

Pattern of Bacterial Isolates and Their Antibiotic Susceptibility in Culture-and-Sensitivity Reports from Quetta, Pakistan

Syed Hafeezullah Shah

MPhil Scholar, Pharmacy Practice, Faculty of Pharmacy and Health Sciences, University of Balochsitan

Noman ul Haq

Associate Professor, Pharmacy Practice, Faculty of Pharmacy and Health Sciences, University of Balochsitan

Asma Mengal

MPhil Pharmacy Practice, Faculty of Pharmacy and Health Sciences, University of Balochsitan

Naveed Qamar

Pharmacist, University of Balochistan

Nazia Saad

Pharmacist, University of Balochistan

Aqeel Nasim

Drug Analyst, Provincial Drug Testing Laboratory Balochistan

Author Details

Keywords: antibiotic resistance; culture and sensitivity; *Salmonella* Typhi; *Staphylococcus aureus*; Quetta; Pakistan

Received on 16 Feb 2026

Accepted on 18 Mar 2026

Published on 27 Mar 2026

Corresponding E-mail & Author*:

Syed Hafeezullah Shah

Email: aghahafeezshah@gmail.com

Abstract

Background: In Pakistan antibiotic resistance has become an escalating problem, but there is little local information available from Balochistan. Identifying common bacteria and what antibiotics are still effective in treating them helps the doctor decide on treatment.

Objective: To present the type of bacteria isolated in the culture and sensitivity reports from Quetta and their antibiotic sensitivity pattern.

Methods: This was a retrospective descriptive study of 321 culture and sensitivity reports from Quetta for the years 2020, 2021 and 2023-2026 with no reports available for the year 2022. Data regarding age, sex, specimen type, bacterial isolate and reported antimicrobial susceptibility category (Sensitive, Intermediate or Resistant) were extracted. All reports were considered as one level of isolation per report. Only isolates cultured against a particular antibiotic were used to determine resistance percentages.

Results: Most patients were male (62.6%) and 44.2% were infants under one year old. Blood was the commonest specimen (90.3%). *Salmonella* Typhi was the commonest bacterium (191, 59.5%), followed by *Staphylococcus aureus* (64, 19.9%).

Among *S. Typhi*, resistance was very high to ampicillin (98.4%), chloramphenicol (92.1%) and co-trimoxazole (83.8%), and about half of isolates were resistant to ceftriaxone (52.7%), cefixime (54.7%) and ciprofloxacin (47.1%). All tested *S. Typhi* isolates were sensitive to azithromycin, meropenem and imipenem. No resistance to vancomycin or linezolid was seen in staphylococci.

Conclusion: Typhoid bacteria in Quetta are resistant to most older antibiotics. Azithromycin and carbapenems still worked in the isolates tested. Doctors should use local sensitivity data when choosing antibiotics, and laboratories should report results in a standard way.

1. Introduction

Antimicrobial resistance (AMR) has become one of the biggest public health concerns of the world, and poses a risk to the successful treatment of common bacterial infections. Resistance is the ability of microorganisms to persist in the presence of antimicrobial agents that would have otherwise prevented or eliminated them, causing therapeutic failure and/or a decreased efficacy. The inappropriate use and over-use of antimicrobial medicines are thought to be the primary causes of the development and dissemination of antimicrobial resistance by the World Health Organization (WHO) [1]. Resistant infections have implications beyond just microbiological resistance: they are linked to longer hospitalizations, higher health care costs, and more second line or reserve antibiotic use and mortality. A global analysis in 2019 estimated the mortality burden of bacterial AMR to be about 1.27 million deaths globally in 2019, and 4.95 million deaths globally due to bacterial AMR [2]. The burden is especially troubling in low and middle resource countries, where infectious diseases continue to be an issue and capacity in diagnostic microbiology, antimicrobial stewardship, infection prevention and surveillance may be lacking. AMR is a formal concern in Pakistan, reflected in the development of a National Action Plan on AMR, which includes strengthening capacity of laboratories, awareness creation, infection prevention, rational antimicrobial use, and surveillance [3]. However, use of antibiotics remains high. Another point prevalence survey across multiple centres in Pakistani hospitals revealed high levels of antimicrobial use, and the importance of antimicrobial stewardship and evidence-based prescribing [4]. The national usage data have also shown a lot of broad-spectrum agents usage such as fluoroquinolones, penicillin combinations, third-generation cephalosporins, macrolides [5]. Such exposures have antibiotic selection pressure on bacteria and has helped increase and develop resistant strains. The results underline the need to have reliable microbiological information locally and regionally to recommend the use of an antimicrobial agent, rather than using empirical prescribing alone.

Typhoid fever is a good example of the emergence of antimicrobial resistance in Pakistan. Typhoid is a systemic disease due to the bacteria *Salmonella enterica* serovar Typhi and remains a significant cause of morbidity in South Asia, such as Pakistan [7]. The earlier drugs used for typhoid fever were chloramphenicol and ampicillin and trimethoprim-sulfamethoxazole (TMP-SMX). Subsequent emergence of multidrug resistant *S. Typhi* (conventionally defined as resistance to these three first line drugs) led to a rise in the use of fluoroquinolones. But, over time, reduced fluoroquinolone susceptibility and resistance became more common, creating even fewer choices for treatment. Soon thereafter the extensively drug-resistant (XDR) *S. Typhi* emerged in Pakistan, marking a critical step in the national AMR situation. An outbreak of XDR was found in Sindh, which was resistant to the traditional first-line agents, as well as to fluoroquinolones and third generation cephalosporins, with the presence of blaCTX-M-15 and qnrS [8]. A subsequent outbreak investigation in Hyderabad yielded the spread of ceftriaxone resistant *S. Typhi* and key epidemiologic features of this new strain [9]. Antimicrobial resistance among typhoidal *Salmonella* isolates from Pakistan also highlights the threat of AMR, as was again shown by the Surveillance for Enteric Fever in Asia Project [10]. In addition, population-based surveillance has also shown that Pakistan continues to suffer from a significant burden of enteric fever [11]. Such changes have significantly limited therapeutic choices and heightened the use of low numbers of available drugs, such as azithromycin and also, for seriously drug-resistant infections, carbapenems. Repeated exposure of humans to antimicrobial agents and the subsequent selection of resistant organisms illustrate how a normally treatable bacterial disease can become a major therapeutic problem like *S. Typhi*. Such concerns apply to other clinically significant bacteria such as *Escherichia coli*, *Klebsiella* spp., *Acinetobacter* spp., *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *Enterococcus* spp. and regular local surveillance of susceptibility patterns is critical.

AMR surveillance mechanisms have been developed at the national level in Pakistan such as participation in the WHO Global Antimicrobial Resistance and Use Surveillance System and the Pakistan Antimicrobial Resistance Surveillance System under the supervision of the National Institute of Health [12]. But, the evidence for AMR is not evenly spread across the geographic regions of Pakistan. A systematic review of 10 years' research on antibiotic resistance in Pakistan revealed high levels of resistance of multiple WHO priority bacterial pathogens and significant deficiencies in national monitoring. Importantly, of all the studies included in the review, about 40.9% were from the province of Sindh and 35.5% from the province of Punjab; however, no studies reporting AMR in Balochistan were found in the literature analysed [6]. This geographical imbalance matters as patterns of antimicrobial susceptibility do not necessarily apply to each hospital or province. Factors such as local antimicrobial use and prescription habits, patient populations, infection control practices, diagnostic service availability, referral processes, and dissemination of specific resistant bacterial strains all affect the emergence of resistance. Moreover, there is still a variable implementation of antimicrobial stewardship activities in hospitals across Pakistan. A national hospital assessment revealed that there were significant gaps in infrastructure for stewardship and that some of the recommended stewardship activities were not always being performed [13]. This often leaves the clinician confronted with the need to begin treatment before definite microbiological results are available. Resistance data from distant geographical locations or from historical patterns or by individual experience are not necessarily up to date with local data, so there is a greater risk of prescribing a drug that is ineffective for the present local situation. Therapy that's not appropriate may delay clinical response, promote repeated or extra antibiotic exposure, extend stay in hospital, raise the cost of treatment, and promote further resistance. On the other hand, unnecessary use of empirical broad-spectrum antibiotic therapy increases the antimicrobial selective pressure. Local culture and sensitivity data are thus a vital link between diagnostic microbiology and sensible prescribing.

The lack of collated information on antimicrobial susceptibilities from Quetta and throughout the Balochistan region is thus a significant clinical and epidemiological dearth of knowledge. The data provided in routine culture and sensitivity reports are useful in real-life situations to know what organisms are causing infections in a given health care setting and what drugs are effective or resistant to them. In Pakistan, it has been shown that adjusting empirical therapy based on culture and sensitivity has a positive impact on the selection of appropriate antibiotics, minimizing exposure to antibiotics and cost of treatment [14]. Similarly, it is known that culture-guided de-escalation can lead to a decrease in the use of broad spectrum anti-microbial drugs in patients that have infections from organisms like *E. coli* and methicillin sensitive *S. aureus* [15]. Routinely generated laboratory data can then be aggregated to reveal the most common organisms being isolated, their patterns of susceptibility and resistance to commonly used antibiotics and offer a local evidence base for guiding empirical treatment recommendations. This data can also be used to assist hospital antimicrobial stewardship committees, clinicians, pharmacists, microbiologists and health authorities in the design of antibiograms, updating institutional antimicrobial prescribing guidelines, establishing a list of antibiotics that should not be unnecessarily used and in the detection of emerging signals of antimicrobial resistance. Having a baseline for Quetta is also significant as resistance patterns can either become more stable, more resistant or more susceptible over time. This is especially important for Balochistan where published data is much scarcer than other provinces, and extrapolation from the cities of Karachi, Lahore or other large urban centres may not reflect the bacterial epidemiology in Balochistan. Local evidence generation is thus required for immediate clinical decision making and to support regional AMR surveillance and stewardship. For these reasons, the objectives of this study were to isolate and identify the bacterial flora present in culture and sensitivity reports from Quetta and to see their susceptibility and resistance pattern to the commonly used antibiotics as to provide locally relevant evidence for empirical treatment; antimicrobial stewardship and future surveillance of antimicrobial resistance in Balochistan.

2. Materials and Methods

2.1 Study design, setting and study period

A retrospective descriptive laboratory-record study was conducted using 321 culture-and-sensitivity reports from patients whose specimens were processed or reported through laboratory services in Quetta, Balochistan, Pakistan. The available reports covered 2020, 2021, and 2023–2026; no eligible reports were available for 2022. Reports originated from hospital patients and laboratory collection services linked to Civil Hospital Quetta and the Shaukat Khanum, Aga Khan, and Dow laboratory networks. Because the study used previously generated reports, no intervention or prospective specimen collection was undertaken for this analysis.

2.2 Eligibility, unit of analysis and sampling

All available culture and sensitivity (C/S) results available in the study dataset for a bacterial isolate with at least one antimicrobial sensitivity test were eligible for inclusion. Reports with no bacterial organism or no bacterial susceptibility information were unsuitable for analysis. All laboratory reports were considered to be one isolate level report. The available reports were treated as a retrospective record series, thus the results reflect laboratory reports submitted and should not be read as prevalence estimates. A unique patient identifier of suitable quality that would allow us to determine whether an individual had more than one culture during the study period was not available in the source records.

2.3 Data extraction and study variables

Data elements were extracted from each report into a uniform data set. Data collected included year of report, patient age, specimen type (blood, urine, pus or sputum), bacterial organism isolated, antibiotic tested, and antibiotic susceptibility reported by the laboratory as sensitive, intermediate or resistant. Age was grouped as <1 year, 1–2 years, 3–6 years, 7–12 years, 13–18 years, 19–55 years, and >55 years for descriptive presentation. If an antibiotic was not reported for a specific isolate, it was reported as missing for the isolate and was not included in the denominator for the antibiotic-specific susceptibility calculation.

2.4 Microbiological identification and antimicrobial susceptibility testing

The identification of the bacteria and the sensitivity tests had already been conducted by the laboratories that had extracted the bacteria from the patients in the normal course of treatment. Standard disk-diffusion methods were reported to be the most commonly used susceptibility testing methods. The study was done using reports produced by various laboratories over a number of years, so that each report could not always be relied upon as a true record of the testing platform, the potency of each antibiotic disc, the quality-control strain used, or the interpretive standard used for each result. Specifically, it was not always clear if Clinical and Laboratory Standards Institute (CLSI) or European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints had been used. Therefore, susceptibility categories were not re-classified after receipt; only as reported by the original laboratory.

2.5 Outcome definitions and data handling

The main results were the distribution of bacterial isolates and the percentage of tested isolates classified as resistant, intermediate, or susceptible to each antimicrobial agent. Denominators were thus not consistent across the antibiotics due to tests not being done on all isolates. Resistant isolates were determined as the proportion of isolates reported resistant to an antibiotic divided by the number of isolates tested, reported as a percentage. Intermediate results kept as a separate category and were not included with resistant results. The

susceptibility results were described and interpreted with caution for organisms with few isolates.

2.6 Statistical analysis

The analysis of data was done descriptively by calculating and using frequencies and percentages. Patient characteristics, specimen distribution, bacterial isolates and antimicrobial susceptibility categories were reported as counts and proportions. To describe the available laboratory reports, no inferential hypothesis testing was conducted. While the overall patient and specimen tables included all 321 records, antibiotic susceptibility percentages included the number of isolates tested for the particular antibiotic.

2.7 Ethical considerations

Ethical clearance and institutional approval were obtained from the Institutional Ethics Committee of the Faculty of Pharmacy and Health Sciences, University of Balochistan. All procedures were performed in accordance with the Declaration of Helsinki. Written informed consent was obtained from all participants prior to enrollment. Participant confidentiality and anonymity were maintained throughout the study

3. Results

3.1 Patient characteristics

A total of 321 isolates were studied (Table 1). Male patients made up 62.6% of the sample. The largest age group was infants under one year (44.2%), followed by children aged 7 to 12 years (19.9%). Only 4.4% of patients were older than 18 years. Blood was the specimen for 90.3% of isolates. The highest number of isolates came from 2021 (84) and 2023 (74), and none from 2022.

Table 1. Characteristics of the 321 patients and specimens.

Characteristic	Number (n)	Percentage (%)
Age group		
Less than 1 year	142	44.2
1–2 years	37	11.5
3–6 years	34	10.6
7–12 years	64	19.9
13–18 years	30	9.3
19–55 years	11	3.4
More than 55 years	3	0.9
Sex		
Male	201	62.6
Female	120	37.4
Specimen		
Blood	290	90.3
Urine	16	5.0
Pus	11	3.4
Sputum	4	1.2
Year		
2020	21	6.5
2021	84	26.2
2023	74	23.1
2024	48	15.0
2025	67	20.9
2026	27	8.4

3.2 Bacteria isolated

Eleven types of bacteria were found (Table 2, Figure 1). *Salmonella* Typhi was the most common (191, 59.5%), followed by *Staphylococcus aureus* (64, 19.9%), *Staphylococcus epidermidis* (22, 6.9%), *Escherichia coli* (14, 4.4%) and *Pseudomonas aeruginosa* (13, 4.0%). All typhoid isolates came from blood. Most of the other bacteria came from infants under one year of age (113 of 130, 86.9%).

Table 2. Bacteria isolated from culture-and-sensitivity reports.

Bacterium	Number (n)	Percentage (%)
<i>Salmonella</i> Typhi	191	59.5
<i>Staphylococcus aureus</i>	64	19.9
<i>Staphylococcus epidermidis</i>	22	6.9
<i>Escherichia coli</i>	14	4.4
<i>Pseudomonas aeruginosa</i>	13	4.0
<i>Klebsiella</i> spp.	6	1.9
<i>Streptococcus mitis</i>	3	0.9
<i>Micrococcus</i> spp.	3	0.9
Diphtheroids	2	0.6
<i>Proteus</i> spp.	2	0.6
<i>Bacillus</i> spp.	1	0.3

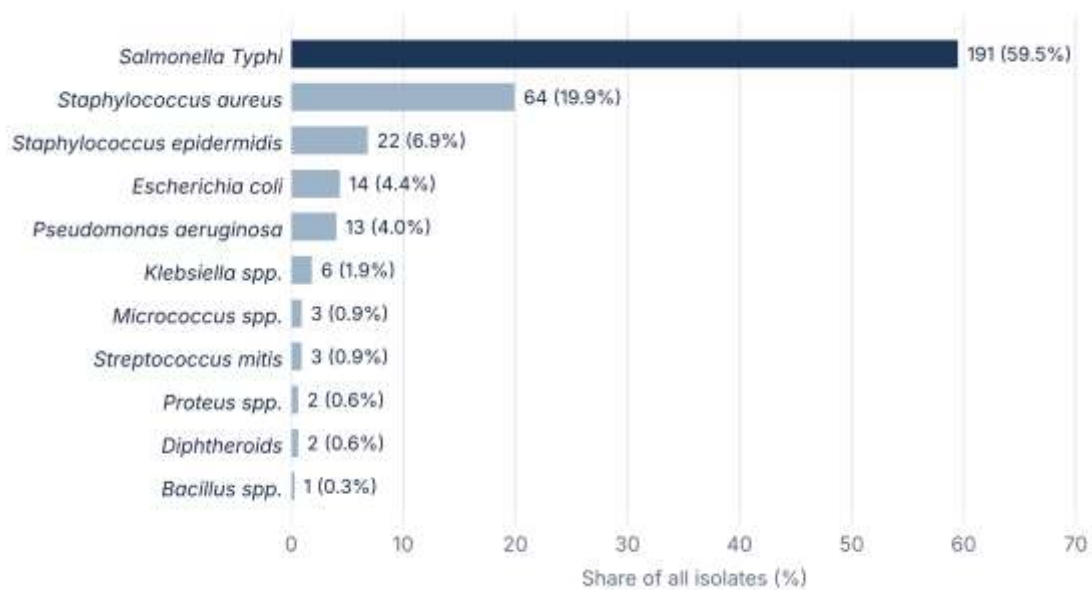


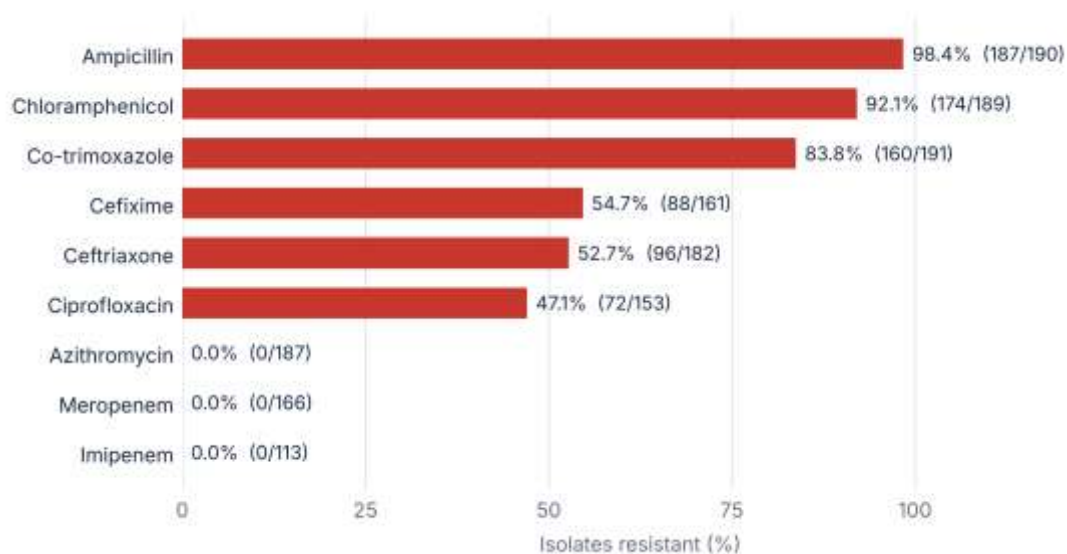
Figure 1. Bacteria isolated from culture-and-sensitivity reports (n=321).

3.3 Antibiotic susceptibility of *Salmonella* Typhi

Resistance of *S. Typhi* to the older antibiotics was very high (Table 3, Figure 2): ampicillin 187/190 (98.4%), chloramphenicol 174/189 (92.1%) and co-trimoxazole 160/191 (83.8%). About half of the isolates were resistant to ceftriaxone (52.7%) and cefixime (54.7%). Ciprofloxacin was resistant in 47.1% and intermediate in a further 14.4%. In contrast, all isolates tested against azithromycin (187), meropenem (166) and imipenem (113) were sensitive. Not every isolate was tested against every antibiotic, so these last three results come from fewer isolates.

Table 3. Antibiotic susceptibility of Salmonella Typhi (n=191).

Antibiotic	Tested (n)	Sensitive n (%)	Intermediate n (%)	Resistant n (%)
Ampicillin	190	3 (1.6)	0 (0.0)	187 (98.4)
Chloramphenicol	189	15 (7.9)	0 (0.0)	174 (92.1)
Co-trimoxazole	191	29 (15.2)	2 (1.0)	160 (83.8)
Cefixime	161	72 (44.7)	1 (0.6)	88 (54.7)
Ceftriaxone	182	86 (47.3)	0 (0.0)	96 (52.7)
Ciprofloxacin	153	59 (38.6)	22 (14.4)	72 (47.1)
Azithromycin	187	187 (100.0)	0 (0.0)	0 (0.0)
Meropenem	166	166 (100.0)	0 (0.0)	0 (0.0)
Imipenem	113	113 (100.0)	0 (0.0)	0 (0.0)

**Figure 2.** Percentage of Salmonella Typhi isolates resistant to each antibiotic

3.4 Antibiotic susceptibility of other bacteria

Numbers of the other bacteria were small, so these results are only a guide (Table 4). Staphylococci showed no resistance to vancomycin (*S. aureus* 0/54; *S. epidermidis* 0/21) or linezolid (0/58 and 0/14). Amikacin resistance in *S. aureus* was low (1/48). *E. coli* was resistant to co-trimoxazole (5/5), ceftriaxone (5/5) and often ciprofloxacin (5/7), but was sensitive to gentamicin, nitrofurantoin and fosfomycin (7/7 each). *P. aeruginosa* was resistant to ciprofloxacin in 8 of 13 isolates (61.5%) but sensitive to imipenem (10/10), tobramycin (11/11) and gentamicin (8/8).

Table 4. Antibiotic susceptibility of other common bacteria (resistant/tested).

Bacterium and antibiotic	Resistant/tested	Resistant (%)
Staphylococcus aureus (n=64)		
Vancomycin	0/54	0.0
Linezolid	0/58	0.0
Amikacin	1/48	2.1
Teicoplanin	4/20	20.0
Doxycycline	9/42	21.4
Staphylococcus epidermidis (n=22)		
Vancomycin	0/21	0.0
Linezolid	0/14	0.0
Ciprofloxacin	7/8	87.5
Co-trimoxazole	6/8	75.0
Escherichia coli (n=14)		
Gentamicin	0/7	0.0
Nitrofurantoin	0/7	0.0
Fosfomycin	0/7	0.0
Piperacillin–tazobactam	0/6	0.0
Ciprofloxacin	5/7	71.4
Ceftriaxone	5/5	100.0
Co-trimoxazole	5/5	100.0
Pseudomonas aeruginosa (n=13)		
Imipenem	0/10	0.0
Tobramycin	0/11	0.0
Gentamicin	0/8	0.0
Piperacillin–tazobactam	1/13	7.7
Ceftazidime	3/7	42.9
Ciprofloxacin	8/13	61.5

4. Discussion

The principal finding of this study was the predominance of *Salmonella* Typhi among the 321 culture-and-sensitivity reports from Quetta, together with very high resistance to traditional first-line antityphoid agents. Resistance to ampicillin (98.4%), chloramphenicol (92.1%), and co-trimoxazole (83.8%) indicates that these agents would be unreliable for empirical treatment of suspected typhoid in the population represented by these reports. The finding is consistent with the broader evolution of multidrug-resistant and extensively drug-resistant typhoid in Pakistan. The XDR outbreak characterized in Sindh demonstrated resistance to traditional first-line drugs, fluoroquinolones, and third-generation cephalosporins [8,9]. Subsequent Pakistani studies have also documented high resistance to first-line drugs and markedly reduced susceptibility to ciprofloxacin and cephalosporins [17–19]. In the present dataset, resistance to ceftriaxone (52.7%), cefixime (54.7%), and ciprofloxacin (47.1%) is therefore clinically important because these agents have historically been used when older first-line therapies failed.

All *S. Typhi* isolates tested against azithromycin, meropenem, and imipenem in this dataset were reported as sensitive. Similar studies from Pakistan have shown that azithromycin and carbapenems were very active, or totally active, against resistant typhoidal *Salmonella* [17–19]. These results confirm their continued significance for drug resistant enteric fever; however, there is no evidence that resistance cannot develop. Resistance to azithromycin has already been reported for typhoidal *Salmonella* in South Asia [20], and increased use of carbapenems may create additional selective pressure. Furthermore, 187 *S. Typhi* isolates were tested against azithromycin, 166 against meropenem, and 113 against imipenem, so the apparent 100% susceptibility applies only to those tested subsets. These agents should therefore be preserved through culture-guided prescribing and stewardship rather than used indiscriminately.

Staphylococcus aureus was the second most common isolate, and no resistance to vancomycin or linezolid was reported among the isolates tested. This pattern is broadly

compatible with Pakistani stewardship and antibiogram studies in which Gram-positive isolates, including *S. aureus*, retained high susceptibility to vancomycin and linezolid [14,15,21]. Nevertheless, oxacillin or ceftiofloxacin results were not available in the present dataset, preventing classification of *S. aureus* as methicillin-resistant or methicillin-susceptible. This is an important limitation because MRSA status directly affects empirical treatment and infection-control decisions. The predominance of non-typhoidal isolates among infants younger than one year also deserves attention, but the retrospective report-based design does not provide sufficient clinical information to determine whether the isolates represented community-acquired infection, healthcare-associated infection, or, in the case of some skin flora, possible contamination.

Although *Escherichia coli* and *Pseudomonas aeruginosa* were much less frequent than *S. Typhi* and staphylococci, their resistance patterns warrant cautious attention. Among the small number of *E. coli* isolates tested, resistance was observed to co-trimoxazole, ceftriaxone, and ciprofloxacin, whereas all seven isolates tested against gentamicin, nitrofurantoin, and fosfomycin were reported sensitive. A previous study conducted in Quetta, Balochistan, similarly identified *E. coli* as the most common uropathogen and reported high resistance to ceftriaxone and fluoroquinolones while retaining comparatively good activity of fosfomycin and selected reserve agents [16]. This local concordance reinforces the worry over the empirical use of cephalosporins and fluoroquinolones. Ciprofloxacin was active against eight of 13 *P. aeruginosa*, while imipenem, tobramycin and gentamicin were active against the few isolates tested. There is no generalisation of these estimates as several organism-antibiotic combinations were based on less than 10 observations.

The study has practical implications for antimicrobial stewardship in Quetta. Local susceptibility data are essential because resistance patterns differ between institutions, patient populations, specimen types, and geographical regions. Pakistani studies have shown that using culture-and-sensitivity results to adjust empirical therapy can reduce unnecessary antibiotic use and treatment costs [14], and culture-guided de-escalation has reduced broad-spectrum antibiotic use in patients with *E. coli* and methicillin-sensitive *S. aureus* infections [15]. Hospital-specific antibiograms have also been recommended as a tool for guiding empirical therapy and stewardship [21]. The current findings therefore support the development of a standardized Quetta-based antibiogram using consistent organism-specific antibiotic panels and a clearly stated interpretive standard. Future surveillance should use standardized CLSI or EUCAST methods, deduplicate repeat isolates at the patient level where possible, stratify results by specimen and healthcare setting, and analyze temporal trends using sufficiently complete annual data.

4.1 Limitations

This study has several limitations. First, it was a retrospective analysis of laboratory reports and therefore cannot estimate the incidence or prevalence of infection in the general population. Second, the reports came from different laboratories and years, and the susceptibility-testing method, interpretive standard, and antibiotic panel were not consistently documented. Denominators were very unevenly distributed for different antibiotics since not all isolates were tested against all of them. Third, the numbers of organisms other than *S. Typhi* and *S. aureus* were small, and several percentages were unstable and do not appear to be generally applicable. Fourth, there were no reports available for 2022, making it impossible to assess year-to-year trends. Fifth, there was no unique patient identifier to determine if some patients had repeat cultures. Lastly, clinical diagnosis, prior antimicrobial exposure, comorbidities, treatment and outcomes were not available, nor was a distinction made between infection, colonization and possible contamination. The results are therefore to be regarded as a snapshot description of the reports available and not as an estimate of AMR prevalence.

5. Conclusion

Salmonella Typhi was the commonest bacterium in culture reports from Quetta and was highly resistant to ampicillin, chloramphenicol and co-trimoxazole, with about half of isolates resistant to ceftriaxone, cefixime and ciprofloxacin. Azithromycin and carbapenems were fully active in the isolates tested, as were vancomycin and linezolid against staphylococci. Regular local antibiograms, standard laboratory reporting and careful use of the remaining effective antibiotics are recommended.

Acknowledgment

Sincere acknowledgment is extended to Dr. Nabidad Bugti, affiliated with Sandeman Civil Hospital, for his valuable guidance, support, and professional contribution toward the completion of this work. His assistance and expertise are highly appreciated.

References

- World Health Organization. Antimicrobial resistance. Geneva: World Health Organization; 2023.
- Antimicrobial Resistance Collaborators. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. *Lancet*. 2022;399(10325):629–655. doi:10.1016/S0140-6736(21)02724-0.
- Ministry of National Health Services, Regulations and Coordination, Government of Pakistan. Antimicrobial Resistance: National Action Plan Pakistan. Islamabad: Government of Pakistan; 2017.
- Saleem Z, Hassali MA, Versporten A, Godman B, Hashmi FK, Goossens H, Saleem F. A multicenter point prevalence survey of antibiotic use in Punjab, Pakistan: findings and implications. *Expert Rev Anti Infect Ther*. 2019;17(4):285–293. doi:10.1080/14787210.2019.1581063.
- Saleem Z, Hassali MA, Hashmi FK, Qaisar S, Ahmad M, Ali SS, Ahmad F. Evaluating consumption and expenditure patterns of antibiotics in tablet and capsule dosage forms: Pakistan Antibiotic Consumption Surveillance (PACS). *J Pharm Pract Res*. 2020;50(1):36–41. doi:10.1002/jppr.1584.
- Bilal H, Khan MN, Rehman T, Hameed MF, Yang X. Antibiotic resistance in Pakistan: a systematic review of past decade. *BMC Infect Dis*. 2021;21:244. doi:10.1186/s12879-021-05906-1.
- GBD 2017 Typhoid and Paratyphoid Collaborators. The global burden of typhoid and paratyphoid fevers: a systematic analysis for the Global Burden of Disease Study 2017. *Lancet Infect Dis*. 2019;19(4):369–381. doi:10.1016/S1473-3099(18)30685-6.
- Klemm EJ, Shakoore S, Page AJ, et al. Emergence of an extensively drug-resistant *Salmonella* enterica serovar Typhi clone harboring a promiscuous plasmid encoding resistance to fluoroquinolones and third-generation cephalosporins. *mBio*. 2018;9(1):e00105-18. doi:10.1128/mBio.00105-18.
- Qamar FN, Yousafzai MT, Khalid M, et al. Outbreak investigation of ceftriaxone-resistant *Salmonella* enterica serotype Typhi and its risk factors among the general population in Hyderabad, Pakistan: a matched case-control study. *Lancet Infect Dis*. 2018;18(12):1368–1376. doi:10.1016/S1473-3099(18)30483-3.
- Qamar FN, Yousafzai MT, Dehraj IF, et al. Antimicrobial resistance in typhoidal *Salmonella*: Surveillance for Enteric Fever in Asia Project, 2016–2019. *Clin Infect Dis*. 2020;71(Suppl 3):S276–S284. doi:10.1093/cid/ciaa1323.
- Garrett DO, Longley AT, Aiemjoy K, et al. Incidence of typhoid and paratyphoid fever in Bangladesh, Nepal, and Pakistan: results of the Surveillance for Enteric Fever in Asia Project. *Lancet Glob Health*. 2022;10(7):e978–e988. doi:10.1016/S2214-109X(22)00119-X.
- National Institute of Health Pakistan. Pakistan Antimicrobial Resistance Surveillance System. Islamabad: National Institute of Health, Pakistan.
- Saleem Z, Hassali MA, Hashmi FK, Godman B, Ahmed Z. Snapshot of antimicrobial stewardship programs in the hospitals of Pakistan: findings and implications. *Heliyon*. 2019;5(7):e02159. doi:10.1016/j.heliyon.2019.e02159.

- Altaf U, Saleem Z, Akhtar MF, et al. Using culture sensitivity reports to optimize antimicrobial therapy: findings and implications of antimicrobial stewardship activity in a hospital in Pakistan. *Medicina (Kaunas)*. 2023;59(7):1237. doi:10.3390/medicina59071237.
- Haseeb A, Saleem Z, Altaf U, et al. Impact of positive culture reports of *E. coli* or MSSA on de-escalation of antibiotic use in a teaching hospital in Pakistan and the implications. *Infect Drug Resist*. 2023;16:77–86. doi:10.2147/IDR.S391295.
- Hussain T, Moqadasi M, Malik S, et al. Uropathogens antimicrobial sensitivity and resistance pattern from outpatients in Balochistan, Pakistan. *Cureus*. 2021;13(8):e17527. doi:10.7759/cureus.17527.
- Aslam A, Kharal SA, Aslam M, Raza A. Trends of antimicrobial resistance in typhoidal strains of *Salmonella* in a tertiary care hospital in Pakistan. *Cureus*. 2021;13(1):e12664. doi:10.7759/cureus.12664.
- Hussain MA, Ahmed I, Akram S, Khan MA, Ali S, Amir M. Extensively drug-resistant typhoidal *Salmonellae*: are these bugs swarming into suburban and rural areas of Pakistan? *Cureus*. 2022;14(6):e26189. doi:10.7759/cureus.26189.
- Yousaf M, Sikandar I, Waqas Z, et al. Antibiotic resistance in *Salmonella* Typhi strains isolated from patients in Pakistan: a hospital database study. *Cureus*. 2024;16(4):e58240. doi:10.7759/cureus.58240.
- Hooda Y, Sajib MSI, Rahman H, et al. Molecular mechanism of azithromycin resistance among typhoidal *Salmonella* strains in Bangladesh identified through passive pediatric surveillance. *PLoS Negl Trop Dis*. 2019;13(11):e0007868. doi:10.1371/journal.pntd.0007868.
- Kursheed F, Tabassum A, Farwa U, Wazir S, Shafiq M, Sheikh AK. The antibiogram of pus cultures in federal tertiary care hospital, Islamabad and its utility in antimicrobial stewardship. *Iran J Microbiol*. 2024;16(1):56–61. doi:10.18502/ijm.v1