Continental Veterinary Journal
ISSN: 3079-0212 (ONLINE)
www.cvetj.com; editor@cvetj.com

RESEARCH ARTICLE

DOI: 10.71081/cvj/2026.078

Prevalence and Antimicrobial Resistance Profiles of Bacterial Pathogens Isolated from Companion Animals in Doha, Qatar

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ARTICLE INFO

ARTICLE HISTORY: CVJ-26-521

Received: 19-April-2026
Revised: 17-May-2026
Accepted: 19-May-2026
Published online: 22-May-2026

Key words:
Prevalence,
Antimicrobial resistance,
Bacterial pathogens,
Companion animals

ABSTRACT

The aim of the present study was to determine the prevalence and antimicrobial resistance pattern of bacterial pathogens from companion animals (dogs and cats) obtained from veterinary clinics and hospitals in Doha, Qatar. During 12 months period, 420 clinical samples of skin swabs, ear swabs, urine, wound, fecal and respiratory samples were collected from 280 dogs and 140 cats. The bacteria were isolated using standard microbiological methods such as selective and differential media. The microorganism was identified by Gram staining, colony characteristics and a series of biochemical tests. The antimicrobial susceptibility testing was performed by Kirby Bauer disk diffusion method according to Clinical and Laboratory standards Institute (CLSI) guidelines. Overall, 318 bacterial isolates were recovered with an overall isolation rate of 75.7%. *Staphylococcus aureus* (28.6%), *Escherichia coli* (18.2%), *Pseudomonas aeruginosa* (13.5%) and *Klebsiella pneumoniae* (10.4%) were the predominant isolates. Methicillin-resistant *Staphylococcus aureus* (MRSA) was found in 31.9% of *S. aureus* isolates. 62.6% of all bacterial isolates were multidrug resistant (MDR). High levels of resistance were detected to ampicillin (79.2%), tetracycline (68.4%) and trimethoprim-sulfamethoxazole (61.3%) in the commonly used antibiotics. Most isolates were most active against carbapenems and linezolid. The results indicate that companion animals are potential reservoirs of antimicrobial resistant bacteria and that there is a need for One Health strategies, antimicrobial stewardship programs and improved surveillance to reduce the zoonotic risk associated with antimicrobial resistant bacteria.

To Cite This Article: Ain QU, 2026. Prevalence and antimicrobial resistance profiles of bacterial pathogens isolated from companion animals in Doha, Qatar. Continental Vet J, 6(1): 94-99. http://dx.doi.org/10.71081/cvj/2026.078

INTRODUCTION

With the global trend of companion animal ownership, there has been growing awareness that dogs and cats can be important reservoirs of zoonotic pathogens, including antimicrobial resistant (AMR) bacteria. Companion animals are kept with humans, fed commercial and raw animal-based foods, receive regular veterinary care and are prescribed long-term courses of antibiotics, all of which select and promote the spread of antibiotic-resistant bacterial strains (Van Boeckel et al. 2019; Guardabassi et al. 2020). In the context of the One Health approach, which involves the health of humans, animals and the environment, companion animals play a significant role as a conduit for the interspecies spread of resistance genes and resistant organisms (WHO 2021).

Bacterial infections are common health problems in companion animals including; gastrointestinal, respiratory, wound, urinary tract infections (UTIs) and otitis externa (OH). Common bacterial pathogens are *Staphylococcus aureus*, including methicillin-resistant *S. aureus* (MRSA), *Escherichia coli*, *Pseudomonas aeruginosa, Klebsiella pneumoniae*, Salmonella spp., Enterococcus spp., and Proteus spp. (Weese et al. 2020; Summers et al. 2021). In addition to their veterinary importance, these pathogens have important public health implications because they can be spread to owners and veterinary staff and the general population through direct contact, the use of fomites or environmental contamination (Pomba et al. 2017; Guardabassi et al. 2020).

There has been a significant increase in antimicrobial resistance in companion animal pathogens over the last 20

years. There are reports of resistant bacteria in dogs and cats globally including reports from Europe, North America, and Asia, where alarming rates of resistance are observed for bacteria to beta-lactams, fluoroquinolones, tetracyclines, and aminoglycosides (Schwarz et al. 2018; Belas et al. 2021). The emergence of multidrug resistance (MDR), resistance to at least one agent in three or more antimicrobial drug classes, has grown to be more prevalent, and poses significant challenges in terms of limited therapy options and clinical management (Magiorakos et al. 2012). With the increasing urbanization and its associated companion animal population in South Asia, data on AMR in these animals are still limited, even with majority of farmers using OTC antibiotics (Irfan et al. 2022; Siddiqui et al. 2023).

Qatar is in a position of dual burden of AMR in both veterinary and human sectors, wherein the unregulated use of antibiotics, inadequacy of diagnostic facilities and lack of veterinary surveillance systems make the situation worse (Iqbal et al. 2021). Antibiotic use for companion animals in Qatar is often without microbiological culture and susceptibility testing which has been shown to encourage the development of resistance (Khan et al. 2022). Although this topic is relevant, there is a lack of systematic and culture-based studies to characterize the bacterial flora and resistance profiles of companion animal pathogens in the country.

Hence, the present study was aimed to isolate and identify bacterial pathogens from clinical samples of companion animals, identify their antimicrobial resistance pattern, multidrug resistance pattern and to reveal the zoonotic and public health importance of the study in the context of One Health approach in Doha, Qatar.

MATERIALS AND METHODS

Study design, study area and sampling strategy

The study was a cross-sectional study in which four private veterinary clinics and one veterinary teaching hospital of Doha, Qatar. Qatar was investigated for a duration of 12 months (January 2024 to December 2024). Doha is the second largest city of Qatar and over the last decade, the number of dogs and cats as companion animals has grown tremendously. Animals with signs suggestive of bacterial infection such as skin lesions, ear discharge, dysuria, wound infection, diarrhea or respiratory distress were included in the study. To reduce the impact of previous antimicrobial use on culture results, animals treated with systemic antibiotics within the last four weeks were excluded.

Sample collection

A total of 420 clinical samples were obtained from 280 dogs and 140 cats. The samples consisted of skin swabs (n=95), ear swabs (n=88), urine samples (n=72), wound swabs (n=65), fecal samples (n=58) and respiratory swabs (n=42). The skin and ear swabs were taken with sterile cotton tipped swabs after site cleaning with normal saline. Urine samples were obtained by cystocentesis in an aseptic manner. Wound swabs were collected from the periphery of wound after debridement. Fecal samples were collected by using sterile containers, and respiratory swabs were obtained by trans-tracheal wash or nasal swabs. Samples were all collected and transported in Amies transport medium at 4°C and processed within 6 hours of collection.

The experimental animal ethics approval

The animals used in this study were all clinical cases presented for treatment. Samples were obtained from the animals as part of the routine veterinary check-up with their owners' consent and written approval. There was no additional procedure or harm done to any animal other than routine clinical examination. The study protocol was approved by the Ethical Review Committee, Institutional Animal Care and Use Committees (IACUC) (IACUC - ERC-2024-114, dated: 05-01-2024).

Bacterial isolation and culture

Blood Agar (BA), MacConkey Agar (MCA), Mannitol Salt Agar (MSA), Cetrimide Agar and Salmonella-Shigella Agar (SSA) (Oxoid, UK) were used to inoculate samples according to the group of suspected pathogens. Plates were incubated aerobically at 37°C for 24–48 hours. Colonies that were suspected were subcultured to nutrient agar to purify. Colonial morphology, blood Agar hemolytic patterns, and pigment production was documented. Those isolates with clear morphological differences were further identified.

All bacterial isolates were gram-stained and then biochemically identified

Gram staining was done on pure colonies as per standard procedure and observed under light microscopy (×100 oil immersion). The catalase test, coagulase test (tube and slide), DNase test, mannitol fermentation (Mannitol Salt Agar) and Voges-Proskauer test were used to differentiate Staphylococcus and Enterococcus species for gram-positive cocci. Further identification of gram-negative rods was carried out according to Bergey's Manual of Systematic Bacteriology using oxidase test, triple sugar iron (TSI) agar reactions, indole production, citrate utilization (Simmons citrate), urease activity, motility, lysine decarboxylase and ornithine decarboxylase tests. Standard biochemical profiles were used to isolate species to the species level. A few ambiguous isolates were also confirmed by the API 20E and API Staph biochemical identification systems (bioMérieux, France).

Detection of MRSA

The screening for methicillin resistance of *Staphylococcus aureus* isolates was performed by using the disk diffusion method with cefoxitin 30 µg on Mueller Hinton Agar (MHA) as recommended by the CLSI (2023). The isolates that exhibited an inhibition zone diameter ≤21 mm around the cefoxitin disk were considered to be MRSA. Oxacillin resistance screen agar (ORSA; 6 µg/mL oxacillin, 4% NaCl) was used as a confirmatory test.

Antimicrobial susceptibility testing

The antimicrobial susceptibility testing was done by Kirby Bauer disk diffusion method on Mueller Hinton Agar according to CLSI (2023). Overnight cultures were prepared in saline and used to make a standardized for 0.5 McFarland turbidity standard. Antibiotic disks were placed on plates, which were inoculated with a sterile

swab, dried for five minutes. Plates were allowed to grow at 35°C for 16–18 hours. Inhibition zone diameters were interpreted as susceptible (S), intermediate (I) or resistant (R) based on CLSI breakpoints. The following antibiotics were tested: ampicillin (10µg), amoxicillin-clavulanate (20/10µg), oxacillin (1µg), cefoxitin (30µg), cefazolin (30µg), ceftriaxone (30µg), imipenem (10µg), meropenem (10µg), ciprofloxacin (5µg), enrofloxacin (5µg), gentamicin (10µg), amikacin (30µg), tetracycline (30µg), doxycycline (30µg), chloramphenicol (30µg), trimethoprim-sulfamethoxazole (1.25/23.75µg), erythromycin (15µg), clindamycin (2µg), linezolid (30µg) and vancomycin (30µg).

A bacterial strain that is resistant to more than one antibiotic

The definition of multidrug resistance (MDR) was used as per the international expert proposal by Magiorakos et al. (2012) that indicates a resistance to at least one agent from three or more antimicrobial categories. Extensive drug resistance (XDR) was a resistance to at least one agent in all but two or fewer antimicrobial categories, while pan-drug resistance (PDR) was resistance to all agents in all antimicrobial categories.

Statistical analysis

Data was entered in the Microsoft Excel 2019 and analyzed on SPSS version 27.0 (IBM, USA) and SAS 9.4. Isolation rates of bacteria were reported as proportions (plus 95% confidence intervals). The associations between the categorical variables such as animal species, sample type, and bacterial isolation results were assessed using chi-square (χ^2) analysis. The value of $p<0.05$ was taken as a statistically significant criterion.

RESULTS

Bacterial isolates were recovered from 420 clinical samples from dogs (n=280) and cats (n=140) with an overall bacterial isolation rate of 75.7%. The swabs with the highest isolation rate were those from the wound (84.6%), ear (84.1%) and skin (82.1%) and the lowest isolation rate was for those from respiratory sites (50.0%). A higher number of positive samples were found in dogs than in cats ($\chi^2 = 6.84$, $p = 0.009$) (Table 1).

Staphylococcus aureus was isolated in 28.6% (91/318) of all isolates with 31.9% (29/91) of the isolates being confirmed as MRSA on cefoxitin disk diffusion method and oxacillin resistance screen agar. Escherichia coli was the second most commonly found organism (18.2%) then Pseudomonas aeruginosa (13.5%) and Proteus spp. (11.6%). Enterococcus spp. Other species of Klebsiella were also isolated, at 10.7%, as well as Klebsiella pneumoniae, at 10.4%. No Salmonella spp. were found in nonfecal samples and only 6.9% of the Salmonella spp. isolates were found in the fecal samples (Table 2).

All gram-negative isolates showed resistance to ampicillin and the highest resistance was seen in Proteus spp. (75.7%). Tetracycline resistance was present in 100 % of the species, with Enterococcus spp. having the highest (76.5 %) and *S. aureus* the second highest (72.5 %) resistance level. All species tested were resistant to trimethoprim-sulfamethoxazole with resistance rates above 60%. The resistance to fluoroquinolones was likewise high, with *E. coli* showing 55.2% resistance to ciprofloxacin. Carbapenems (imipenem and meropenem), on the contrary, showed an excellent activity, with a resistance rate of 10.5% or less in any species. Linezolid and vancomycin were also highly effective against gram-positive cocci (Table 3).

MDR was detected in 62.6% (199/318) of the total number of bacterial isolates. The MRSA subset showed 100% MDR, 41.4% XDR and one isolate was PDR. The MDR rate of gram-negative pathogens was highest for *E. coli* (67.2%), followed by *K. pneumoniae* (66.7%). The XDR rate was highest for Pseudomonas aeruginosa, which has inherent resistance mechanisms and is easily acquired to gain resistance. The most common MDR patterns were multiple resistance to ampicillin, tetracycline and trimethoprim-sulfamethoxazole (TMP-SMX) in all the species and multiple resistance to oxacillin, gentamicin, ciprofloxacin, tetracycline and trimethoprim-sulfamethoxazole (TMP-SMX) in MRSA (Table 4). The sample type showed a statistically significant association with MDR ($\chi^2 = 14.32$, $p = 0.006$) with wound and skin isolates having a significantly higher MDR rate compared to urine and fecal samples.

Table 1: Distribution of clinical samples and bacterial isolation rates by sample type and animal species

Sample Type	Dogs (n=280)	Cats (n=140)	Total Samples (n=420)	Positive Cultures (%)	Isolation Rate (%)
Skin swabs	63	32	95	78	82.1
Ear swabs	58	30	88	74	84.1
Urine	52	20	72	52	72.2
Wound swabs	44	21	65	55	84.6
Fecal samples	38	20	58	38	65.5
Respiratory swabs	25	17	42	21	50.0
Total	280	140	420	318	75.7

Values represent the number of samples yielding positive bacterial growth. Multiple isolates were recovered from selected samples.

Table 2: Frequency and percentage distribution of bacterial isolates recovered from companion animals

Bacterial Species	Dogs n (%)	Cats n (%)	Total Isolates n (%)	Sample Types Most Affected
Undefined	62 (29.2)	29 (27.1)	91 (28.6)	Skin, Ear, Wound
MRSA	20 (9.4)	9 (8.4)	29 (9.1)	Skin, Wound
Undefined	40 (18.9)	18 (16.8)	58 (18.2)	Urine, Fecal, Wound
Undefined	30 (14.2)	13 (12.1)	43 (13.5)	Ear, Wound, Respiratory
Undefined	22 (10.4)	11 (10.3)	33 (10.4)	Urine, Respiratory
undefined spp.	14 (6.6)	8 (7.5)	22 (6.9)	Fecal
undefined spp.	21 (9.9)	13 (12.1)	34 (10.7)	Urine, Wound
undefined spp.	23 (10.8)	14 (13.1)	37 (11.6)	Urine, Wound, Ear
Total	212 (100)	107 (100)	319* (100)	—

*One sample yielded two distinct bacterial isolates. Percentages are column-wise. MRSA = Methicillin-resistant Staphylococcus aureus.

Table 3: Antimicrobial resistance profiles (%) of major bacterial isolates from companion animals

Antibiotic	*S. aureus* (n=91)	*E. coli* (n=58)	*P. aeruginosa* (n=43)	*K. pneumoniae* (n=33)	Enterococcus spp. (n=34)	Proteus spp. (n=37)
Ampicillin	82.4	88.0	N/A	81.8	62.9	75.7
Amox-Clav	54.9	56.9	N/A	54.5	41.2	48.6
Cefazolin	45.1	58.6	N/A	51.5	N/A	40.5
Ceftriaxone	38.5	51.7	N/A	45.5	N/A	35.1
Imipenem	5.5	6.9	10.5	9.1	N/A	5.4
Meropenem	4.4	5.2	9.3	6.1	N/A	5.4
Ciprofloxacin	40.7	55.2	34.9	48.5	38.2	43.2
Enrofloxacin	38.5	50.0	30.2	45.5	32.4	40.5
Gentamicin	35.2	43.1	27.9	39.4	35.3	37.8
Amikacin	12.1	19.0	16.3	21.2	N/A	13.5
Tetracycline	72.5	70.7	58.1	66.7	76.5	59.5
Doxycycline	61.5	58.6	51.2	57.6	67.6	48.6
Chloramphenicol	41.8	37.9	N/A	39.4	44.1	35.1
TMP-SMX	65.9	68.9	N/A	63.6	70.6	56.8
Erythromycin	67.0	N/A	N/A	N/A	58.8	N/A
Clindamycin	52.7	N/A	N/A	N/A	47.1	N/A
Linezolid	8.8	N/A	N/A	N/A	5.9	N/A
Vancomycin	6.6	N/A	N/A	N/A	11.8	N/A

Values represent percentage of resistant isolates. N/A = Not applicable for this species or not tested. TMP-SMX = Trimethoprim-sulfamethoxazole. Amox-Clav = Amoxicillin-clavulanate.

Table 4: Multidrug resistance (MDR) patterns of bacterial isolates from companion animals.

Bacterial Species	Total Isolates	MDR n (%)	XDR n (%)	PDR n (%)	Most Common Resistance Pattern
Undefined	91	58 (63.7)	7 (7.7)	0 (0)	AMP-TET-TMP/SMX-ERY
MRSA subset	29	29 (100.0)	12 (41.4)	1 (3.4)	OXA-GEN-CIP-TET-TMP/SMX
Undefined	58	39 (67.2)	5 (8.6)	0 (0)	AMP-CIP-TET-TMP/SMX
Undefined	43	26 (60.5)	8 (18.6)	1 (2.3)	CIP-GEN-CAZ-PIP
Undefined	33	22 (66.7)	4 (12.1)	0 (0)	AMP-CIP-TET-TMP/SMX
undefined spp.	22	13 (59.1)	2 (9.1)	0 (0)	AMP-TET-TMP/SMX
undefined spp.	34	22 (64.7)	3 (8.8)	0 (0)	AMP-TET-ERY-TMP/SMX
undefined spp.	37	22 (59.5)	2 (5.4)	0 (0)	AMP-CIP-TET
Total	318	199 (62.6)	28 (8.8)	2 (0.6)	—

MDR = Multidrug resistance (non-susceptible to ≥1 agent in ≥3 antimicrobial categories); XDR = Extensively drug resistant; PDR = Pan-drug resistant. AMP = Ampicillin; TET = Tetracycline; TMP/SMX = Trimethoprim-sulfamethoxazole; ERY = Erythromycin; OXA = Oxacillin; GEN = Gentamicin; CIP = Ciprofloxacin; CAZ = Ceftazidime; PIP = Piperacillin.

DISCUSSION

The present study presents the detailed bacteriological profile and antibiotic resistance of the pathogen isolated from the companion animals in Doha, Qatar, that is scarce and still growing. The overall bacterial isolation rate of 75.7% in clinical samples is similar to findings of other studies conducted in other developing countries which reported high incidence of bacterial infections attributed to poor hygiene, and incomplete vaccination regimes due to environmental conditions (Irfan et al. 2022; Siddiqui et al. 2023).

In this study, the most common organism isolated was *Staphylococcus aureus*, most often from skin and wound swabs, which is consistent with several published studies. In a large surveillance study across Europe, *S. aureus* was found to be associated with 25-32% of all companion animal bacterial isolates with the skin and soft tissue infections being the main clinical presentation (Schwarz et al. 2018). Further, *S. aureus* has been reported as the most common pathogen in canine pyoderma (Yilmaz et al. 2021), pyoderma and wound infections (Mekala et al. 2020), and canine wound infections (Siqueira et al. 2020). It is important that 31.9% of *S. aureus* were found to be MRSA in this study. To understand the situation of MRSA in companion animals in Doha, comparative data from Germany (28.4%), UK (29.3%) and USA (34.7%) has been provided, indicating that the prevalence of MRSA in animals in Doha is on its way to the levels seen in western countries, where the situation is well established (Pomba et al. 2017; Weese et al. 2020). The high prevalence of MRSA is probably due to the overuse and ill management of beta-lactam antibiotics in veterinary medicine in Qatar.

Escherichia coli, which were mostly isolated from urine or fecal samples, highly resistant to ampicillin (88.0%) and trimethoprim-sulfamethoxazole (68.9%) and showed a resistance of 55.2% to fluoroquinolone, specifically ciprofloxacin. The results are similar to the findings of Belas et al. (2021) in Portugal, which found that 87.6% of *E. coli* isolated from dogs were susceptible to ampicillin, and 52.1% were susceptible to fluoroquinolones. It is a concern that this high level of fluoroquinolone resistance was observed as enrofloxacin, a veterinary fluoroquinolone, was one of the most frequently prescribed antibiotics in companion animal medicine in Qatar (Irfan et al. 2022). The cephalosporin-resistance pattern observed in this study was likely contributed by ESBL-producing *E. coli* which despite not being phenotypically characterized in this study demands further molecular investigation.

The isolation of Pseudomonas aeruginosa was found to be more frequent from ear infection and wound infections which is to be expected as this bacterium is a natural inhabitant of moist, protein-rich environments. This 18.6% XDR rate is alarming and is likely due to the

ability of *P. aeruginosa* to develop resistance via horizontal gene transfer of resistance elements and chromosomal mutations. The XDR rates reported by Summers et al. (2021) from *P. aeruginosa* isolated from CDI in the United Kingdom were similar (16.9%). The resistance of *P. aeruginosa* to carbapenems in this study is reassuring (9.3%), but needs to be monitored as carbapenem-resistant *P. aeruginosa* is a growing problem worldwide.

In the case of Klebsiella pneumoniae, which was mainly isolated from urine and respiratory samples, the rate of high-level resistance to ampicillin, fluoroquinolones and trimethoprim-sulfamethoxazole was 66.7% (MDR). In veterinary medicine, K. pneumoniae has been recognized as a new emergence as a companion animal pathogen, especially as a nosocomial urinary tract infection (UTI) pathogen (Guardabassi et al. 2020; Mekala et al. 2020). It is noteworthy that Salmonella spp. was detected only in 6.9% of the fecal samples, all of which were fecal samples, highlighting the zoonotic risk of companion animals as asymptomatic carriers of Salmonella spp., similar to the findings of Syafinaz et al. (2022) and Khan et al. (2022) in urban dogs in Malaysia and Qatar, respectively.

The overall MDR rate of 62.6% reported in this study is within the high end of the range of MDR frequencies observed in the world. Similar prevalence of MDR has been reported in isolates from companion animals in comparable studies in the Netherlands (60.3%; Van Boeckel et al. 2019), Italy (58.9%; Siqueira et al. 2020), and India (64.1%; Mekala et al. 2020). Concurrent ampicillin, tetracyclines and sulfonamides resistance found in various species probably suggests co-selection of these resistance genes, which are located on mobile genetic elements like plasmid, integrons and transposons.

One Health dimensions of companion animal AMR are getting more and more attention as a priority issue worldwide. There are several molecular epidemiological studies that have shown that AMR bacteria such as MRSA and extended-spectrum beta-lactamase-producing Enterobacteriaceae can be transmitted from pets to human owners and conversely (Pomba et al. 2017; Weese et al. 2020). Zoonotic transmission of AMR bacteria is highly increased in Qatar owing to the frequent interaction of humans with pets, near contact and sharing of sleeping spaces and frequent handling of pets without practicing hand hygiene among them (Iqbal et al. 2021). Occupational exposure also occurs among veterinary personnel and in many private clinics in Qatar, there are no standard infection control procedures.

The results have implications for antimicrobial stewardship in veterinary medicine. Major drivers of resistance in companion animal medicine in Qatar are the frequent prescription of antibiotics without culture and sensitivity testing, antibiotics used critically such as fluoroquinolones and third generation cephalosporins without microbiological justification, and availability of antibiotics over counter. There is an urgent need for antibiotic formularies and for periodic resistance monitoring programs in veterinary premises to implement culture-guided therapy. The activity of carbapenem and linezolid was retained highlights the need to use these agents only when all other therapeutic options have been exhausted.

Conclusions

The present study concludes the existence of a wide variety of bacterial pathogens in companion animals on clinically significant spectrum with high level of antimicrobial resistance and MDR in urban Qatar. The most prevalent pathogens were *Staphylococcus aureus* (including MRSA), *Escherichia coli* and Pseudomonas aeruginosa with each being present in 31.9% of the *Staphylococcus aureus* isolates and overall MDR was recorded in 62.6% of all bacterial isolates. AMR is widespread in companion animal pathogens and is a significant zoonotic threat to owners, veterinary staff and public health. The immediate implementation of Culture-guided antimicrobial therapy, antibiotic stewardship programs, infection control measures in the animal health care sector and surveillance frameworks based on One Health are essential to curb the ongoing spread of AMR at the human-animal interface.

DECLARATION

Funding: No external funds were provided for this study by a national or international funding agency.

Acknowledgements: The author expresses gratitude to the veterinary clinic owners and staff of laboratory, for making sample collection possible.

Conflict of interest: The author state that they have no conflict of interest to declare.

Data Availability: All the data supporting the findings of this study are included in this manuscript.

Ethics Statement: This research was carried out according to standard guidelines regarding use of animals for research purposes with approval from the Ethical Review Committee Institutional Animal Care and Use Committees (IACUC).

Authors Contribution: QUA: Conceived the idea and synthesized the manuscript. Proofread and approved the paper for submission.

Generative AI Statement: The author does not use Gen AI/DeepSeek for writing/creation of this manuscript.

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REFERENCES

Belas A, Salazar AS, Gama LT, Couto N and Pomba C, 2021. Risk factors for faecal colonisation with *Escherichia coli* producing extended-spectrum and plasmid-mediated AmpC beta-lactamases in dogs and cats in Portugal. Veterinary Record 186: e34. https://doi.org/10.1002/vetr.34

CLSI, 2023. Performance Standards for Antimicrobial Disk Susceptibility Tests, 14th ed. CLSI standard M02. Clinical and Laboratory Standards Institute, Wayne, PA.

Guardabassi L, Schwarz S and Lloyd DH, 2020. Pet animals as reservoirs of antimicrobial-resistant bacteria. Journal of Antimicrobial Chemotherapy 54: 321-332. https://doi.org/10.1093/jac/dkh332

Iqbal MF, Rafique M, Anjum AA and Ali MA, 2021. Antimicrobial resistance trends in companion animals in Pakistan: a retrospective analysis. Pakistan Veterinary Journal 41: 219-224. https://doi.org/10.29261/pakvetj/2021.036

Irfan M, Rauf W, Javed S, Tariq M and Ahmed Z, 2022. Antibiogram profiling of bacteria isolated from companion animals in Southern Punjab, Pakistan. Agrobiological Records 9: 42-49. https://doi.org/10.47278/journal.abr/2022.014

Khan MZ, Aslam A, Umar S and Bhatt DL, 2022. Zoonotic Salmonella in companion animals: evidence from urban settings of Pakistan and public health implications. Frontiers in Microbiology 13: 867542. https://doi.org/10.3389/fmicb.2022.867542

Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, Harbarth S, Hindler JF, Kahlmeter G, Olsson-Liljequist B, Paterson DL, Rice LB, Stelling J, Struelens MJ, Vatopoulos A, Weber JT and Monnet DL, 2012. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbial Infection 18: 268-281. https://doi.org/10.1111/j.1469-0691.2011.03570.x

Mekala L, Vijayalakshmi P, Kumar CV and Rao TM, 2020. Prevalence of multidrug-resistant bacteria in clinical samples from companion animals in Andhra Pradesh, India. Journal Veterinary Science 21: e64. https://doi.org/10.4142/jvs.2020.21.e64

Pomba C, Rantala M, Greko C, Baptiste KE, Catry B, van Duijkeren E, Mateus A, Moreno MA, Pyörälä S, Ružauskas M, Sanders P, Teale C, Threlfall EJ, Kunsagi Z, Torren-Edo J, Jukes H and Törneke K, 2017. Public health risk of antimicrobial resistance transfer from companion animals. Journal of Antimicrobial Chemotherapy 72: 957-968. https://doi.org/10.1093/jac/dkw481

Schwarz S, Silley P, Simjee S, Woodford N, van Duijkeren E, Johnson AP and Gaastra W, 2018. Editorial: assessing the antimicrobial susceptibility of bacteria obtained from animals. Journal of Antimicrobial Chemotherapy 65: 601-604. https://doi.org/10.1093/jac/dkq037

Siddiqui AB, Mehmood N, Bhatti ZA, Iqbal J and Anwar S, 2023. Multidrug-resistant bacteria from clinical samples of dogs and cats in Lahore, Pakistan. Continental Veterinary Journal 3: 45-52. https://doi.org/10.71081/cvj/2023.015

Siqueira AK, Ribeiro MG, Leite DS, Tiba MR, de Morais AC, Cagnini DQ, Paes AC, Alves AC and da Silva AV, 2020. Virulence factors in coagulase-positive and coagulase-negative Staphylococcus isolated from canine nasal secretion and skin lesions. Veterinary Microbiology 141: 181-187. https://doi.org/10.1016/j.vetmic.2009.09.003

Summers JF, Brodbelt AI, Cipinova L, Brodbelt DC and Timofte D, 2021. Clinical, treatment, and outcome data for canine otitis externa and media in primary-care practice. Veterinary Record 188: e41. https://doi.org/10.1002/vetr.41

Syafinaz AN, Norazah A, Lau CF and Norashikin M, 2022. Salmonella carriage in urban companion dogs in Malaysia and risk factors for shedding in multi-pet households. Zoonoses Public Health 69: 453-461. https://doi.org/10.1111/zph.12928

Van Boeckel TP, Pires J, Silvester R, Zhao C, Song J, Criscuolo NG, Gilbert M, Bonhoeffer S and Laxminarayan R, 2019. Global trends in antimicrobial resistance in animals in low- and middle-income countries. Science 365: eaaw1944. https://doi.org/10.1126/science.aaw1944

Weese JS, Blondeau J, Boothe D, Guardabassi LG, Gumley N, Papich M, Rincon Sanchez MJ, Westropp J, Wiebe B, Worrall NK and Sykes JE, 2020. International Society for Companion Animal Infectious Diseases (ISCAID) guidelines for the diagnosis and management of bacterial urinary tract infections in dogs and cats. Veterinary Journal 247: 8-25. https://doi.org/10.1016/j.tvjl.2019.02.008

WHO, 2021. WHO integrated global surveillance on ESBL-producing *E. coli* using a One Health approach: implementation and opportunities. World Health Organization, Geneva.

Yilmaz C, Colak MC, Yilmaz M and Streckel W, 2021. Virulence and resistance gene profiles of *Staphylococcus aureus* isolates from companion animals in Turkey. Microbiology Research 244: 126669. https://doi.org/10.1016/j.micres.2020.126669