The characteristic of antibiotic drug resistance of Salmonella Typhi isolated from tertiary care hospital in Faisalabad

Babar Hayat, Abu Baker Siddique*, Zeeshan Nawaz and Muhammad Usman Qamar

Institute of Microbiology: Government College University Faisalabad, Pakistan.

Abstract: *Salmonella* Typhi, a human-restricted pathogen, is demonstrating multi-drug resistance (MDR) due to widespread and inappropriate antibiotic use. This study aims to molecular identify the pattern of antibiotic resistance. Blood samples from 2456 suspected patients were assessed. Molecular identification of *Salmonella* Typhi was performed by amplifying the fliC gene. The Disc diffusion method was used to measure the susceptibility of antibiotics. 2456 patient samples, bacterial growth and *Salmonella* Typhi were 152 (6.2 %) positive. PCR analysis confirmed that all 152 isolated strains were *Salmonella* Typhi (100%) through the amplification of the *fliC* gene. *Salmonella* Typhi isolates showed resistance to trimethoprim (58%), ampicillin (63%), ciprofloxacin (79%) and chloramphenicol (58%). Fifty-eight percent of the isolates showed multi-drug resistance, whereas 26 percent had extensive drug resistance. Antibiotic resistance gene of quinolones was isolated as 44 (36.4%), whereas 88 (57.9 %) were positive for *blactical among carbapenem-resistance* bacteria. For the azithromycin resistance, *more* genes were detected as a percentage 03 (50 %) from isolates. It concludes that several multidrug resistance and extensive drug-resistance *Salmonella* Typhi were found. The majority of isolates were sensitive to meropenem, Imipenem and *Azithromycin*.

Keywords: Multidrug resistance, extensive drug resistance, polymerase chain reaction.

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INTRODUCTION

Typhoid fever, caused by *Salmonella* Typhi, is a critical infectious disease, particularly impacting children and young adults studies by (Goay *et al.*, 2016). Symptoms encompass diarrhea, enlarged spleen, meningitis, systemic temperature elevation, nausea, loss of appetite and severe headaches (Baker *et al.*, 2020). *Salmonella* Typhi, a Gramnegative, rod-shaped, motile bacterium with flagella, poses a mortality risk of 12-30% if untreated, contrasting with a 99% survival rate with timely treatment (Osuntokun and Olajubu, 2015).

One of the nations with the highest rates of typhoid is Pakistan. 451.7 cases per 100,000 people is the annual incidence rate. It is uncertain what molecular mechanism S. Typhi uses to cause enteric fever. Clinical signs and symptoms that connect with other bacterial infections (Yasin et al., 2022). From 2016 to 2018, the Health Authority of Pakistan reported that out of 8188 cases in Sindh, 5274 cases were extensively drug-resistant (XDR) typhoid. XDR resistance often arises when multidrugresistant (MDR) bacteria acquire plasmids. In densely populated places with inadequate sanitation, tainted water and compromised immune systems, the prevalence of typhoid fever is higher. MDR strains of Salmonella are to resistant co-trimoxazole, ampicillin and chloramphenicol (Hooda et al., 2019). Resistance to ampicillin, trimethoprim-sulfamethoxazole and chloramphenicol is known as an MDR, whereas resistance to fluoroquinolones, ampicillin, co-trimoxazole and

chloramphenicol is also known the XDR (Akram *et al.*, 2020). First identified between the late 1970s to early 1980s. MDR *Salmonella* Typhi is resistant to these two groups (ceftriaxone, a third-generation cephalosporin, or quinolones) of antibiotics are known as extensively drugresistant (XDR). In areas with limited resources, azithromycin is a cost-effective and effective oral first-line antibiotic for treating XDR typhoid (khan *et al.*, 2024). Carbapenem antibiotics are the final opetion for treating infections caused by MDR and XDR bacteria. MBL is produced by bacteria that are sensitive to colistin but resistant to β-lactam antibiotics (carbapenems and other antibiotics) (Sawa *et al.*, 2020).

MATERIALS AND METHODS

Study design

Before starting the research project ethical permission was obtained from the Ethics Review Committee at Faisalabad University, Government College with code CUF/ERC/4173, dated December 21 and also obtained the informed consent forms to collect clinical samples.

Collection of clinical samples

A total of 2456 blood samples were taken from patients exhibiting symptoms such as fever, drowsiness and stomach discomfort in accordance with the doctor's prescription for the blood culture test. The samples were taken from a tertiary care center in Faisalabad.

Isolation, biochemical identification

The blood samples were grown using Tryptic Soy Broth Medium (Oxoid, United Kingdom). Two milliliters of

*Corresponding author: e-mail: absiddique@gcuf.edu.pk

blood were collected immediately after and 16 milliliters of TSB (1:8) were added without any anticoagulant. Mixture incubated at 37°C for 48-72 hours.

The Tryptic Soy Broth Medium (Oxoid, United Kingdom) was used to cultivate the blood samples. Following the collection of two millilitres of blood, 16 millilitres of TSB (1:8) were added without the use of an anticoagulant. mixture incubated for 48-72 hours at 37°C.

Then mixture was used to create a loopful culture that was streaked on both *Salmonella* Shigella and MacConkey's agar (Oxoid) (Ain *et al.*, 2022).

Primary identification of the isolate used methyl red, citrate test, Gramme staining and triple sugar iron agar (Oxoid) for colony morphology, culture and biochemical test.

Molecular confirmation of Salmonella Typhi

The molecular identification of *Salmonella* Typhi involved the utilization of a specific primer set known as *flic*. Thermo Fisher Scientific's Gene JET genomic DNA extraction kit was used for the extraction and purification of genomic DNA. The isolated DNA was then immediately refrigerated at -20°C. According to the study by Kumar *et al.* 2005), 36 cycles made up the reaction amplification conditions: 30 seconds of denaturation at 95°C, 30 seconds of annealing at 96°C, 1 minute of extension at 72°C and 5 minutes of final extension at 72°C. After being separated by gel electrophoresis, the PCR product was deposited onto a 2% agarose gel with ethidium bromide and examined under gel documentation. (Fermantis, USA,). table 1

Antibiotic susceptibility test

Salmonella Typhi resistance to antibiotics, such as ciprofloxacin (CIP) (10 μg), ampicillin (AMC) (20 μg), cefixime (CFM) (5 μg), ceftriaxone (CFT) (30 μg), trimethoprim (TRI) (23.75 μg), chloramphenicol (C) (30 μg), azithromycin (AZT) (15 μg) and imipenem (IMP) (10 μg) were evaluated using Kirby- Bauer disc diffusion testing, using Oxoid, UK. Every host strain was uniformly distributed on a Mueller-Hinton agar plate after being diluted to a turbidity equal to the 0.5 McFarland standard. To determine antibiotic susceptibility, the clear zone surrounding the antibiotic discs was measured. The CLSI standards were used to classify strains as susceptible (S) or resistant (R) based on the size of the zone.

Molecular identification antimicrobial resistance genes

Molecular identification of the genes responsible for Cephalosporin antibiotic resistance (blaCTX-M) and Carbapenemase resistance (blaIMP, blaOXA-48 and blavim) (Qamar et al., 2020). genes for plasmid resistance The qnrA, qnrB and qnrS quinole-resistant genes were amplified (Herrera-Sánchez et al., 2021). Using a PCR assay, the azithromycin msrA, eraA, ere A and mefA genes

were identified. (Yasin *et al.*, 2022). The details of primers and annealing temperature is provided below table 2.

RESULTS

Bacterial isolation and identification

Out of the 2456 samples collected and examined, 152 (6.2%) isolates of *Salmonella* Typhi were identified from individuals suspected of typhoid. The data reveals more infections in males (57.9 %) as compared to females (42.1 %) (table 3). Within the age group of 1 to 61 years. Notably, typhoid was more prevalent among age groups between 1 to 10 years (8.66 %) and 21-30 years (20%) (table 4). The pure *Salmonella* Typhi samples were preserved as stock in 20% (v/v) glycerol at -80°C.

From our data, it looks like we are comparing proportions (percentage of infected) between two groups (Male and Female), which suggests that a chi-squared test for independence would be appropriate. The P-value from the chi-squared test is approximately 0.467. This P-value suggests that there is no significant difference in the infection rates between males and females in your data because the P-value exceeds the usual thresholds for significance (e.g., 0.05). Therefore, we cannot reject the null hypothesis that the proportion of infected individuals is the same for both genders.

The degree of freedom for this test is 4. The expected frequencies, based on the assumption that there's no effect of age group on infection rates. Since the p-value is much less than 0.05, we reject the null hypothesis, suggesting a significant in infection rates among the age groups. In other words, the age range of individuals with notable bacterial proliferation is not uniform (table 4).

Morphological properties and identification of isolates

Out of the 2456 samples, 152 (6.2%) tested positive for *Salmonella* Typhi. On XLD, all pure isolates were identified by their dark metallic sheen. Results are shown in fig. 1. *Salmonella* Typhi is detected by nitrate, citrate test and methyl red positive. The isolates' TSI test results show a significant blackening of the slant as a result of increased H2S production and the butt's medium is positioned above the bottom side, indicating high acid production.

Molecular identification of bacterial isolated strains Amplification of the *fliC* gene identified 152 (100%) of the isolates as *Salmonella* Typhi, as indicated in fig. 2.

Antimicrobial susceptibility testing

According to tests for antibiotic susceptibility, *Salmonella* Typhi pure strains were resistant to ciprofloxacin, ampicillin, trimethoprim and chlorphenicol (C) in 79%, 63%, 58% and 58% of cases, respectively. All of the purified isolates, however, showed complete susceptibility to imipenem (IMP) and azithromycin (AZT). Of the

isolates, only 26% showed extensive drug resistance, while 58% showed resistance to multiple drugs (table 5).

Molecular detection of resistance gene

The results of this research proved that 121 of the 152 S. Typhi strain isolates tested positive for ciprofloxacine (CIP) resistance. For quinolones, 44 (36.4%) tested positive for the *QnrS* gene. For *QnrA*, no amplification was seen. Of the isolates, 11 (9.0%) had *QnrB* identified.

The bla_{CTX-M} gene has been identified to be present in 88 (57.9%) of the cephalosporin-resistant bacteria. Among the bacteria resistant to carbapenem, 56 (36.8%) had resistance bla_{IMP} and 40 (26.3%) had resistance $blaOXA_{-48}$. Six isolates were positive for azithromycin resistance. Three genes linked to azithromycin resistance were examined. Three isolates (50%) were positive for the msrA gene. Only 02 (33%) had mefA gene positivity.



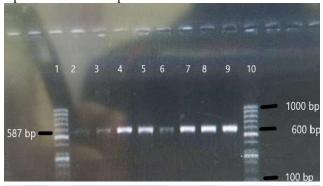
Fig. 1: On the plate, the colonies are smooth and red. And have a diameter of 2-3 mm, with a discernible black center.

DISCUSSION

Salmonella Typhi, responsible for typhoid, presents a serious risk to public health. The study characterizes typhoid patients based on clinical symptoms, age distribution and gender prevalence. In our study total of 152 (6.2%) isolates of Salmonella Typhi were identified from individuals suspected of having typhoid. The data reveals a higher prevalence of infections in males (57.9%) as compared to females (42.1%). within the age group of 1 to 61 years (Qamar et al., 2020) according to the study,

Typhoid was higher in age groups between one and ten years 8.66 % and 21 to 30 years (20%). Sepsis was observed in 66.6% of males compared to 33.3% of females. Because of their lower immune systems, males may be unfavorable in septic conditions, whereas females may have innate advantages due to the sex hormones they produce. It has been demonstrated that male sex

hormones inhibit the immune system's response to cellular mediation. (Lin *et al.*, 2021). Ten antibiotics from seven groups of antimicrobials were used in antimicrobial susceptibility assays for all 152 isolates. 79%, 63%, 58% and 58% of the pure *Salmonella* Typhi strains tested positive for antimicrobial sensitivity to trimethoprim, ciprofloxacin, ampicillin and chlorphenicol (C), respectively. An alarming issue is the resistance to ciprofloxacin and ampicillin.



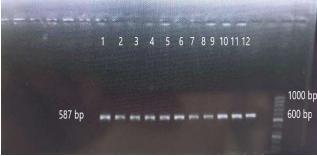


Fig. 2: (A) The Gene ruler with bands of 1000, 900, 800, 700, 600, 500, 400, 300, 200 and 100 bps displayed in lanes 01 and 10; Lanes 2–09: Isolated *Salmonella* Typhi was identified with the use of the *fliC* gene (587 bps) amplification. (B): Lane 12: Bands of 1000, 900, 800, 700, 600, 500, 400, 300, 200 and 100 bps are displayed by the gene ruler; Lanes 01-12: Isolated *Salmonella* Typhi was identified with the use of the *fliC* gene (587 bps) amplification.

All of the purified isolates, however, showed complete susceptibility to imipenem (IMP) and azithromycin (AZT).

With resistance levels of 45%, 31% and 35% for ciprofloxacin, levofloxacin and ofloxacin, respectively, the fluoroquinolones performed better (Afzal *et al.*, 2012).

According to another study, 30.4% of adolescents are infected. The impact was greater on men. While men are outside for work and may consume more unhygienic food, women tend to stay at home for a variety of reasons (Hasan et al., 2023). One of the main causes of antibiotic-resistant bacterial infections in people is Salmonella Typhi, which poses a serious threat to public health. The development of antibiotic resistance as a result of improper antibiotic use has given rise to MDR and XDR strains of S. Typhi. Many factors contribute to the prevalence of resistant pathogens,

including the overuse of antibiotics, bed-sharing, careless behavior, crowded wards with insufficient medical staff and pathogen colonization on hands and medical equipment. (Ullah *et al.*, 2025).

According to a study, S. Typhi (n = 415) shown a significant level of resistance to ciprofloxacin and cefotaxime (33%) distinct from meropenem and colistin. (Das et al., 2021). Additional findings included the discovery that a sizable portion of isolates had resistance to Cefoperazone (11%) Ceftazidime (25%), Ceffixime (20%), Cefotaxime (16%) and Cefepime (13%). 75 % of the isolates were azithromycin-resistant (Mahmood et al., 2025). In our study, 26 % of isolates had extensive drug resistance displayed and 58% of the isolates showed resistance to multiple drugs. Data from Aga Khan University in Pakistan shows that between 2001 and 2006, the rate of ciprofloxacin resistance rose from 1.6% to 64.1%, while the prevalence of MDR S Typhi remarkably increased from 34.2% to 48.5% (Huss, & Raman, 2020).

In the Pakistani province of Sindh, the first reports of XDR S. Typhi were received in 2016. While local instances of XDR S. Typhi dominate, certain tragic cases have been reported from other countries, including Italy, which has a history of sending people to Pakistan (Procaccianti *et al.*, 2020). *Salmonella* Typhi may be correctly identified by amplifying the flagellin (fliC) gene locus. Of 152 (100%) isolates were confirmed to belong to *Salmonella* Typhi this was confirmed. Kumar *et al.*, 2010 Study has shown that the fliC genes are particular genes that are used to identify S. typhi in enteric fever patients. This gene acts as a diagnostic for quickly identifying isolates of S. typhi from various samples. No other species of bacterium have it.

The molecular analysis of antimicrobial resistance genes revealed that 48 (31.6%) isolates had resistance genes against quinolones and among bacteria resistant to cephalosporins, 88 (57.9%) were positive for $bla_{\rm CTM}$ genes, while among bacteria resistant to carbapenems, 56 (36.1%) had resistance genes for $bla_{\it IMP}$ and $bla_{\rm OXA-48}$. There were found to be 40 (26.3%) more genes related to azithromycin resistance in isolates. Sixty-two (34%) of the $\it Salmonella$ Typhi isolates in Lahore research were XDR.

The common resistance gene was ampC, which had a 47% prevalence. Genes to be examined were isolates with 45, 40, 21, 6, 18, 3, 11, 6 and 2% of gyrA, catA1, tet(A), aac (3)-la, qnrS, blaNDM-1 and blaCTX-M-15, respectively (Zahid *et al.*, 2022). Ciprofloxacin (CIP) resistance was detected in the S. Typhi strain 121 isolates used in our study. For quinolones, 44 (36.4%) tested positive for the *QnrS* gene. For *QnrA*, no gene was found. Of the isolates, 11 (9.0%) had *QnrB* identified. Three genes linked to azithromycin resistance were examined. Three isolates (50%) were positive for the msrA gene. The mefA gene was positive in just 02 (33%) cases.

Ain et al., 2022 studied an analogous investigation was carried out on 40 isolates that produced ESBL; blaTEM (n = 37, 92.5%), blaCTX15 (n = 11; 27.5%) and blaSHV1 (n = 3; 7.5%) were found. Salmonella Typhi was shown to contain genes resistant to fluoroquinolones, such as 164 for gyrA, 160 for gyrB, 164 for parC and 160 for parE, qnrS (n = 15) and qnrB (n = 3). Furthermore, dfrA7 was found in 145 isolates, the cat gene in 147 isolates and the ac(6)-ib-cr gene in 163 isolates; no isolate had the resistance genes qnrA, qnrC, blaOXA, or drfA14. Seven genes were examined in 37 isolates resistant to azithromycin; only one of the genes tested positive for mefA, whereas three tested positive for msrA (Yasin et al., 2022).

The overall occurrence of S. typhi from blood samples attending tertiary care hospitals in Faisalabad, was 152 (6.2%). Patients aged 21-30 years harbored more bacteria. Gender influence on occurrence 88 (57.9%) in males. The antibiotics Azithromycin (AZT), Imipenem (IMP) and Meropenum (MEM) were the most effective against the isolates.

It concludes that a rise in the dosage of ciprofloxacin is causing clinical isolates of *Salmonella* Typhi from the Faisalabad district to exhibit growing fluoroquinolone resistance.

Significant research has revealed that *Salmonella* Typhi is developing a resistance to carbapenem. This means that physicians must carefully consider their alternatives when using antibiotics, as the bacteria may have been exposed to this most effective class of medications. Azithromycin, Imipenem (IMP) and Meropenum (MEM) were recommended as the best medications to treat XDR *Salmonella* Typhi (Mahmood *et al.*, 2025).

The oral medicine azithromycin is used to treat XDR typhoid. Additional therapeutic selections include Intravenous carbapenems like meropenem and imipenem. Although all the extensive drug resistance isolates were not resistant to carbapenems, carbapenem resistance is not common globally. A new study published from Punjab, Pakistan, 48% of isolates had carbapenem resistance (Shah *et al.*, 2020).

CONCLUSION

In conclusion, this study supports the hypothesis that patients from various geographic regions may have different host variations and transmission protocols. These results also indicate that almost all locally circulating S. Typhi will probably eventually acquire molecular markers for resistance to azithromycin and carbapenem. This may soon become a worldwide issue. Further research would have helped discover mechanisms of resistant and potential antibiotic-resistant connections

Table 1: Specific primer sequences to identify S. Typhi

| Target | Primer name | Gene | Sequence (5'-3') | Product size | References |
|---------------------|----------------|------|---|--------------|------------------------------|
| Salmonella Typhi | fliC | fliC | GCTTAATGTCCAAGATGCCTAC(F) GAGCAACGCCAGTACCATCTG(R) | 587bp | (Kumar <i>et al.</i> , 2005) |

 Table 2: The details of primers and annealing temperatures

| Target | Primer name | Gene | Sequence (5'-3') | Product size | Annealing Temperature |
|----------------|----------------------|----------------|------------------------------|--------------|--------------------------|
| | QnrS | QnrS | ACGACATTCGTCAACTGCAA-F | 417bp | 55°C |
| Quinolone | | | TAAATTGGCACCCTGTAGGC- R | | |
| resistant gene | qnrA | qnrA | F- CCGCTTTTATCAGTGTGACT | 188 bp | 55∘C |
| | | | R- ACTCTATGCCAAAGCAGTTG | | |
| | qnrB | qnrB | F-GATCGTGAAAGCCAGAAAGG | 469 bp | 54∘C |
| | | | R-ACGATGCCTGGTAGTTGTCC | | |
| | bla_{IMP} | bla_{IM} | F 5-GGAATAGAGTGGCTTAATTCTC-3 | 232bp | 52∘C |
| | | P | R 5 -CCAAACCAC TACGTTATC-3 | | |
| Carbapenemase | $bla_{\rm OXA}$ | bla_{OX} | F- GCGTGGTTAAGGATGAACAC | 438bp | 52∘C |
| gene | 48 | A-48 | R- CATCAAGTTCAACCCAACCG | - | |
| | bla_{vim} | $bla_{ m vim}$ | F 5 -GATGGTGTTTGGTCGCATA-3 | 390 bp | 52∘C |
| | | | R 5 -CGAATGCGCAGCACCAG-3 | | |
| Cephalosporin | bla_{CTX} - | bla_{CTX} | F 5-ATGTGCAGYACCAGTAARGT-3 | 593 bp | 52∘C |
| gene | M | - M | R 5-TGGGTRAARTARGTSACCAGA-3 | _ | |
| | msrA | msrA | F-TCCAATCATTGCACAAAATC | 163bp | 58∘C |
| | | | R- AATTCCCTCTATTTGGTGGT | | |
| | $ere\ A$ | ereA | F- GCCGGTGCTCATGAACTTGAG | 420 bp | 60 ∘C |
| Azithromycin | | | R-CGACTATTCGATCAGAGGC | | |
| | mefA | mefA | F-AGTATCATTAATCACTAGTGC | 345bp | 54∘C |
| | | | R:TTCTTCTGGTACTAAAAGTGG | | |

 Table 3: Sex distribution of bacterial isolates from patient

| SEX | No. of Infected | Percentage of infected | No. of Un-Infected | Percentage of Un-Infected | Total No. of samples |
|--------|-----------------|------------------------|--------------------|------------------------------|----------------------|
| Male | 88 | 57.9 % | 1256 | 54.5 % | 1344 |
| Female | 64 | 42.1% | 1048 | 45.5 % | 1112 |
| Total | 152 | 100 % | 2304 | 100 % | 2456 |

Table 4: The Age distribution of patients with notable bacterial growth

| Age Group | Infected No. | Percentage of infection (%) | Total Number | Chi-square | p-value |
|-------------------|--------------|-----------------------------|--------------|------------|---------|
| Children 0-10 | 60 | 39 % | 1016 | | |
| Adolescent 11- 19 | 41 | 27 % | 108 | | |
| 20-30 | 24 | 16 % | 223 | | |
| 31-59 | 20 | 13 % | 625 | | < 0.001 |
| Above 61 | 7 | 4.6 % | 484 | 54.8 | |
| Total | 152 | 100 % | 2456 | | |

 Table 5: Antibiotic susceptibility pattern of bacterial isolates from Typhoid Patients.

| Sr.no | Antibiotic class | Antibiotics | Susceptibility Pattern | | |
|--------|-----------------------|---------------------------------------|------------------------|--------------|-----------|
| Sr.110 | Antibiotic class | Anubiotics | Sensitive | Intermediate | Resistant |
| 1 | Penicillin | Amicilllin (AMP) | 46 (30 %) | 10 (7%) | 96 (63%) |
| | rememm | Ammoxillin | 30 (20 %) | 15(10%) | 106(70 %) |
| 2 | Cephalosporins | Ceftriaxone | 38 (25 %) | 41 (27%) | 71 (47%) |
| 2 | Серпагозротніз | Cefixime (CEF) | 46 (30%) | 46 (30 %) | 60 (40%) |
| 3 | Diaminopyrimidins | Trimethoprim (TRI) | 30 (20 %) | 33 (22%) | 88(58%) |
| 4 | Quinolones | Ciprofloxacine (CIP) | 18 (12 %) | 14 (9%) | 120 (79%) |
| | Cholorophenicol | | | | |
| 5 | inhibit peptide | Cholorophenicol(C) | | | |
| | bond form | | 38 (25 %) | 26 (17%) | 88 (58%) |
| 6 | Macrolides | Azithromycin (AZT) | 173 (90 %) | 15 (10%) | 0 (0%) |
| 7 | Carbapenems | Imipenem (IMP) | 129 (85 %) | 22 (15%) | 0 (0%) |
| , | c ur c up c i c i i i | Meropenum (MEM) | 124 (82 %) | 27 (18%) | 0 (0%) |
| | | MDR: Resistance to AMPICILLIN, | | | |
| 8 | | TRIMETHOPRIM (Third generation | | | |
| Ü | Multidruge | cephalosporin), | | | |
| | resistance | CHLORAMPHENICOL | 49 (32%) | 15 (10%) | 88 (58%) |
| | | Resistance to AMPICILLIN, | | | |
| | | TRIMETHOPRIM (Third generation | | | |
| 9 | | cephalosporin), CHLORAMPHENICOL, | | | |
| 9 | | Ciprofloxacin (fluoroquinolones), and | | | |
| | Extensive drug | a ceftriaxone third-generation | | | |
| | resistance | cephalosporin. | 91 (60%) | 21 (14%) | 40 (26%) |

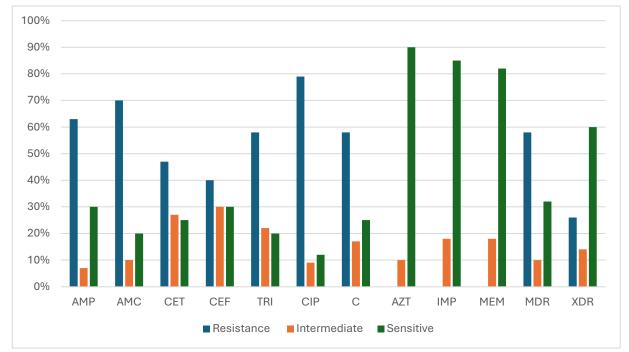


Fig. 3: The comparison of Salmonella Typhi antibiotic resistance profile is shown in this graph.

S-Sensitive, R-Resistant, AP-Amicillin, AM-Ammoxillin, SXT: Ceftriaxone, TRI: Trimethoprim, MEM: Meropenum, CIP: Ciprofloxacine, C: Cholorophenicol, AZT: Azithromycine, IMP: Imipenem, CEF: Cefixime.

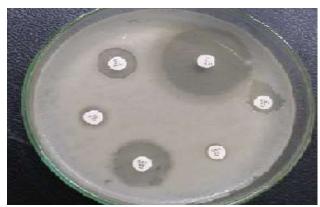


Fig. 4: *S.* Typhi resistance to antibiotics was determined by the Kirby Bauer method on Mueller Hinton Agar.

Ethical approval and consent to participate

The procedures for taking blood samples from human subjects were closely adhered to in this investigation. The Institutional Ethics Committee granted ethical clearance under code GCUF/ERC/4173 on December 20, 2021, ensuring compliance with ethical standards for research involving human participants. Furthermore, informed consent was provided by every participant in research involving human subjects.

Conflict of interest

The authors declare that the research was no conflict of interest.

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