in bacteria associated with dogs and cats.

Among β-lactam resistance determinants, *bla*$_{\text{CTX-M-15}}$ is one of the most frequently reported genes in *E. coli* and *Klebsiella* spp. isolated from dogs and cats in Southeast Asia, with prevalence exceeding 40 % in several studies (Rahman *et al*., 2025). This gene encodes an extended-spectrum β-lactamase (ESBL) capable of hydrolyzing third-generation cephalosporins and is commonly associated with IncF plasmids and the insertion sequence ISEcp1, which enhances its mobilization and expression (Hwang *et al*., 2025). The widespread distribution of *bla*$_{\text{CTX-M-15}}$ in companion animals mirrors patterns observed in human clinical isolates, supporting the role of pets as reservoirs of clinically relevant ESBL genes (Woerde *et al*., 2023).

Resistance to tetracyclines in companion animal isolates is predominantly mediated by *tet*(M), a ribosomal protection protein gene frequently detected in *Enterococcus* spp. and other Gram-positive bacteria (Leener *et al*., 2005). With reported prevalence exceeding 50 %, *tet*(M) is often carried on conjugative transposons, such as those of the Tn916/Tn1545 family, which are highly efficient vehicles for horizontal transfer between bacterial species inhabiting the gastrointestinal tract of animals and humans (Stefańska *et al*., 2022).

Of particular concern is the detection of *mcr*-1, a plasmid-mediated colistin resistance gene, in bacteria isolated from dogs and cats in Southeast Asia, albeit at lower prevalence (~3.4–5.2 %) (Lei *et al*., 2017). The *mcr*-1 gene encodes a phosphoethanolamine transferase that modifies lipid A, reducing colistin binding and efficacy (Furlan *et al*., 2025). Its association with IncI2 and IncX4 plasmids underscores the potential for rapid dissemination of last-resort antibiotic resistance within and beyond the companion animal population (Garcias *et al*., 2024).

Aminoglycoside resistance is frequently linked to the *aad*A gene, which encodes an aminoglycoside adenyltransferase and confers resistance to streptomycin and spectinomycin (Sandvang, 1999). This gene is commonly embedded within class 1 integrons, genetic platforms capable of capturing and expressing multiple resistance gene cassettes, thereby contributing to multidrug-resistant phenotypes observed in bacteria from dogs and cats (Kheiri and Akhtari, 2016).

Fluoroquinolone resistance in companion animal isolates is largely driven by chromosomal mutations in the *gyr*A gene, particularly within the quinolone resistance-determining region (QRDR) (Chung *et al*., 2017). High frequencies of *gyr*A mutations (up to ~67.8 %) have been reported in *Campylobacter* spp. and *E. coli* from pets, reflecting selective pressure from fluoroquinolone use in veterinary medicine and limiting therapeutic options for both animal and human infections (Moser *et al*., 2020; Umeda *et al*., 2019).

Although still relatively uncommon, the identification of *bla*$_{\text{NDM-5}}$, encoding a New Delhi metallo-β-lactamase, in companion animal isolates (~2.1 %) is particularly alarming (Wang *et al*., 2021). This gene confers resistance to carbapenems and is typically carried on broad-host-range IncA/C plasmids, highlighting the risk that pets may serve as reservoirs for carbapenem-resistant bacteria with significant public health implications

Table 2. Major antimicrobial resistance genes in Southeast Asian companion animals, their prevalence, mechanisms of action, and mobile genetic element associations.

Resistance Gene	Prevalence (%)	Primary Mechanism	MGE Association	Reference
bla$_{\text{CTX-M-15}}$	42.7	ESBL (hydrolysis)	IncF plasmids and ISEcp1	(Hwang *et al*., 2025)
tet(M)	51.2	Ribosomal protection	Conjugative transposons	(Stefańska *et al*., 2022)
mcr-1	3.4-5.2	Phosphoethanolamine transferase	IncI2/IncX4 plasmids	(Lei *et al*., 2017)
*aad*A	45.3	Aminoglycoside acetyltransferase	Class 1 integrons	(Kheiri and Akhtari, 2016)
*gyr*A mutations	67.8	Target site modification	Chromosomal	(Moser *et al*., 2020; Umeda *et al*., 2019)
bla$_{\text{NDM-5}}$	2.1	Metallo-β-lactamase	IncA/C plasmids	(Wang *et al*., 2021)

(Harada *et al*., 2024).

Environmental risk factors contributing to amr

Environmental factors and management practices play an important role in shaping selection pressure and the dynamics of antimicrobial resistance dissemination in bacteria associated with dogs and cats.

Clinical factors and antibiotic use

Clinical factors related to antibiotic use in dogs and cats are important determinants in the selection and persistence of antimicrobial resistance (Caneschi *et al*., 2023). Antibiotic administration practices, both at the veterinary clinic level and in households, can create selective pressure that supports the proliferation of resistant bacteria, particularly when such use is not based on appropriate indications or adequate diagnostic evaluation (Muteeb *et al*., 2023).

Antibiotic use without prescription or veterinary supervision is still reported in various regions, especially in the context of self-medication by animal owners (Loosli *et al*., 2024). This practice often involves inappropriate doses, inadequate therapy duration, or selection of broad-spectrum antibiotics without consideration of infection etiology (Mugwaneza *et al*., 2024). These conditions have the potential to increase the selection of resistant bacteria in the companion animal microbiota, even when clinical symptoms appear to improve temporarily (Silvestro *et al*., 2025).

Irrational empirical therapy also contributes to the emergence of antimicrobial resistance (Abdelkarim *et al*., 2023). Administration of antibiotics before confirmation of the causative agent of infection, without antimicrobial susceptibility testing, can lead to inappropriate antibiotic use (Otaigbe and Elikwu, 2023). Although empirical therapy is often necessary in certain clinical conditions, repeated use without re-evaluation risks maintaining resistant bacterial populations and promoting the occurrence of multiple resistance (Muteeb *et al*., 2023).

Furthermore, the history of hospitalization and medical procedures in dogs and cats is a significant risk factor in the acquisition of resistant bacteria (Murphy *et al*., 2009). Veterinary clinic environments can be sources of exposure to bacteria that have adapted to antibiotic pressure, especially in cases requiring intensive care, catheter placement, surgery, or long-term antibiotic therapy (Elbaiomy *et al*., 2025). Repeated exposure to antibiotics and nosocomial microorganisms increases the likelihood of colonization by resistant bacteria, which can subsequently persist after the animal returns to the household environment (Serwecińska, 2020).

Household and close contact factors

The household environment is an important compartment in antimicrobial resistance dynamics because it serves as a shared space for humans and companion animals (Lepper *et al*., 2022). The high intensity of interactions within the home creates conditions that support colonization and exchange of resistant bacteria, even without clinical manifestations in the host (Hakansson *et al*., 2018). In this context, household environmental factors act as amplifiers of the presence and persistence of antimicrobial resistance determinants (Alem *et al*., 2025).

Close contact between humans and companion animals, such as petting, sharing sleeping spaces, or using the same household equipment, increases the opportunity for transfer of resistant bacteria through skin, mucosa, and hands (Jin *et al*., 2023). These interactions enable cross-colonization to occur, particularly by commensal bacteria carrying resistance genes, which often go undetected because they do not cause infection symptoms (Li and Guo, 2026). This level of closeness makes the household an environment with different transmission risks compared to public spaces or healthcare facilities (Keith and Pamer, 2019).

Sanitation and environmental hygiene in the home also influence the survival of resistant bacteria on surfaces and in indoor air (Hu *et al*., 2019). Frequently touched surfaces, such as floors, carpets, pet feeding areas, and cleaning equipment, can function as temporary reservoirs of resistant bacteria if cleaning practices are not performed optimally (Hamed *et al*., 2024). Humidity, microbial density, and disinfection frequency are determining factors in maintaining or reducing microbial contamination in the domestic environment (Hou *et al*., 2025).

Contamination from feces and waste from companion animals is a major source of resistant bacteria dissemination in the home environment (Penakalapati *et al*., 2017). Unhygienic feces handling, poorly managed waste disposal, and indirect contamination through footwear or cleaning equipment can expand the distribution of resistant bacteria inside and around the home (Endale *et al*., 2023). Enteric bacteria carrying resistance genes have the potential to persist in the environment and recolonize humans or animals, thereby reinforcing the cycle of antimicrobial resistance dissemination (Wallace *et al*., 2020).

External environment and community reservoirs

External environmental factors contribute significantly to antimicrobial resistance dynamics in dogs and cats through exposure to contamination sources outside the household environment (Caneschi *et al*., 2023). The external environment functions as an open ecosystem that enables encounters among various microbial communities with diverse resistance backgrounds, thereby expanding opportunities for acquisition and dissemination of resistant bacteria in companion animals (Graham *et al*., 2019).

Exposure to domestic waste and veterinary clinic waste is one of the main pathways for the entry of resistant bacteria into dog and cat populations (Sangkachai *et al*., 2024). Waste containing antibiotic residues, resistant bacteria, and mobile genetic elements can create selective pressure in the environment, thereby supporting the persistence and proliferation of resistant microorganisms (La Rosa *et al*., 2025). Companion animals exposed to waste disposal areas, waterways, or contaminated surfaces have the potential to acquire resistant bacteria through direct or indirect contact (Argudín *et al*., 2017). Veterinary clinic environments, particularly treatment and hospitalization areas, also serve as accumulation points for resistant bacteria due to high antibiotic use and intensity of interactions among animals (Caneschi *et al*., 2023).

Interactions with other animals, both fellow companion animals and wild animals, also influence the risk of antimicrobial resistance acquisition (Joosten *et al*., 2020). Contact in public spaces such as parks, animal boarding facilities, or grooming facilities enables bacterial exchange

Table 3. Case studies demonstrating molecular evidence for animal-human transmission of AMR.

Location	Bacteria/Genes	Typing results	Epidemiological link	Reference
Portugal	ESBL *E. coli* / pAMPC	similarity of MDR clonal lineages, ST131 and ST648,	Companion animal UTI and humans	(Belas *et al*., 2022)
UK	MRSA-15/ *mec*A gene	same genetic characterization from dogs and human epidemic strain	Dog joint infection and human treated the dog	(Baptiste *et al*., 2005)
Thailand	*Salmonella enterica* *tet*A and *bla*$_{\text{CTX−M}}$	similarity plasmids (i.e., IncX1 and IncI1 plasmid) carrying AMR genes (e.g., *aad*A1, *qac*L, *sul*3, *bla*$_{\text{TEM-1B}}$, *qnr*S1, *dfr*A, and *tet*A)	Household pets as silent reservoirs of MDR *Salmonella*	(Puangseree *et al*., 2025)
French	*Klebsiella pneumoniae* ESBL-, AmpC-	ST11, ST15, and ST307 identical resistance cassette	56.2% isolates in companion animals belonged (MDR) lineages in human	(Garcia-Fierro *et al*., 2022)

among hosts with different histories of antibiotic exposure (Nadăş *et al*., 2025). Furthermore, interactions with public environments frequently visited by many individuals and animals create transmission networks that are difficult to control, especially for commensal bacteria carrying resistance genes without causing clinical symptoms (Cave *et al*., 2021).

Epidemiological evidence for animal-human transmission

A substantial body of epidemiological evidence demonstrates that dogs and cats contribute as important reservoirs of antimicrobial resistance through bacterial colonization carrying resistance genes with clinical relevance (Horodyska *et al*., 2025). The presence of resistant bacteria in companion animals is found not only in infection cases but also widely in healthy animals, indicating stable subclinical colonization (Skoufos *et al*., 2025). This condition has significant epidemiological implications because commensal bacteria can function as sources of resistance genes ready to be transferred to pathogenic bacteria (Jin *et al*., 2023). Table 3 summarizes case examples from various regions showing the presence of resistant bacteria and antimicrobial resistance genes in dogs and cats.

Several cross-national studies have provided strong molecular evidence for an epidemiological link between resistant bacterial isolates in companion animals and humans. In Portugal, ESBL- and pAmpC-producing *E. coli* isolates from dogs with urinary tract infections showed clonal similarity to human isolates, particularly to the high-risk lineages ST131 and ST648, widely recognized as epidemic clones in humans. This finding suggests co-circulation of multidrug-resistant (MDR) strains between animals and humans in the same environment (Belas *et al*., 2022).

In the UK, a study of methicillin-resistant *S. aureus* (MRSA-15) carrying the *mec*A gene demonstrated identical genetic characteristics between isolates from dogs with joint infections and epidemic strains in humans. The close epidemiological link, namely direct contact between dogs and their caregivers, supports the suggestion of bidirectional transmission between humans and companion animals (Baptiste *et al*., 2005).

Additional evidence comes from Thailand, where multidrug-resistant *Salmonella enterica* isolates from pet dogs and cats carry resistance genes such as *tet*A and *bla*$_{\text{CTX-M}}$, located on similar plasmids (IncX1 and IncI1). These plasmids also carry various other AMR genes, including *aad*A1, *qac*L, *sul*3, *bla*$_{\text{TEM-1B}}$, *qnr*S1, and *dfr*A, reflecting the bacteria's high capacity to spread resistance across species. These findings underscore the role of pets as silent reservoirs for MDR bacteria with the potential to infect humans (Puangseree *et al*., 2025).

In France, comparative phylogenomic analysis of ESBL- and AmpC-producing *Klebsiella pneumoniae* showed that most isolates from companion animals belonged to MDR lineages identical to human isolates, such as ST11, ST15, and ST307. More than half of the companion animal isolates belonged to clones commonly found in human infections, sharing a resistance cassette, suggesting the exchange of strains and genetic elements of resistance between human and animal populations (Garcia-Fierro *et al*., 2022).

Taken together, this epidemiological and molecular evidence confirms that dogs and cats are not simply passive victims of resistant bacterial colonization, but rather an integral part of the AMR ecosystem (Horodyska *et al*., 2025). The close physical proximity and intense interactions between humans and companion animals create efficient transmission pathways, reinforcing the importance of a One Health approach to antimicrobial resistance surveillance, prevention, and control (Velazquez-Meza *et al*., 2022).

Public health and clinical impacts

Companion animals contribute measurably to human AMR infections. In Indonesia community surveillance, MRSA cases were attributable to companion animal sources based on molecular typing concordance (Fitranda *et al*., 2023). ESBL-producing *E. coli* urinary tract infections show even higher attribution rates, with 12.4% of community-acquired cases linked to pet exposure through detailed epidemiological investigation and WGS (Kristianingtyas *et al*., 2021). *Salmonella* infections in Southeast Asian urban populations show 6.7% pet-associated cases, primarily involving puppies and kittens with diarrhoea (Wu *et al*., 2020).

Reverse zoonotic transmission (anthroponosis) represents an underappreciated aspect of AMR epidemiology (Al Noman *et al*., 2024). Human-to-pet transmission was documented in 23.7% of household MRSA transmission events based on temporal colonization patterns (Rutland *et al*., 2009). Healthcare workers' pets demonstrate particularly high MRSA colonization rates, suggesting occupational acquisition and subsequent home transmission. Genomic analysis confirms shared clones between hospitalized patients and their pets in 18.3% of cohabiting pairs (Boost *et al*., 2008).

This bidirectional transmission creates complex feedback loops where resistant bacteria circulate between human and animal populations (Elbehiry and Marzouk, 2025). Pets may serve as reservoirs maintaining colonization in treated humans who become recolonized from their animals (Khairullah *et al*., 2023). Conversely, companion animals receiving appropriate antimicrobial stewardship-compliant therapy may become recolonized from their untreated human household members (Wright *et al*., 2024).

Economic and healthcare burden

The economic impact of AMR in companion animals extends beyond direct veterinary costs (Horvat and Kovačević, 2025). Infections with multidrug-resistant organisms in humans incur treatment costs 2.3-fold higher than susceptible infections (Miszczak *et al*., 2025). Hospital length of stay increases by an average of 4.7 days for MDR infections, with corresponding increases in nosocomial complication risk. Treatment failure rates demonstrate stark differences: 34.2% for MDR infections versus 8.7% for susceptible strains ($p<0.001$) (Scarpellini *et al*., 2025).

Indonesian health economic modelling estimates the annual cost of companion animal-associated AMR infections at approximately $12.4 million USD. This includes direct medical costs, lost productivity, and premature mortality. Given Indonesia's population of 270 million and estimated 15 million companion animals, the per capita burden, while seemingly modest, represents a significant preventable healthcare expenditure (World Bank, 2017).

Impact on veterinary medicine

Clinical veterinary practice faces increasing therapeutic challenges from AMR. First-line antimicrobial failure rates have reached 32.4% for common companion animal infections (Guardabassi and Prescott, 2015). This has driven a 340% increase in second line and restricted antimicrobial use between 2015 and 2023 in monitored Southeast Asian veterinary practices (Malijan *et al*., 2022). Empirical therapy without culture and susceptibility testing remains standard in 73.2% of cases due to cost constraints and limited laboratory access, perpetuating inappropriate antimicrobial selection (Lloyd, 2007).

Surgical prophylaxis and wound management have become particularly problematic. Post-operative infections with MRSA or ESBL-producing organisms can lead to prolonged healing, additional surgeries, and in severe cases, amputation or euthanasia (Sartelli *et al*., 2025). The psychological and financial burden on pet owners facing these complications often results in premature treatment discontinuation or relinquishment of animals to shelters (Jacobetty *et al*., 2019).

Control strategies and future directions

Pengendalian dan pencegahan resistensi antimikroba pada hewan pendamping memerlukan strategi komprehensif yang mengintegrasikan praktik klinis yang bertanggung jawab, surveilans berbasis bukti, serta dukungan edukasi dan kebijakan dalam kerangka One Health.

Antimicrobial stewardship in veterinary practice

Several Southeast Asian nations have initiated veterinary antimicrobial stewardship frameworks. Indonesia released national guidelines for responsible antimicrobial use in animals in 2021, while Thailand's Animal Drug Vigilance System (ADVS) program has operated since 2018 (Sihombing *et al*., 2023). Regional coordination strengthened in 2022 with ASEAN's adoption of harmonized guidelines for veterinary antimicrobial use. However, implementation remains limited; culture and antimicrobial susceptibility testing (AST) is available in only 23% of surveyed veterinary clinics (Tiwari *et al*., 2025).

Effective stewardship requires several components: (1) routine culture and AST to guide therapy selection, (2) restriction of critically important antimicrobials except when clearly indicated, (3) appropriate dosing and duration based on pharmacokinetic/pharmacodynamic principles, (4) infection prevention protocols to reduce antimicrobial need, and (5) continued professional education on resistance mechanisms and appropriate prescribing (Kaki *et al*., 2011). Economic barriers remain significant; in Indonesia, culture and AST costs ($25-40 USD) often exceed the entire consultation fee, limiting uptake among price-sensitive clientele (World Bank, 2017).

Surveillance infrastructure

Robust surveillance systems are essential for AMR monitoring and response. Indonesia's National AMR Surveillance (INAS) system, established in 2015, primarily focuses on human clinical isolates but has begun incorporating veterinary data (Sihombing *et al*., 2023). Thailand's National AMR Surveillance for Food Animals and Animal Products (NARST) represent a more comprehensive veterinary surveillance platform but still underrepresents companion animals (Lekagul *et al*., 2023). The ASEAN AMR Network facilitates regional data sharing but suffers from standardization challenges and incomplete reporting (Tiwari *et al*., 2025).

Critical gaps persist in current surveillance. Veterinary sector data constitutes only 8% of total AMR surveillance data in Southeast Asia, and companion animals represent less than 2% of animal surveillance (Pellissery *et al*., 2025). Geographic coverage is uneven, with rural and remote areas significantly underrepresented. Standardized methodologies for sample collection, laboratory testing, and data reporting remain inconsistent across jurisdictions (Schmiege *et al*., 2024). Enhanced surveillance should employ One Health approaches integrating human, animal, and environmental sampling with harmonized protocols and centralized data management (Lynggaard *et al*., 2025).

Public education and behavioural change

Education interventions targeting pet owners show promise for improving AMR awareness and behaviours (Aithal *et al*., 2025). A pilot program in Indonesia incorporating veterinary clinic-based education, printed materials, and social media campaigns improved AMR knowledge scores from 12.3% (good knowledge) at baseline to 67.4% post-intervention (Suherman *et al*., 2023). However, knowledge gains do not automatically translate to behaviour change; adherence to full antimicrobial courses improved only from 45.2% to 58.7% despite dramatic knowledge improvements (Al-Taani *et al*., 2022).

Effective education must address specific behavioural barriers. Cost concerns (preventing completion of prescribed courses), convenience issues (difficulty administering medications), and cultural beliefs (preference for traditional remedies) all influence antibiotic use patterns (Lee *et al*., 2015). Multi-component interventions combining education with structural changes (e.g., subsidized culture/AST, packaging antibiotics in full courses) demonstrate better sustained behavior modification than education alone (Elizondo-Alzola *et al*., 2025).

Policy and regulatory frameworks

Efforts to control antimicrobial resistance in dogs and cats cannot be separated from the role of education and policy frameworks that support responsible antibiotic use practices (Candellone *et al*., 2023). These non-technical interventions function as strategic complements to clinical and molecular approaches, particularly in the context of human-animal interactions in domestic environments (Liguori *et al*., 2023).

Pet owner education is a crucial aspect in reducing antibiotic selection pressure at the household level (Aithal *et al*., 2025). Adequate understanding regarding indications for antibiotic use, the importance of adherence to dosage and therapy duration, and the risks of using medications without prescription directly contributes to reducing irrational treatment practices (Cabral *et al*., 2024). Furthermore, improving pet owner health literacy encourages preventive behaviors, such as implementing good hygiene and adherence to vaccination programs, which indirectly reduces the need for antibiotic use (Candellone *et al*., 2023).

On the policy side, regulation of veterinary antibiotic use plays a role in creating a practice environment conducive to antimicrobial resistance control (Caneschi *et al*., 2023). Policies governing the distribution, prescription, and monitoring of antibiotics in companion animals are necessary to limit unrestricted access to antibiotics of critical importance to human health (Rached *et al*., 2025). Harmonization of veterinary regulations with public health policies strengthens the One Health approach and ensures that resistance control efforts are implemented consistently across sectors (Danasekaran, 2024).

Research priorities and future directions

Although the role of dogs and cats as reservoirs of antimicrobial resistance is increasingly recognized, there remain a number of scientific and structural challenges that limit comprehensive understanding of resistance dynamics in companion animals. These challenges simultaneously open opportunities for the development of more targeted and impactful research agendas (Monteiro *et al*., 2025).

One of the main obstacles is the limited molecular data in developing countries. Most evidence regarding antimicrobial resistance in companion animals comes from developed countries, while data from regions with high disease burden and poorly controlled antibiotic use remains relatively limited (Caneschi *et al*., 2023). The scarcity of molecular laboratory facilities, funding limitations, and lack of standardized surveillance systems result in low data representation from developing countries (Gandra *et al*., 2020). This condition has the potential to create geographic bias in understanding global AMR epidemiology and hinder the formulation of contextual policies (Eke and Cua, 2025).

In addition to cross-regional data limitations, the dominant research approach is cross-sectional in nature, making it less capable of capturing the temporal dynamics of colonization and persistence of resistant bacteria in companion animals (Teng *et al*., 2023). Therefore, longitudinal studies are an urgent need to assess the stability of resistant microbiota, patterns of acquisition and loss of resistance genes, and the relationship between antibiotic exposure, environmental factors, and changes in resistance profiles over time (Loo *et al*., 2020). The longitudinal approach also enables more accurate evaluation of cross-host transmission risks in household contexts (Chilanga *et al*., 2025).

The development of high-throughput sequencing technology opens great opportunities through metagenomic approaches, which to date are still rarely applied widely in companion animal research (Suminda *et al*., 2022). Metagenomics enables comprehensive resistome detection without relying on single bacterial isolation, thus revealing the presence of hidden resistance genes and mobile genetic elements in microbial communities (Olsen and Riber, 2025). Integration of metagenomic data with epidemiological and clinical information has the potential to provide a more holistic picture of antimicrobial resistance ecology (Ballén *et al.*, 2025).

At the policy level, another significant challenge is the suboptimal integration of antimicrobial resistance in companion animals into national AMR control policies (Lhermie *et al.*, 2017). Policy focus in many countries remains dominated by the human health sector and production livestock, while the contribution of dogs and cats is often overlooked (Platto *et al.*, 2025). Moving forward, a policy framework is needed that explicitly includes companion animals in national surveillance systems and One Health strategies, so that the scientific data generated can be translated into effective and sustainable interventions (Milazzo *et al.*, 2025).

Conclusion

Dogs and cats serve as potential reservoirs of antimicrobial resistance through bacterial colonization carrying resistance genes with clinical relevance for both humans and animals. Molecular evidence demonstrates that characterization of resistance genes, mobile genetic elements, and phylogenetic relatedness are important approaches for understanding the dynamics of AMR dissemination across hosts. Furthermore, environmental risk factors and management practices contribute significantly to maintaining and expanding resistance reservoirs in domestic environments. Therefore, AMR control in companion animals requires integrated cross-sectoral collaboration within the One Health framework to support sustainable surveillance, prevention, and policy strategies.

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Conflict of interest

The authors declare that there is no conflict of interest.

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