Volume 3, Number 1, 2026
Pages 234-246
Bioscience Insights
ISSN: 3080-3489 (Print)
ISSN: 3080-3497 (Online)
BiosciInsights.com

ANTIMICROBIAL RESISTANCE PATTERNS OF BACTERIAL ISOLATES FROM FELINE CLINICAL INFECTIONS IN A PRIVATE VETERINARY PRACTICE IN LAHORE, PAKISTAN

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Article Information

Article History

Received:	January 15, 2026
Revised:	February 15, 2026
Accepted:	May 03, 2026
Available Online:	June 30, 2026

Keywords:
Antimicrobial resistance; feline; multidrug resistance; antibiogram; Pakistan; One Health

Abstract

Antimicrobial resistance (AMR) in companion animals is a recognized One Health concern, yet feline-specific AMR data from Pakistan is absent from the published literature. We retrospectively reviewed bacterial culture and antimicrobial sensitivity reports from 200 feline clinical infection cases (urinary, skin/wound, otic, respiratory, and other sites) presenting to a private veterinary hospital in Lahore, Pakistan, between 2021 and 2025. Multidrug resistance (MDR) was defined as non-susceptibility to at least one agent in three or more antimicrobial classes. Escherichia coli (33.0%) and Staphylococcus pseudintermedius (21.0%) were the most frequently isolated organisms, predominating in urinary and skin/wound infections respectively, while Pseudomonas aeruginosa (11.5%) predominated in otic infections. Our primary MDR definition excluded organism-drug combinations attributable to intrinsic resistance. On that basis, prevalence was 62.5% (125/200; 95% CI 55.6-68.9%). The unadjusted panel-based figure, reported for comparability with published series, was 80.0% (160/200; 95% CI 73.9-85.0%). Twelve comparisons were run, so a Bonferroni-corrected threshold of $P<0.004$ was applied. Only infection site survived it ($P<0.001$ under both definitions), with urinary isolates carrying the highest adjusted burden (81.9%). Apparent

associations with chronicity (P=0.049) and clinical outcome (P=0.023) appeared only under the unadjusted definition, did not persist after adjustment (P=0.097 and P=0.589), and do not survive correction. Both should be regarded as unconfirmed. Organism identity was the more consistent correlate of outcome: infections caused by Pseudomonas aeruginosa, Enterococcus faecalis or Proteus mirabilis resolved in 24.0% of cases versus 48.0% for other organisms (P=0.003). Resistance to amikacin (17.0%) and imipenem/meropenem (4.6%) remained low across all organisms, in contrast to high resistance to ampicillin (73.6%) and clindamycin (77.3%). Two constraints limit how these figures may be used. Concurrent ATCC quality-control strains were not available in this setting, so individual susceptibility calls carry unquantified imprecision. And every isolate came from a culture-submitted, treatment-enriched caseload. These are descriptive findings from one practice. They are not population prevalence estimates, and they should not be used as an empirical-therapy reference for first-presentation infections.

Novelty Statement

To our knowledge, this is the first descriptive characterization of antimicrobial resistance (AMR) in feline clinical bacterial isolates from Pakistan. The country is absent from the companion-animal AMR literature, despite established surveillance in East Asia, Europe and North America. Two features distinguish this work. First, it applies an intrinsic-resistance-adjusted multidrug-resistance definition as its primary analysis, so that acquired resistance is not conflated with resistance that is simply a property of the organism. Second, it uses that adjustment to show which apparent associations survive and which do not: infection site holds, while chronicity and clinical outcome do not. The result is a descriptive baseline for a population that currently has none, not a reference table for empirical prescribing.

INTRODUCTION

Introduction

Antimicrobial resistance (AMR) is recognized by the World Health Organization as one of the top ten global public health threats, with companion animals increasingly identified as both a consequence of, and a contributor to, resistance patterns relevant to human health through shared households, environments, and, at times, antimicrobial classes (WHO, 2023). Surveillance in companion animals has expanded substantially over the past five years across East Asia, Europe and North America (Marco-Fuertes et al., 2022; Sobkowich et al., 2023; Seo et al., 2025; Monteiro et al., 2025). Two organisms recur across these series. Escherichia coli and Staphylococcus pseudintermedius are consistently the leading isolates, with concerning rates of multidrug resistance (MDR) in urinary, dermatological and otic infections (Moon et al., 2023).

Pakistan, despite this global expansion of companion-animal AMR surveillance, remains entirely unrepresented in the published literature on the subject. This is a meaningful gap in practice, not just in the literature: empirical antimicrobial selection, made before culture results are available or in place of culture testing altogether where owners cannot afford it, is currently guided by international data of uncertain local relevance, underscoring the urgent need for culture-based diagnostics and local surveillance. International guidelines such as those of the International Society for Companion Animal Infectious Diseases (ISCAID) for urinary tract infection management (Weese et al., 2019) were developed primarily from North American and European data and may not reflect resistance patterns actually circulating in this population.

We therefore set out to do three things. First, characterize the bacterial organisms isolated from feline clinical infections across common sites in a Pakistani private practice. Second, determine resistance patterns for the antibiotics most frequently prescribed here. Third, identify which clinical and signalment factors are associated with multidrug resistance, applying the classification framework validated for companion animal pathogens (Sweeney et al., 2018).

Materials and Methods

This retrospective study was conducted at General Veterinary Hospital, Lahore, Pakistan, using bacterial culture and antimicrobial sensitivity reports generated during routine clinical care of feline patients between 2021 and 2025. Cases were included if a positive bacterial culture with a completed sensitivity panel was on file, together with basic signalment data; cultures with no growth or judged contaminated were excluded. Two hundred eligible cases were identified. The sample size was determined by the number of eligible feline culture-positive cases presenting during the study period; no a priori power calculation was performed, as the primary aim was descriptive characterization rather than hypothesis testing.

Bacterial identification was performed using standard phenotypic and conventional biochemical panels (including Gram staining, catalase, coagulase, oxidase, IMViC, and urease tests). Antimicrobial susceptibility testing was performed via the standardized Kirby-Bauer disk diffusion method on Mueller-Hinton agar and interpreted using the Clinical and Laboratory Standards Institute (CLSI) veterinary antimicrobial susceptibility testing (VET01) criteria current at the time of testing.

For each case, age, sex, neuter status, infection site (urinary, skin/wound, otic, respiratory, or other), episode chronicity (first episode versus recurrent/chronic), prior antibiotic exposure for the current episode, the organism isolated, treatment adjustment following culture, and clinical outcome were extracted from clinical records. Susceptibility (susceptible, intermediate, or resistant) was recorded for twelve antimicrobials spanning nine classes commonly used in this practice: amoxicillin-clavulanate and ampicillin (penicillins), cephalexin and ceftriaxone (cephalosporins), enrofloxacin and marbofloxacin (fluoroquinolones), gentamicin and amikacin (aminoglycosides), doxycycline (tetracycline), trimethoprim-sulfamethoxazole (folate pathway inhibitor), clindamycin (lincosamide), and imipenem/meropenem (carbapenem). Not every antimicrobial was tested against every isolate; resistance percentages were calculated among isolates actually tested for each agent.

Operational definitions for chronicity and outcome were extracted directly from the medical history. “Recurrent/chronic” was assigned if the record documented previous episodes of the same infection type within the preceding six months, or ongoing signs persisting for more than 14 days despite initial empirical therapy. “First episode” denoted acute presentations with no prior history of similar signs. Because follow-up microbiological cultures are rarely affordable for owners in this setting, clinical outcomes were defined based on the final follow-up visit or documented owner communication: “resolved” (complete cessation of presenting signs with no further antimicrobial therapy required), “improved” (documented reduction in severity but requiring extended management or monitoring), “unresolved/refractory” (no clinical improvement or worsening of signs requiring escalation to a different antimicrobial class), or “lost to follow-up”.

Multidrug resistance was defined, following the standardized framework validated for companion animal pathogens (Sweeney et al., 2018), as non-susceptibility to at least one agent in three or more of

the nine antimicrobial classes tested, applied uniformly to the raw susceptibility data for all 200 isolates. Because several organism-drug combinations in the panel reflect intrinsic rather than acquired resistance, a second, more conservative MDR classification was calculated in parallel, in which classes were counted only where the agent is expected to have activity against that organism. Combinations excluded from the adjusted count were: lincosamides against Gram-negative isolates; aminopenicillins, first-generation cephalosporins, ceftriaxone, tetracyclines and folate-pathway inhibitors against Pseudomonas aeruginosa; lincosamides, cephalosporins, folate-pathway inhibitors and aminoglycosides against Enterococcus faecalis; tetracyclines against Proteus mirabilis; and aminopenicillins against Klebsiella pneumoniae. Both classifications are reported throughout. The adjusted classification is designated the primary analysis, because a uniform panel-based count systematically overstates resistance in organisms that are intrinsically non-susceptible to several agents on the panel. The panel-based figure is retained alongside it for comparability with published series that use unadjusted panels.

Descriptive statistics summarized organism distribution, site distribution, and resistance rates. Associations between MDR status and categorical variables (age group, sex, infection site, chronicity, prior antibiotic exposure, and clinical outcome) were tested using Pearson's chi-square test under both MDR definitions. Prior antibiotic exposure was analysed as a three-level variable, with cases in which exposure could not be established from the record retained as a distinct “unknown” category rather than excluded. Isolates were additionally grouped by organism. One group comprised P. aeruginosa, E. faecalis and P. mirabilis, all of which carry extensive intrinsic resistance; the other comprised every remaining organism. This grouping was tested against clinical outcome.

Twelve comparisons were performed in total: six variables under two MDR definitions. A Bonferroni-corrected significance threshold of $P<0.004$ was therefore adopted, and results not meeting it are reported as unconfirmed regardless of their uncorrected P-value. Confidence intervals were calculated by the Wilson score method. Analyses were performed in Python (pandas, SciPy).

This study used retrospective clinical data collected during routine care, with no new animal experimentation. Data use was reviewed and approved under an institutional exemption for retrospective clinical audits by the Ethical Review Committee of General Veterinary Hospital, Lahore (Ref: GVH-ERC-2025-AMR), consistent with national animal welfare regulations.

Results

The 200 included cats skewed toward adults (39.0% aged 3-7 years); 51.5% were male and 75.5% were neutered. Infections were most often urinary (41.5%), followed by skin/wound (29.5%), otic (14.5%), respiratory (12.5%), and other sites (2.0%). Recurrent or chronic infections made up 57.5% of the cohort, and 57.0% had documented prior antibiotic exposure for the current episode (Table 1).

Escherichia coli was the most frequently isolated organism overall (33.0%), followed by Staphylococcus pseudintermedius (21.0%) and Pseudomonas aeruginosa (11.5%). Organism

distribution varied markedly by site: E. coli predominated in urinary infections (56/83, 67.5%), S. pseudintermedius in skin/wound infections (33/59, 55.9%), and P. aeruginosa in otic infections (13/29, 44.8%), while Pasteurella multocida and Bordetella bronchiseptica together accounted for most respiratory isolates (19/25, 76.0%) (Table 2).

Resistance rates varied substantially by antimicrobial and organism (Table 3). Resistance was lowest to amikacin (17.0%) and imipenem/meropenem (4.6%) and highest to clindamycin (77.3%) and ampicillin (73.6%). Pseudomonas aeruginosa isolates showed particularly high resistance to beta-lactams, including complete resistance to amoxicillin-clavulanate, ampicillin, and cephalexin (100.0% each), consistent with known intrinsic resistance in this organism; even here, amikacin (5.3%) and imipenem/meropenem (9.5%) resistance remained comparatively low.

Adjusted MDR prevalence was 62.5% (125/200; 95% CI 55.6-68.9%). The unadjusted panel-based figure was 80.0% (160/200; 95% CI 73.9-85.0%). The gap between them is not trivial: roughly one isolate in five counted as MDR on the raw panel qualified through intrinsic resistance alone.

Adjusted MDR prevalence ranged from 50.0% in 2022 to 68.8% in 2023 (Table 7). While the overlapping confidence intervals suggest general stability, the sample size per year lacks the statistical power to definitively rule out temporal changes or material drift in testing practice over the five years.

Infection site was the only variable to meet the corrected threshold, and it did so under both definitions (adjusted χ^2=27.24, df=4, P<0.001; panel-based χ^2=34.73, df=4, P<0.001). Urinary isolates carried the highest burden either way (81.9% adjusted, 95% CI 72.3-88.7%; 92.8% panel-based, 95% CI 85.1-96.6%). Otic infections behaved differently. Their apparent burden fell from 86.2% to 41.4% on adjustment, which reflects the predominance of P. aeruginosa at that site rather than acquired resistance. No other variable survived correction. Chronicity reached nominal significance under the panel-based definition only (recurrent/chronic 85.2% versus first episode 72.9%; P=0.049) and lost it on adjustment (P=0.097). Prior antibiotic exposure showed a consistent trend but never reached significance (P=0.079 and P=0.071). Age group and sex were unassociated with MDR status throughout (Table 4).

Under the panel-based definition, MDR status was associated with clinical outcome (χ^2=9.57, df=3, P=0.023), with resolution achieved in 36.9% of MDR cases compared with 62.5% of non-MDR cases. This association did not persist under the intrinsic-resistance-adjusted definition (χ^2=1.92, df=3, P=0.589; resolution 39.2% versus 46.7%), indicating that it was substantially attributable to organisms carrying extensive intrinsic resistance rather than to acquired multidrug resistance itself (Table 5).

Isolate identity proved more informative than resistance classification. All 50 isolates in the high-intrinsic-resistance group were classified MDR on the raw panel. Infections caused by these organisms resolved in 24.0% of cases against 48.0% for all others, and unresolved or refractory infection was twice as frequent (28.0% versus 14.0%; χ^2=14.24, df=3, P=0.003, Table 6). Treatment was escalated to a reserve-class antibiotic in 24 cases, all of them MDR on the raw panel; this reflects clinicians responding to susceptibility reports rather than an independent effect of resistance on outcome.

Discussion

This appears to be the first characterization of feline clinical AMR patterns from Pakistan. The existing literature is concentrated in East Asia, Europe and North America (Marco-Fuertes et al., 2022; Sobkowich et al., 2023; Seo et al., 2025; Monteiro et al., 2025), and South Asia is largely absent from it. The predominance of E. coli in urinary infections and S. pseudintermedius in skin/wound infections mirrors findings from companion animal AMR surveillance elsewhere (Moon et al., 2023; Seo et al., 2025), which is reassuring given this dataset comes from a single resource-limited practice rather than a multi-center surveillance network.

The MDR prevalence found here (62.5% adjusted, 80.0% unadjusted) sits well above rates reported in feline isolates from South Korea (14.4-26.7%) (Moon et al., 2023; Seo et al., 2025). That comparison should be read loosely rather than literally. Those studies sampled healthy or community animals, used different antimicrobial panels, and applied their own MDR definitions; a like-for-like comparison would require clinical-infection series using matched panels, which are not available for this region. Several factors nonetheless plausibly contribute to the gap. This sample was drawn exclusively from clinical infections submitted for culture, a population already enriched for treatment failure and prior antibiotic exposure, whereas some comparator studies sampled healthy or community animals. Over half of this cohort had documented prior antibiotic exposure and recurrent or chronic disease, both plausible drivers of resistance selection. Antimicrobials in this practice setting are also frequently available without prescription restriction, and empirical, culture-independent use is common where owners cannot afford susceptibility testing — a pattern that likely accelerates local resistance selection relative to settings with more regulated antimicrobial access.

The outcome analysis requires careful interpretation, and the sensitivity analysis is instructive here. Under the panel-based definition, MDR infections resolved barely more than half as often as non-MDR infections, a difference that would appear to make a strong case for changing prescribing behaviour. That association did not survive adjustment for intrinsic resistance. The explanation is largely one of organism identity: P. aeruginosa, E. faecalis and P. mirabilis are intrinsically non-susceptible to several agents on the panel and were therefore classified MDR in every case, and these same organisms are recognised as difficult to treat for reasons that extend beyond acquired resistance, including biofilm formation, anatomical site and host factors. The apparent MDR-outcome relationship is thus confounded by which organism was isolated, and we do not interpret these data as demonstrating that acquired multidrug resistance caused treatment failure in this cohort.

What the data do support is more modest but still clinically actionable: infections caused by this group of organisms carried substantially poorer resolution rates. For the practising clinician, organism identity on culture is therefore a more reliable early signal of likely difficulty than the MDR label alone. Establishing whether acquired resistance independently worsens outcome would require a larger cohort with multivariable adjustment for organism, site and severity, which the present sample cannot support.

The elevated MDR prevalence in urinary infections has implications for how empirical choices are reasoned about here, and the site pattern is clearer once intrinsic resistance is accounted for: urinary isolates retained a high adjusted MDR rate (81.9%), which is not explained by intrinsic resistance. What does explain it cannot be determined here; acquired resistance, nosocomial or environmental transmission, and circulating resistant clones would all be consistent with these data. The otic rate, by contrast, halved on adjustment and is better read as the intrinsic profile of P. aeruginosa than as multidrug resistance. Ampicillin and amoxicillin-clavulanate, both reasonable first-line choices under ISCAID's urinary tract infection guidance (Weese et al., 2019), showed resistance exceeding 70% and 45% respectively in this population. This is not a flaw in those guidelines, which were built from different populations. Nor does it license using the present figures as a substitute. Resistance rates drawn from culture-submitted, treatment-enriched cases will overstate what a clinician faces at first presentation, and applying them empirically would push prescribing toward broader agents than most cases require. What these data support is a case for building a local antibiogram from unselected first-presentation cultures, not the use of this one as that reference. The consistently low resistance to amikacin and imipenem/meropenem, including in intrinsically resistant P. aeruginosa isolates, likely reflects their restricted use as reserve agents in this practice rather than any regional advantage, and supports continuing to preserve them for confirmed resistant infections rather than empirical use.

The most serious limitation is the absence of concurrent quality control. Standard ATCC reference strains (E. coli ATCC 25922, S. aureus ATCC 25923, P. aeruginosa ATCC 27853) were not run alongside clinical isolates, because routine access to and supply of these strains is not feasible in this setting. Testing followed standard phenotypic protocols on Mueller-Hinton agar. Even so, without concurrent controls we cannot quantify day-to-day variation in disc potency, media performance or incubation conditions, and individual susceptibility calls therefore carry imprecision we are unable to bound. This constrains what any single resistance percentage in this paper can bear. It is stated in the abstract for that reason.

The second constraint is generalisability. Every isolate was submitted for culture during clinical care, usually after empirical therapy had failed or in cats with chronic or recurrent disease. The population is heavily enriched for treatment-refractory infection. Neither the 62.5% nor the 80.0% figure represents multidrug resistance among feline infections in Pakistan generally, and community-level resistance is almost certainly lower. These are descriptive figures from one caseload.

Several analytical limitations also apply. Not every antimicrobial was tested against every isolate, and we could not verify retrospectively whether panel composition shifted over the study period; annual MDR rates were broadly consistent (Table 7), but yearly sample sizes are too small to exclude drift. Organism-specific resistance estimates based on small denominators carry wide intervals and should not guide individual prescribing decisions; amikacin resistance in P. aeruginosa, for instance, is 5.3% with a 95% confidence interval of 0.9-24.6%. Chronicity and outcome definitions were taken from the

clinical record rather than applied prospectively against standardized criteria. We did not perform multivariable regression, which would be needed to separate the contributions of organism, site and severity, and which the size of this sample does not comfortably support. Genotypic confirmation of resistance mechanisms was not performed.

Conclusion

To our knowledge, this is the first feline-specific antimicrobial resistance data reported from Pakistan. Adjusted multidrug resistance among cultured clinical isolates was 62.5%, and infection site was the only variable associated with it after correction for multiple testing, with urinary isolates carrying the highest burden. Apparent associations with chronicity and clinical outcome did not survive either adjustment for intrinsic resistance or correction; organism identity was the more consistent correlate of poor resolution.

Two caveats govern the use of these figures. They derive from a culture-submitted, treatment-enriched caseload and are not community prevalence estimates. And they were generated without concurrent quality-control strains, so individual percentages carry imprecision we cannot quantify. What the data support is narrower than an empirical-therapy reference: resistance to common first-line agents appears high enough in this population to justify culture and sensitivity testing wherever affordable, particularly in recurrent urinary infections, and to justify building a local antibiogram from unselected first-presentation cultures. Antimicrobial stewardship warrants attention in this setting.

Acknowledgment

None.

Conflict of Interest

The authors declare no conflict of interest.

Authors' Contribution

ZA conceived and designed the study, extracted the clinical data, performed the statistical analysis, and drafted the manuscript. IH supervised the laboratory procedures (phenotypic bacterial identification and antimicrobial susceptibility testing) and critically reviewed the manuscript for intellectual content. MTA, TY, IHB and FR helped for doing experiments and data collection. And all authors approved the final version.

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Tables

Table 1. Case characteristics (n=200)

Variable	Category	n	%
Age group	Adult (3-7y)	78	39.0
	Young adult (1-3y)	50	25.0
	Mature adult (7-10y)	32	16.0
	Senior (>10y)	20	10.0
	Young (<1y)	20	10.0
Sex	Male	103	51.5
	Female	97	48.5
Neuter status	Neutered	151	75.5
	Intact	49	24.5
Infection site	Urinary	83	41.5
	Skin/Wound	59	29.5
	Otic	29	14.5
	Respiratory	25	12.5
	Other	4	2.0
Chronicity	Recurrent/Chronic	115	57.5
	First episode	85	42.5
Prior antibiotic exposure	Yes	114	57.0
	No	70	35.0

Variable	Category	n	%
	Unknown	16	8.0

Table 2. Organism distribution by infection site

Organism	Urinary	Skin/Wound	Otic	Respiratory	Other	Total
Escherichia coli	56	9	0	0	1	66
Staphylococcus pseudintermedius	0	33	9	0	0	42
Pseudomonas aeruginosa	0	10	13	0	0	23
Pasteurella multocida	0	3	0	12	0	15
Proteus mirabilis	9	0	5	0	0	14
Enterococcus faecalis	11	0	0	0	2	13
Staphylococcus spp.	6	0	0	3	0	9
Bordetella bronchiseptica	0	0	0	7	0	7
Streptococcus spp.	0	4	2	0	0	6
Klebsiella pneumoniae	1	0	0	3	0	4
Staphylococcus aureus	0	0	0	0	1	1
Total	83	59	29	25	4	200

Table 3. Antimicrobial resistance rates, overall and for the three most frequently isolated organisms (% resistant among isolates tested)

Antimicrobial	Overall % R (n tested)	E. coli % R (n)	S. pseudintermedius % R (n)	P. aeruginosa % R (n)
Amoxicillin-clavulanate	47.0 (200)	45.5 (66)	47.6 (42)	100.0 (23)*
Ampicillin	73.6 (182)	83.1 (59)	87.5 (40)	100.0 (19)*
Cephalexin	58.0 (200)	57.6 (66)	45.2 (42)	100.0 (23)*
Ceftriaxone	46.6 (174)	35.2 (54)	50.0 (38)	87.0 (23)*
Enrofloxacin	44.0 (200)	42.4 (66)	45.2 (42)	73.9 (23)
Marbofloxacin	35.8 (190)	37.1 (62)	40.0 (40)	50.0 (22)
Gentamicin	42.4 (184)	44.6 (65)	25.6 (39)	71.4 (21)
Amikacin	17.0 (171)	9.4 (53)	16.2 (37)	5.3 (19)
Doxycycline	62.2 (180)	80.0 (55)	40.5 (37)	100.0 (22)*
Trimethoprim-sulfamethoxazole	64.2 (179)	79.4 (63)	44.7 (38)	100.0 (19)*
Clindamycin	77.3 (172)	100.0 (55)*	55.3 (38)	100.0 (20)*
Imipenem/Meropenem	4.6 (174)	6.7 (60)	2.9 (35)	9.5 (21)

*Percentages are calculated among isolates actually tested for each agent; n tested is shown in parentheses. * denotes an organism-drug combination affected by recognised intrinsic resistance, excluded from the adjusted MDR classification.*

Note: Organism-specific resistance estimates based on fewer than 30 isolates (e.g., P. aeruginosa) carry wide confidence intervals and should be interpreted with caution. For example, amikacin resistance in P. aeruginosa (n=19) was 5.3% (95% CI 0.9-24.6%).

Table 4. Association between clinical/signalment variables and multidrug resistance (MDR) status under both definitions (chi-square)

Variable	Panel-based χ^2 (df)	Panel-based P	Adjusted χ^2 (df)	Adjusted P
Age group	5.66 (4)	0.226	6.51 (4)	0.164
Sex	0.15 (1)	0.697	0.07 (1)	0.798
Infection site	34.73 (4)	<0.001	27.24 (4)	<0.001
Chronicity	3.87 (1)	0.049	2.76 (1)	0.097
Prior antibiotic exposure	5.07 (2)	0.079	5.29 (2)	0.071
Clinical outcome	9.57 (3)	0.023	1.92 (3)	0.589

Table 5. Clinical outcome by multidrug resistance (MDR) status under both definitions

MDR Status	Resolved	Improved	Unresolved/Refractory	Lost to Follow-up
Panel-based: MDR (n=160)	59 (36.9%)	60 (37.5%)	31 (19.4%)	10 (6.2%)
Panel-based: Non-MDR (n=40)	25 (62.5%)	8 (20.0%)	4 (10.0%)	3 (7.5%)
Adjusted: MDR (n=125)	49 (39.2%)	44 (35.2%)	22 (17.6%)	10 (8.0%)
Adjusted: Non-MDR (n=75)	35 (46.7%)	24 (32.0%)	13 (17.3%)	3 (4.0%)

Panel-based χ^2=9.57, df=3, P=0.023; adjusted χ^2=1.92, df=3, P=0.589.

Table 6. Clinical outcome by organism group

Organism group	Resolved	Improved	Unresolved/Refractory	Lost to Follow-up
High intrinsic resistance* (n=50)	12 (24.0%)	23 (46.0%)	14 (28.0%)	1 (2.0%)
All other organisms (n=150)	72 (48.0%)	45 (30.0%)	21 (14.0%)	12 (8.0%)

** Pseudomonas aeruginosa, Enterococcus faecalis, Proteus mirabilis. χ^2=14.24, df=3, P=0.003.*

Table 7. Adjusted MDR prevalence by year of isolation

Year	MDR / total	% MDR	95% CI
2021	22/35	62.9	46.3-76.8
2022	20/40	50.0	35.2-64.8
2023	33/48	68.8	54.7-80.1
2024	23/36	63.9	47.6-77.5
2025	27/41	65.9	50.5-78.4

Confidence intervals calculated by the Wilson score method. Intervals overlap across all five years, though annual sample sizes are too small to exclude temporal drift.