



Original Article

Prevalence and antimicrobial susceptibility of bacterial species isolated from diarrheal stool of patients at Al-Zawiya Medicine Hospital, Libya

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Abstract:

Background: Bacterial diarrhea is a common health problem affecting many patients, including hospitalized patients. It is caused by various microorganisms, and these bacteria contribute to the rise in antibiotic resistance, making it a major public health issue. **Aim:** This study aimed to determine the prevalence of bacterial strains isolated from patients and to investigate their susceptibility to commonly used antibiotics at Al-Zawiya Hospital in Al-Zawiya, Libya. **Methods:** The study examined stool sample collection methods for patients seen at Al-Zawiya Hospital between January 1 and July 2024. Isolated samples were cultured using standard methods. Diagnosis was established using microbiological methods, and antibiotic susceptibility was tested using the Kirby-Bauer disk diffusion method. **Results:** The results were analyzed descriptively, where approximately 99 stool samples were collected from individuals aged 9 to approximately 50 years. Salmonella was detected in 26 of 31 samples (78.8%), Escherichia coli in 2 of 31 samples (6%), Shigella in 1 of 31 samples (3%), Staphylococcus aureus in 1 of 31 samples (3%), and Pseudomonas aeruginosa in 1 of 31 samples (3%). The majority of isolated strains showed susceptibility to imipenem, amikacin, and several cephalosporins, commonly used antibiotics. These results confirm the prevalence of enteric bacterial pathogens that contribute significantly to diarrhea, highlighting the need for targeted interventions. **Conclusion :** Diarrhea is an illness that affects people of all ages. Therefore, patients with diarrhea, often accompanied by various bacterial infections, require regular monitoring and appropriate antibiotic treatment. Studies have shown that diarrhea poses a significant threat to individual health due to several factors, including the use of antibiotics, the effectiveness of which is compromised by significant bacterial resistance. Research has also revealed variations in antibiotic resistance among isolated bacteria, leading to increased risks associated with this resistance. Consequently, close monitoring is essential to limit the spread of more resistant strains and explore alternative treatments.

Keywords: Stool samples, Antibiotic resistance, diarrhea.

Introduction:

The human gut is the natural habitat of many types of bacteria, most of which are involved in various metabolic activities and play a major role in maintaining the human immune system. [1] Diarrhea is a major cause of death worldwide, accounting for 21% of deaths in children under five and 12% of all deaths from infectious diseases. There are different types of diarrhea, with acute watery diarrhea being the most common (80% of cases), while persistent diarrhea accounts for 10% of cases (REF). The causes are varied and include malnutrition. The mortality rate associated with diarrhea can reach 35% (REF).

Diarrhea is caused by various types of microorganisms, such as bacteria or viruses.[2,3] Bacteria can be transmitted through fecal-oral contamination via unsanitary water, contaminated food, or contact with infected individuals.[4] People with low stomach acid are most susceptible to diarrhea **REF**. Consuming contaminated food and water, unsanitary practices, and

poor hygiene are all factors that can lead to an increase in diarrhea and, consequently, a rise in the mortality rate.[5] The total number of deaths due to diarrhea in 2016 exceeded 270,000, representing 16.88% of the total number of deaths.[6,7]

Bacteria can be transmitted in many ways, and high temperatures can also alter water availability, making it difficult to obtain drinking water and water for handwashing.[8] Faced with increasing demand for water and its scarcity, and given its important role in diseases, particularly in low-income countries where high temperatures and the resulting pollution are significant, the number of heat-related deaths worldwide is expected to be between 21,000 and 68,000 in 2030, before decreasing to between 15,000 and 49,000 by 2050, which would lead to a decrease in cases of bacterial infections causing acute diarrhea.[9]

The early 20th century was marked by a true revolution in the treatment of many diseases thanks to the discovery of antibiotics. More recently, however, antibiotic



resistance has emerged as a worrying global phenomenon, posing numerous challenges and limiting hospital capacity due to the increasing harmful effects of antibiotic-resistant bacteria, which ultimately constitute a serious threat to human health.[10]. Bacteria have the ability to adapt to their environment by changing through mutations, thereby acquiring new resistance characteristics.[11]. Bacteria can resist antibiotics through several mechanisms, such as enzymatic modification of the antibiotic's structure or its destruction, and sometimes by preventing it from entering the cell or expelling it from the cell, in addition to other means that allow them to resist the effect of these drugs.[12]

The widespread use of antibiotics in human medicine, veterinary medicine, and agriculture during the second half of the last century led to the production of large quantities of these drugs, which put increasing pressure on bacteria, which were able to adapt to these changing conditions thanks to their ability to adapt to their environment.[13] The discovery of antibiotics during the 20th century led to significant improvements in patient health. However, antibiotic resistance poses a weakness in the treatment of infections, resulting in increased morbidity and mortality rates.[14] Some pathogens represent a significant burden for countries in general, and particularly for low-income countries, such as Salmonella and Shigella.[15]

In recent years, concern has grown over antimicrobial resistance, which is responsible for approximately 1.2 million deaths worldwide each year. This resistance occurs when bacteria alter their response to antibiotics, thus reducing their effectiveness. Studies suggest that this phenomenon could lead to a significant number of human deaths, potentially reaching 10 million per year by 2050.[16] The World Health Organization, along with many other organizations and studies, has confirmed that the growing resistance to antimicrobials represents a major challenge that threatens public health and calls for concerted and intensified global efforts to combat it and reduce its effects.[17].

Materials and methods:

In this study, a group of 99 patients suffering from diarrheal diseases, from the outpatient clinics of Al-Zawiya Medical Hospital, were identified and studied within the Al-Zawiya Medical Laboratory by collecting stool samples from patients with diarrhea in a sterile manner in special sterile bottles.

1. Stool Sample Collection:

Stool samples were collected between January and July 2024 using special sealed containers. These samples were then transported directly to the microbiology laboratory at Al-Zawiya Hospital for bacterial culture and identification.

2. Sample Processing and Identification of Bacteria:

The bacteria were isolated on MacConkey agar and then incubated at 37°C for 24 hours. The bacterial isolates were then identified by standard methods, including the urease enzyme production test.

3. Antimicrobial Susceptibility Testing:

The antibiotic susceptibility of the isolates was assessed using the Kirby-Bauer disk diffusion method. This method employed 16 antibiotics produced by a Turkish company (including lofycin) in a culture medium (Mueller-Hinton agar). Petri dishes were incubated at 37°C for 24 hours. A zone of inhibition appeared around the disks containing the active antibiotic, due to its diffusion from the filter paper to the agar. The area of inhibition was measured in millimeters using a transparent ruler, and the zone of inhibition was marked with a circle indicating the location of the bacteria.

The bacteria were classified as susceptible (S), resistant (R), or intermediate (I) according to the standard specifications defined in the laboratory standards of the National Committee for Clinical Laboratories. The antibiotic tested was amikacin, Amoxicillin, Augmentin, Cefotaxime, Gentamycin, Ciprofloxacin, Ceftriaxone, Cefotaxime, Nitrofurantoin, Nitrofurantoin, Cefoxitin, Nalidixicacin, Imipenem, Norfloxacin, Bactrim, Tetracycline, Tobramycin [18, 19]

Statistical Analysis:

Data were analyzed using SPSS V27. Descriptive statistical methods were applied to summarize the study findings, including frequencies and percentages. Tables were used to present the demographic characteristics of the study population, distribution of bacterial isolates according to age and sex, and antimicrobial susceptibility patterns of the isolated microorganisms. The prevalence of bacterial pathogens was calculated as a percentage of the total examined stool samples. Antimicrobial susceptibility results were expressed as frequencies and percentages of susceptible isolates for each tested antibiotic.

Results:

Of the 99 diarrhea stool samples in this study, bacterial species were isolated from 31 samples (33%). The isolation rate was 9 samples (20.5%) in males and 24 samples (43.6%) in females.

Table 1. Frequency distribution of gender and percentage of infection in all studied samples

| Gender | Frequency | Percentage |
|--------|-----------|------------|
| Female | 55 | 55.6% |
| Male | 44 | 44.4% |
| Total | 99 | 100% |



The results in Table 1) show the frequency distribution of diarrheal stool samples by gender among patients at Zawia Medicine Hospital. Of the total 99 examined samples, females accounted for 55 cases (55.6%), whereas males accounted for 44 cases (44.4%). These

findings indicate a slightly higher prevalence of bacterial infection among female patients compared with male patients in the studied sample. This distribution suggests that females represented the majority of infected cases in the present study population.

Table 2: Age and sex distribution of patients with bacteria types in stools

| Age group (years) | Male | | Female | | Sample | Positive no. (%) |
|-------------------|---------------|------------------|---------------|------------------|--------|------------------|
| | No. of sample | Positive no. (%) | No. of sample | Positive no. (%) | | |
| 0 – 9 | 19 | 3(15.7) | 22 | 8(36.3) | 41 | 11 |
| 10 – 19 | 3 | 1(33.3) | 6 | 3(50) | 9 | 4 |
| 20 – 29 | 6 | 1(16.6) | 6 | 2(33.3) | 12 | 3 |
| 30 – 39 | 6 | 3(50) | 2 | 0(0) | 8 | 3 |
| 40 – 50 | 2 | 1(50) | 6 | 3(50) | 8 | 4 |
| >50 | 8 | 0(0) | 13 | 8(61.5) | 21 | 6 |
| Total | 44 | 9(20.5) | 55 | 24(43.6) | 99 | 31 |

The results presented in Table 2 describe the age and sex distribution of patients with bacteria-positive stool samples. Overall, 31 out of 99 examined samples were positive for bacterial isolates. Females showed a higher proportion of positive cases (24 positive cases out of 55 samples, 43.6%) compared with males (9 positive cases out of 44 samples, 20.5%). Regarding age groups, the highest number of positive cases was observed in the 0–9 years group (11 positive cases out of 41 samples),

followed by the >50 years group (8 positive cases out of 21 samples).

In contrast, lower numbers of positive cases were recorded in the 10–19 years (4 out of 9 samples), 20–29 years (3 out of 12 samples), 30–39 years (3 out of 8 samples), and 40–50 years (4 out of 8 samples) age groups. These findings indicate that bacterial infection was more frequent among females than males and was particularly common among younger children (0–9 years) and older adults (>50 years).

Table 3: Distribution of isolated microbes by defined age group

| Age group (years) | No. of sample | S.typhimurium | S.aureus | E.coli | Shigella | Pseudomonas | C.albicans |
|-------------------|---------------|---------------|----------|---------|----------|-------------|------------|
| 0 – 9 | 11 | 11(100.) | 0(0) | 0(0) | 0(0) | 0(0) | 0(0) |
| 10 – 19 | 4 | 2(50) | (25)1 | 1(25) | 0(0) | 0(0) | 0(0) |
| 20 – 29 | 3 | 3(100) | 0(0) | 0(0) | 0(0) | 0(0) | 0(0) |
| 30 – 39 | 3 | 3(100) | 0(0) | 0(0) | 0(0) | 0(0) | 0(0) |
| 40 – 50 | 4 | 3(75) | 0(0) | 1(25) | 0(0) | 0(0) | 0(0) |
| >50 | 8 | 4(50) | 0(0) | 0(0) | 1(12.5) | 1(12.5) | 2(25) |
| Total | 31(33.3) | 26(78.8) | 1(3.0%) | 2(6.0%) | 1(3.0%) | 1(3.0%) | 2(6.0%) |

The results in Table 3) show the distribution of isolated microbial species across different age groups among patients with bacteria-positive stool samples. In the 0–9-year age group, all isolates were identified as *Salmonella typhimurium* (11 cases, 100%), indicating that this species was the only detected pathogen in this group. Similarly, in the 20–29 and 30–39 years age groups, all positive isolates were also *S. typhimurium* (3 cases in each group, 100%). In the 10–19-year age group, mixed isolates were observed, including *Escherichia coli* (1 case, 25%), *Staphylococcus aureus* (1 case, 25%), and *S. typhimurium* (2 cases, 50%). For the 40–49-year age group, the majority of isolates were *S. typhimurium* (3 cases, 75%), with a smaller proportion of *Candida albicans* (1 case, 25%).

In patients older than 50 years, greater microbial diversity was noted, with *S. typhimurium* remaining the most frequent isolate (4 cases, 50%), followed by *C. albicans* (2 cases, 25%), *Pseudomonas* spp. (1 case, 12.5%), and *Shigella* spp. (1 case, 12.5%). Overall, *S. typhimurium* was the predominant isolate across all age groups (26 cases, 78.8%), whereas *E. coli*, *S. aureus*, *Pseudomonas* spp., *Shigella* spp., and *C. albicans* were detected at much lower frequencies. These findings indicate that *S. typhimurium* was the most common etiological agent of diarrhea across all age categories, with broader microbial diversity observed mainly among patients older than 50 years.

**Table 4: Age and sex distribution of isolated microbes No. of positive male and Female**

| Age group (years) | Total | No. of positive males | | | | | Total | No. of positive females | | | | |
|-------------------|-------|-----------------------|----------|--------|----------|-------------|-------|-------------------------|----------|--------|----------|-------------|
| | | S.typhimurium | S.aureus | E.coli | Shigella | Pseudomonas | | S.typhimurium | S.aureus | E.coli | Shigella | Pseudomonas |
| | | | | | | | | | | | | |
| 0 - 9 | 3 | 3 | 0 | 0 | 0 | 0 | 8 | 8 | 0 | 0 | 0 | 0 |
| 10 - 19 | 1 | 1 | 0 | 0 | 0 | 0 | 3 | 1 | 1 | 1 | 0 | 0 |
| 20 - 29 | 1 | 1 | 0 | 0 | 0 | 0 | 2 | 2 | 0 | 0 | 0 | 0 |
| 30 - 39 | 3 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 40 - 50 | 1 | 1 | 0 | 0 | 0 | 0 | 3 | 2 | 0 | 1 | 0 | 0 |
| >50 | 0 | 0 | 0 | 0 | 0 | 0 | 6 | 4 | 0 | 0 | 1 | 1 |
| Total | 9 | 9 | 0 | 0 | 0 | 0 | 22 | 8 | 1 | 2 | 1 | 1 |



The results presented in Table 4) describe the age- and sex-specific distribution of isolated microbial species among patients with bacteria-positive stool samples. Overall, females accounted for the majority of positive isolates (22 cases), whereas males contributed 9 positive cases. In the 0–9-year age group, only *Salmonella typhimurium* was isolated in both females (8 cases) and males (3 cases), indicating complete dominance of this pathogen in this group. In the 10–19 years group, isolates among females included *Escherichia coli* (1 case) and *S. typhimurium* (1 case), while males showed only *S. typhimurium* (1 case).

Similarly, in the 20–29 years group, *S. typhimurium* was the sole isolate in both females (2 cases) and males (1 case). In the 30–39 years group, all positive isolates were

restricted to males and identified as *S. typhimurium* (3 cases), with no isolates recorded among females. For the 40–49 years group, females showed isolates of *E. coli* (1 case) and *S. typhimurium* (2 cases), whereas males again showed only *S. typhimurium* (1 case). In patients older than 50 years, females exhibited greater microbial diversity, including *Pseudomonas* spp. (1 case), *Shigella* spp. (1 case), and *S. typhimurium* (4 cases), while no positive isolates were recorded among males in this age group. Overall, *S. typhimurium* was the predominant isolate in both sexes and across all age groups, with a higher overall frequency among females than males, as shown in Table 4).

Table 5: Antibiogram used against bacterial isolates

| S/N | Drugs | S.Typhimurium (n= 26) | <i>S.aureus</i> (n=1) | E.coli (n=2) | Shigella sp (n=1) | P. aeruginosa (n= 1) |
|-----|-------------------|-----------------------|------------------------|---------------|-------------------|----------------------|
| 1 | Amikacin AK | 21(80.7) | 1(100) | 2(100) | 1(100) | 1(100) |
| 2 | Augmentin AMC | 14(53.8) | 1(100) | 1(50) | 1(100) | 0 |
| 3 | Amoxicillin AMX | 4(15.3) | 1(100) | 1(50) | 1(100) | 0 |
| 4 | Ceftazidime CAZ | 22(84.6) | 1(100) | 1(50) | 0 | 1(100) |
| 5 | Gentamycin CN | 21(80.7) | 0 | 2(100) | 1(100) | 1(100) |
| 6 | Ciprofloxacin CIP | 18(69.2) | 1(100) | 2(100) | 1(100) | 0 |
| 7 | Ceftriaxone CRO | 16(61.5) | 0 | 2(100) | 1(100) | 1(100) |
| 8 | Cefotaxime CTX | 13(50) | 1(100) | 1(50) | 1(100) | 1(100) |
| 9 | Nitrofurantoin F | 15(57.6) | 1(100) | 2(100) | 1(100) | 0 |
| 10 | Cefoxitin FOX | 11(42.3) | 1(100) | 1(50) | 1(100) | 0 |
| 11 | Nalidixicacid NA | 7(26.9) | 0 | 1(50) | 0 | 0 |
| 12 | Imipenem IMP | 25(96.1) | 1(100) | 1(50) | 1(100) | 1(100) |
| 13 | Norfloxacin NOR | 15(57.6) | 0 | 2(100) | 0 | 1(100) |
| 14 | Bactrim SXT | 9(34.6) | 0 | 0 | 0 | 1(100) |
| 15 | Tetracycline TE | 6(23.0) | 0 | 1(50) | 1(100) | 1(100) |
| 16 | Tobramycin TOB | 20(76.9) | 1(100) | 2(100) | 1(100) | 1(100) |

The antimicrobial susceptibility patterns of the isolated bacteria are presented in Table 5). *Salmonella typhimurium* (n = 26) showed the highest susceptibility to imipenem (96.1%), followed by ceftazidime (84.6%), amikacin (80.7%), gentamicin (80.7%), and tobramycin (76.9%). Moderate susceptibility was observed for ciprofloxacin (69.2%), ceftriaxone (61.5%), nitrofurantoin (57.6%), norfloxacin (57.6%), and amoxicillin–clavulanic acid (53.8%), whereas lower susceptibility rates were recorded for cefoxitin (42.3%), trimethoprim–sulfamethoxazole (34.6%), nalidixic acid (26.9%), tetracycline (23.0%), and amoxicillin (15.3%). All isolates of *Staphylococcus aureus* (n = 1) were susceptible to amikacin, amoxicillin–clavulanic acid, amoxicillin, ceftazidime, ciprofloxacin, cefotaxime, cefoxitin, imipenem, nitrofurantoin, and tobramycin, while resistance was observed to gentamicin, ceftriaxone, nalidixic acid, norfloxacin, trimethoprim–sulfamethoxazole, and tetracycline. *Escherichia coli* (n = 2) exhibited complete susceptibility to amikacin,

gentamicin, ciprofloxacin, ceftriaxone, nitrofurantoin, norfloxacin, and tobramycin, but showed reduced susceptibility to amoxicillin, amoxicillin–clavulanic acid, ceftazidime, cefotaxime, cefoxitin, nalidixic acid, imipenem, and tetracycline (50% each).

The single isolate of *Shigella* spp. demonstrated full susceptibility to most tested antibiotics, including amikacin, amoxicillin–clavulanic acid, amoxicillin, gentamicin, ciprofloxacin, ceftriaxone, cefotaxime, cefoxitin, imipenem, nitrofurantoin, and tobramycin, but resistance to ceftazidime, nalidixic acid, trimethoprim–sulfamethoxazole, and norfloxacin was observed. The *Pseudomonas* sp. isolate showed complete susceptibility to amikacin, ceftazidime, gentamicin, ceftriaxone, cefotaxime, imipenem, norfloxacin, trimethoprim–sulfamethoxazole, tetracycline, and tobramycin, while resistance was noted to amoxicillin–clavulanic acid, amoxicillin, ciprofloxacin, nitrofurantoin, cefoxitin, and nalidixic acid.



Overall, imipenem, amikacin, and third-generation cephalosporins demonstrated the highest overall activity against the isolated pathogens, whereas amoxicillin, tetracycline, nalidixic acid, and trimethoprim–

Discussion:

stool samples were examined, of which 31 (33.3%) were positive for bacterial isolates. Females constituted a higher proportion of the study population (55.6%) than males (44.4%), and they also showed a higher proportion of positive bacterial isolates (43.6% in females vs. 20.5% in males), indicating a greater burden of infection among female patients.

With respect to age distribution, bacterial infections were most frequently detected among children aged 0–9 years and adults older than 50 years. These two age groups accounted for the highest numbers of positive cases, whereas lower frequencies were observed in the intermediate age groups (10–49 years). This pattern suggests that young children and older adults represent the most vulnerable populations to diarrheal bacterial infections in the study setting.

Analysis of the isolated microorganisms revealed that *Salmonella typhimurium* was the predominant pathogen, accounting for the majority of isolates across nearly all age groups and both sexes. Other pathogens, including *Escherichia coli*, *Staphylococcus aureus*, *Shigella* spp., *Pseudomonas* spp., and *Candida albicans*, were detected at much lower frequencies and were mainly observed in older age groups, particularly those above 50 years. The distribution by sex showed that females harbored a wider diversity of microbial isolates compared with males, although *S. typhimurium* remained the dominant organism in both groups.

Antimicrobial susceptibility testing demonstrated variable resistance patterns among the isolated bacteria. *S. typhimurium* showed the highest susceptibility to imipenem, ceftazidime, amikacin, gentamicin, and tobramycin, while reduced susceptibility was observed for amoxicillin, tetracycline, nalidixic acid, and trimethoprim–sulfamethoxazole. Other bacterial isolates, although few in number, were generally susceptible to imipenem, aminoglycosides, and third-generation cephalosporins, but exhibited resistance to commonly used antibiotics such as amoxicillin and tetracycline. Overall, imipenem and aminoglycosides demonstrated the greatest effectiveness against the isolated pathogens, whereas older and frequently prescribed antibiotics showed lower efficacy.

Conclusions:

- The overall prevalence of bacterial pathogens among diarrheal patients was 33.3%, with *Salmonella typhimurium* accounting for 78.8% of positive isolates.
- Females (43.6%) were more frequently affected than males (20.5%).
- Children aged 0–9 years and adults older than 50 years were the most vulnerable age groups.

sulfamethoxazole showed comparatively lower effectiveness, indicating varying degrees of antimicrobial resistance among the isolates.

The spread of bacteria that cause diarrhea, particularly in developing countries, is a widespread phenomenon. Diarrhea can lead to dehydration and, consequently, increased mortality, especially when bacteria become resistant to antibiotics. Furthermore, developing effective treatments is complex and requires significant time, effort, and financial resources.[20] In this study, after examining 99 stool samples, 31 isolates were identified as the causative agents of diarrhea in patients at Al-Zawiya Hospital. Among these isolates, 26 were identified as *Salmonella typhimurium* and 2 as *Escherichia coli*. One isolate of *Staphylococcus aureus*, one of *Shigella*, one of *Pseudomonas*, and two were also identified. These results are consistent with [20]. Studies conducted on stool samples in Bangladesh have revealed the presence of *Salmonella* spp. bacteria among the isolated organisms, confirming that this bacterium is a major cause of intestinal diarrhea, given the high incidence of infections of varying severity. It is therefore essential to take appropriate preventive measures to reduce contamination and control the spread of infection.[21].

In this study, Imipenem exhibited a high susceptibility rate (96.1%), and Tobramycin showed a susceptibility rate of 76.9% in *S. typhimurium*. Conversely, Amikacin demonstrated the highest susceptibility rate (80.7%), while Cefotaxime showed a susceptibility rate of approximately 50%. Resistance rates varied among the antibiotics, as shown in Table 5. Furthermore, strains resistant to these antibiotics were associated with cases of diarrhea, with *Salmonella typhimurium* strains representing the largest proportion (26.2%) of the frequently affected strains, an observation confirmed by the results.[22] A study was[23,24] conducted on 40 *Salmonella* strains isolated in southern Mozambique to assess their susceptibility and resistance to antibiotics.

The results showed resistance to nalidixic acid in only 3% of the strains. In this study, imipenem exhibited the highest susceptibility rate (96.1%), while *Shigella* showed 100% susceptibility. Numerous studies indicate that pathogenic bacteria, particularly drug-resistant strains, pose a serious threat to public health. While antibiotic treatments are often effective in controlling cases of bacterial diarrhea, the emergence of resistance to these drugs reduces their effectiveness and increases the risk of infection spreading.[25,26,27]

Summary of the Results:

This study investigated the prevalence of bacterial pathogens and their antimicrobial susceptibility patterns among diarrheal stool samples collected from patients attending Zawia Medicine Hospital, Libya. A total of 99



aminoglycosides or third-generation cephalosporins with caution.

3. The use of antibiotics with high resistance rates (e.g., amoxicillin and tetracycline) should be limited to avoid further development of antimicrobial resistance.
4. Special attention should be given to children and elderly patients, as they represent high-risk groups for bacterial diarrhea.
5. Continuous surveillance of enteric pathogens and their resistance patterns is recommended to monitor trends over time.
6. Public health interventions focusing on hygiene, sanitation, and safe food and water practices should be strengthened to reduce the burden of diarrheal infections.

Conflict of interest:

The authors declare that there is no conflict of interest regarding the publication of this paper.

- Imipenem, amikacin, and third-generation cephalosporins showed the highest *in vitro* activity. However, imipenem should be reserved for severe or multidrug-resistant cases only.
- High resistance rates were observed for amoxicillin (15.3% susceptibility), tetracycline (23.0%), nalidixic acid (26.9%), and trimethoprim–sulfamethoxazole (34.6%).
- The small sample size limits generalizability; larger studies are needed.

Recommendations:

1. Routine microbiological examination and antimicrobial susceptibility testing should be performed for diarrheal stool samples to guide appropriate therapy.
2. Imipenem should not be used as first-line empirical therapy; it should be reserved for severe or resistant infections only. Empirical treatment may rely on

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