

Available online at *www.ujpronline.com*
Universal Journal of Pharmaceutical Research
An International Peer Reviewed Journal
ISSN: 2831-5235 (Print); 2456-8058 (Electronic)
Copyright©2026; The Author(s): This is an open-access article distributed under the terms of the CC BY-NC 4.0 which permits unrestricted use, distribution, and reproduction in any medium for non-commercial use provided the original author and source are credited

RESEARCH ARTICLE

PREVALENCE, BIOTYPING, AND ANTIBIOTIC SUSCEPTIBILITY PROFILES OF *AEROMONAS* SPECIES ISOLATED FROM DIARRHOEAL PATIENTS IN SANA'A CITY, YEMEN

Sami Sultan Ahmed Abdu[1], Sami Mohammed Abdo Hassan[2], Hassan Abdulwahab Al-Shamahy[3*], Ibrahim Mohammed Amed Nahshal[3], Ibrahim Ali Al-Arashi[4], Amirh Abdullah Sa'aed Aljabri[5], Ahmed Mohammed Al-Haddad[6], Naif Mohammed Al-Haidary[7]

[1]*Medical Microbiology and Clinical Immunology Department, Faculty of Medicine and Health Sciences, Sana'a University, Yemen.* [2]*Medical Microbiology and Clinical Immunology Department, Faculty of Medical Sciences, Al-Nasser University, Yemen.* [3]*Medical Microbiology and Clinical Immunology Department, Faculty of Medicine and Health Sciences, Sana'a University.* [4]*Medical Microbiology and Clinical Immunology Department, Faculty of Health Sciences, Thamar University, Yemen.* [5]*Medical Microbiology and Clinical Immunology Department, Faculty of Medical Sciences, Al-Nasser University, Yemen.* [6]*Department of Medical Laboratories, College of Medicine and Health Sciences, Hadhramout University, Al-Mukalla, Yemen.* [7]*Medical Microbiology and Clinical Immunology Department, Faculty of Medicine and Health Sciences, Sana'a University.*

Article Info:

Article History:
Received: 26 July 2026
Reviewed: 3 September 2026
Accepted: 9 October 2026
Published: 15 November 2026

Cite this article:
Abdu SSA, Hassan SMA, Al-Shamahy HA, Nahshal IMA, Al-Arashi IA, Aljabri AAS, Al-Haddad AM, Al-Haidary NM. Prevalence, biotyping, and antibiotic susceptibility profiles of *Aeromonas* species isolated from diarrhoeal patients in Sana'a city, Yemen. Universal Journal of Pharmaceutical Research 2026; 11(5): 8-14. ***http://doi.org/10.22270/ujpr.v11i5.1662***

***Address for Correspondence:**
Dr. Hassan A. Al-Shamahy, Medical Microbiology and Clinical Immunology Department, Faculty of Medicine and Health Sciences, Sana'a University, Yemen. Tel: +967-770299847
E-mail: *hassanalshamahii@gmail.com*

Abstract

Background and Aims: The genus *Aeromonas* is one of new and increasingly important bacterial genera which have been included as a cause of human gastritis. The aims of the study include determination of the prevalence of *Aeromonas* species among diarrhoeal patients, as well as biotyping, and studying the antibiotic susceptibility of the isolates.

Methods: Initially patients suffering from diarrhoea were selected from patients who attended the main hospitals in Sana'a and sent to NCPHL for stool culture. A total of 1991 diarrheal stool specimens were collected during the period of two-year period (2023–2024). In order to identify *Aeromonas* the stool specimens were inoculated into alkaline peptone water, *Aeromonas* agar and TCBS agar, and then the isolates were identified by the relevant biochemical tests.

Results: Presents data on 1,991 diarrhea patients, predominantly children aged 2 months to 9 years (34.0%). There was a slight male predominance (52.9%). The mean age was 22.4 years, with a range of 2 months to 75 years. The leading bacterial causes were non-Salmonella typhoid serogroups (25.0%), Shigella serogroups (13.0%), and *Vibrio cholerae* (7.7%). Moderate to low prevalence included enteropathogenic *E. coli* (5.1%) and *Aeromonas* (1.9%). Resistance rates for *Aeromonas* were 100% for PG-penicillin, Ampicillin-sulbactam, Oxacillin, and Ampicillin, with high resistance to nalidixic acid (84.2%).

Conclusion: Diarrheal illness in this study population heavily burdens young children and is primarily driven by non-Salmonella typhoid and Shigella serogroups.

Keywords: *Aeromonas*, antibiotic susceptibility, diarrhea, gastritis, Yemen.

INTRODUCTION

Members of the genus *Aeromonas* as human and animal pathogens have attracted a great deal of scholarly attention in the last ten years, and the number of scientific and medical publications on the genus has increased significantly[1]. The Gram-negative bacillus's link to human gastrointestinal disorders is mostly responsible for increased attention, but other areas of growing significance included the genus's complex taxonomy and virulence-related variables in infections in humans and animals[2]. Because there are few long-term investigations and it is difficult to distinguish between pathogenic and non-pathogenic strains, the involvement of *Aeromonas* species in bacterial gastroenteritis remains unclear[3]. There are two main types of serious human infections linked to *Aeromonas*. One of these is gastroenteritis, which primarily affects young children or the elderly, although it can also strike travellers and patients with weakened immune systems[4,5]. In addition to gastroenteritis, adults can get extra-intestinal infections. The Mesophile groups of motile *Aeromonas* species are considered to be potential human pathogens, but *A. salmaonicida*, the

only member, which has not been recovered from humans[6]. *Aeromonas* species infections are contracted through ingestion, and in a few documented cases, refrozen or undercooked shellfish and oysters have been strongly suspected of causing food-borne gastroenteritis[7]. Additionally, contact of damaged skin or mucosal surfaces to contaminated water or soil can result in extraintestinal infections[8]. Due to years of civil conflict, widespread population displacement, economic collapse, and the deterioration of water, sanitation, and hygiene (WASH) infrastructures, Yemen is experiencing a serious public health crisis caused by bacterial and parasite illnesses[9-14]. These preventable and treatable diseases spread quickly, especially among vulnerable rural communities and internally displaced persons (IDP) camps, because less than half of the country's healthcare facilities are completely operational[15,16].

About 26% of Yemen's reported neglected infectious diseases are caused by bacterial infections, which are closely associated with tainted food and water sources[9]. Cholera epidemics in Yemen have historically been unusual[12]. The aims of the study include determination of the prevalence of *Aeromonas* species among diarrhoeal patients, as well as bio-typing, and studying the antibiotic susceptibility of the *Aeromonas* isolates.

MATERIAL AND METHODS

Sample size and patient selection

Study population and sample size: A total of 1,991 patients presenting with diarrheal symptoms were enrolled in this study. The sample size reflects the total volume of symptomatic individuals who met the inclusion criteria during the designated study timeframe.

Selection criteria and study period

Participants were selected based on the following criteria**:** Patients presenting with acute or chronic diarrhea symptoms. Clinical cases were consecutively accumulated over a two-year period (from 1st January, 2022, to 31st December, 2023).

Study setting: The selection was restricted to patients who actively sought medical attention or were referred directly to the National Central Public Health Laboratory (NCPHL)**.**

Fecal specimens: The stool specimens from selected diarrhoeal patients were collected according to the standard method of Bialy and Scott Diagnostic Microbiology[17]. Each stool specimen was collected in a sterile disposable 25 ml container. Loose stools were collected only. All stool specimens were transported within two hours of collection to the National Central Public Health Laboratory (NCPHL) for processing, culture and identification. A transport medium (Cary-Blair) was used when stool specimens were not delivered within two hours to the National Central Public Health Laboratory (NCPHL).

Data collection: A full history was taken from each patient. The findings were recorded in a predesigned questionnaire which included sex, age, risk factors of contracting gastritis.

Culture and identification: All stool specimens were inoculated into alkaline peptone water, TCBS[18] and *Aeromonas* agar then incubated aerobically at 37ºC for 48 hours[19]. The suspected colonies then picked for bacterial identification by microscopy, Gram-stain reaction, and biochemical tests, and bio-typing was done by API.

Sensitivity test: Stoke disc diffusion sensitivity test was used to test the isolates for 13 different antibiotics. Both the test and control (*S. aureus* NCTC6571) organisms were inoculated onto Muller Hinton agar (Oxoid), the same plate using an inoculum which gives semi confluent growth. This means that the activity of each disc is controlled, the inhibition zone size of the test organism can be compared directly with that of the control, and errors due to using too heavy or too light an inoculum would be detected.

RESULTS

Table 1 illustrates the distribution by age and gender of 1,991 patients suffering from diarrhoea who visited the central laboratory for stool culture testing in Sana'a, Yemen, over a two-year period (2023–2024). Regarding age distribution, children and young people constituted the majority of cases; the 2-month to 9-year age group recorded the highest prevalence, accounting for 34.0% (677 patients) of the total. As for gender distribution, a slightly higher proportion of males (52.9%) were observed compared to females (47.1%).

Table 1: The age and sex distribution of patients suffering from diarrhea attending central laboratory for stool culture for 2 years period (2023 and 2024).

Character	N (%)
Age groups	
2 months–9 years	677 (34)
10–19 years	293 (14.7)
20–29 years	364 (18.3)
30–39 years	239 (12)
40–49 years	187 (9.4)
50–59 years	99 (5)
60–69 years	85 (4.3)
More than 70 years	46 (2.4)
Sex	
Males	1053 (52.9)
Females	938 (47.1)
Total	1991 (100)
Summary Statistics	
Mean age	22.4 years
SD	18.8 years
Median	20.0 years
Mode	1.0 year
Youngest	2 months
Oldest	75 years

Analysis of the age statistics reveals a mean patient age of 22.4 years, with significant age variation (a standard deviation of 18.8 years); the most frequent age (mode) among patients seeking treatment was one year, while ages ranged from a minimum of two months to a maximum of 75 years. Table 2 shows that the most common cause of diarrhoea, in which parasitic causes were the most frequently isolated, accounted for 31.0%

(617 cases) of the total. Considering the leading bacterial causes among the pathogenic bacteria, non-Salmonella typhoid serogroups were the most prevalent at 25.0% (498 cases), followed by Shigella serogroups at 13.0% (259 cases) and *Vibrio cholerae* at 7.7% (153 cases).

Table 2: Bacterial isolates among diarrheal patients.

Organisms	n (%)
Enteropathogenic E. coli serogroups	101 (5.1)
Shigella serogroups	259 (13.0)
Non-*Salmonella* typhoid serogroups	498 (25.0)
Campylobacter jejuni	2 (0.1)
Aeromonas species	38 (1.9)
S. aureus	14 (0.7)
Yersinia enterocolitica	14 (0.7)
Clostridium difficile	12 (0.6)
V. cholerae	153 (7.7)
Non-*Vibrio cholerae*	18 (0.9)
Bacillus cereus	2 (0.1)
Clostridium perfringens	2 (0.1)
Parasitic causes	617 (31.0)
Non-Diagnostic cases	261 (13.1)

Considering moderate to low prevalence: Entero-pathogenic *E. coli* serogroups made up 5.1% (101 cases), while *Aeromonas* species were found in 1.9% (38 cases) of patients. Considering rare pathogens, several organisms were extremely rare in this sample, each appearing in less than 1% of the cases. These include *Campylobacter jejuni*, *Bacillus cereus*, and *Clostridium perfringens*, which were each isolated in only 2 patients (0.1%). Furthermore, Other Isolates: Non-pathogenic bacterial isolates accounted for 13.1% (261 cases) of the total findings. Table 3 outlines the prevalence rate of different isolated *Aeromonas* species collected from 38 specimens of diarrheal patients. *Aeromonas hydrophila* is the most prevalent species found in the specimens, accounting for 17 cases (44.7%); *Aeromonas sobria* is the second most common species, closely following at 16 cases (42.1%); and *Aeromonas caviae* is the least prevalent species isolated, representing only 5 cases (13.2%). Table 4 displays the antibiotic susceptibility patterns of 38 *Aeromonas* species isolates collected from patients experiencing diarrhea in Sana'a, Yemen. It categorizes the bacteria's response to 13 different antibiotics into three levels: sensitivity, intermediate, and resistant, showing both the raw count and the percentage. The *Aeromonas* isolates showed 100% resistance (38 out of 38 isolates) to four specific antibiotics, including PG-penicillin, ampicillin-sulbactam, oxacillin, and ampicillin.

Table 3: The prevalence rate of isolated *Aeromonas* species from diarrheal patient's specimens.

Species	n (%)
A. hydrophila	17 (44.7)
A. sobria	16 (42.1)
A. caviae	5 (13.2)
Total	38 (100)

Several other antibiotics faced high rates of bacterial resistance, including nalidixic acid (84.2%, 32 isolates), ofloxacin (76.3%, 29 isolates), trimethoprim (57.9%, 22 isolates), and gentamicin (57.9%, 22 isolates). The antibiotics that successfully inhibited the highest percentage of isolates were chloramphenicol (60.5%, 23 isolates), nitrofurantoin (57.9% sensitive, 22 isolates), and cefotaxime (57.9% sensitive, 22 isolates). Ciprofloxacin showed a highly divided split, with 42.1% sensitivity, 28.9% intermediate, and 28.9% resistance. Gentamicin showed 57.9% resistance; the remaining 42.1% fell entirely into the intermediate category, leaving 0% fully sensitive. Clindamycin showed a relatively even spread across sensitivity (31.6%), intermediate (26.3%), and resistance (42.1%).

DISCUSSION

The findings of this study provide a detailed epidemiological insight into the etiology of diarrheal illness within the studied cohort. A striking observation is that parasitic pathogens emerged as the primary cause of diarrhea, accounting for 31.0% (617 cases) of the total sample. This exceptionally high burden of parasitic isolates highlights a significant public health concern. Globally, intestinal protozoa and helminths remain deeply endemic in areas constrained by poor sanitation infrastructure, compromised water safety, and inadequate personal hygiene.

Table 4: Antibiotic susceptibility of Aeromonas species isolates from patients with diarrhea in Sana'a city, Yemen (n=38).

Antibiotic	Sensitivity %	Intermediate %	Resistant %
Ciprofloxacin	16 (42.1)	11 (28.9)	11 (28.9)
Trimethoprim	2 (5.3)	14 (36.8)	22 (57.9)
Chloramphenicol	23 (60.5)	8 (21.0)	7 (18.4)
PG-penicillin	0 (0.0)	0 (0.0)	38 (100)
Clindamycin	12 (31.6)	10 (26.3)	16 (42.1)
Ofloxacin	5 (13.2)	4 (10.5)	29 (76.3)
Ampicillin-sulbactam	0 (0.0)	0 (0.0)	38 (100)
Oxacillin	0 (0.0)	0 (0.0)	38 (100)
Ampicillin	0 (0.0)	0 (0.0)	38 (100)
Gentamicin	0 (0)	16 (42.1)	22 (57.9)
Nitrofurantoin	22 (57.9)	0 (0.0)	16 (42.1)
Nalidixic acid	5 (13.2)	1 (2.6)	32 (84.2)
Cefotaxime	22 (57.9)	0 (0.0)	16 (42.1)

The predominant isolation of parasites over viral or bacterial agents in this study underscores the critical necessity for localized targeted interventions, such as enhanced water treatment systems and aggressive health sanitation campaigns[15,16].

Among the pathogenic bacteria isolated, non-Salmonella typhoid serogroups were identified as the most prevalent bacterial etiology, comprising 25.0% (498 cases) of the sample. This high frequency indicates substantial fecal-oral contamination routes, likely tied to contaminated food or municipal water networks. Following closely, *Shigella* serogroups accounted for 13.0% (259 cases). This finding aligns robustly with global data, including the *Global Burden of Diseases Study*, which consistently positions *Shigella* as a leading bacterial driver of moderate-to-severe diarrheal morbidity and mortality worldwide, particularly due to its low infectious dose and high transmissibility. The detection of *V. cholerae* at 7.7% (153 cases) further signifies an active risk of acute secretory diarrheal outbreaks within the community, reinforcing the demand for rapid diagnostic tracking and immediate rehydration protocols[9,20,21].

Pathogens exhibiting a moderate-to-low prevalence included *Enteropathogenic E. coli* (EPEC) serogroups (5.1%, 101 cases) and *Aeromonas* species (1.9%, 38 cases). *EPEC* pathotypes are well-documented contributors to persistent infantile and childhood diarrhoea via the disruption of intestinal microvilli. Meanwhile, *Aeromonas* species, though less frequently discussed, are increasingly recognized as opportunistic aquatic pathogens capable of inducing gastroenteritis following the consumption of untreated well water or contaminated seafood[15,16].

Conversely, certain classic bacterial Enteropathogens were exceptionally rare in this population. *Campylobacter jejuni*, *Bacillus cereus*, and *Clostridium perfringens* were each isolated in a mere 0.1% (2 cases) of patients. While *Campylobacter* stands as a dominant cause of bacterial foodborne diarrhea in high-income, developed countries, its sparse distribution in this sample suggests variations in regional livestock exposure, dietary habits, or potential under-isolation due to strict microaerophilic culture requirements. The low incidence of *B. cereus* and *C. perfringens* indicates that acute, toxin-mediated food poisoning outbreaks were not the driving factor behind the steady burden of diarrheal presentations during the study period[9,15,16].

Finally, non-diagnostic cases constituted 13.1% (261 cases) of the total findings. This subset represents instances where standard laboratory diagnostic work-flows failed to identify a definitive pathogen. This diagnostic gap can reasonably be attributed to several factors: viral etiologies (such as Rotavirus or Norovirus) that may not have been screened for in the baseline panel, preceding self-medication with over-the-counter antimicrobials by patients prior to sample collection, or non-infectious causes of acute diarrhea such as dietary intolerances and functional bowel disorders. Implementing molecular multi-pathogen testing, such as multiplex polymerase chain reaction (PCR) assays, in future surveillance could significantly reduce this undiagnosed fraction and improve therapeutic precision[15,16].

No surveys, have been performed in Yemen to determine the prevalence of *Aeromonas* species as a cause of diarrhoea, nor have any cases been reported. However, *Aeromonas* gastritis has been reported from areas in Europe, America, and Asia[4,5,22]. This study has demonstrated that human gastritis due to *Aeromonas* species is currently 1.9% from Yemen, while in India the prevalence of *Aeromonas* was (3.1%)[23], in Bangladesh 7%[24], and in Africa 2.7%, in Latin America 1.8%, and 2.3% in Asia as whole[2,3,22]. The low rate in our study might be due the facts, First, *Aeromonas* species are significant pathogens of animals, and cause serious opportunistic infection only in immune-compromised individuals[3,25]. The second point is that there is no association between *Aeromonas species* and gastroenteritis in Yemen because *Aeromonas* species are found everywhere in the environment, so most people in Yemen may be immunized against *Aeromonas species*, due to the high frequency of exposure to these species resulting from poor environmental hygiene. This is converse of the situation in developed countries where it is less frequent, so that the chance to develop immunity among the general population against *Aeromonas* species is rare; most probably for this reason accidental exposure to *Aeromonas* species leads to clinical infections. This hypothesis is supported by the findings of Kirov *et al*. and Jiang *et al*.[25,26]. A third key factor involves the bacteria themselves: identifying *Aeromonas* as a definitive cause of diarrhea is challenging because the genus is highly heterogeneous, and only specific subgroups may be pathogenic[27]. Furthermore, although various virulence factors have been identified in *Aeromonas* species such as entero-toxins, cytotoxins, hemolysins, aerolysins, proteases, hemagglutinins, and tissue-culture adherence or invasion capabilities a clear link between these factors and actual diarrheagenic ability remains unproven[28,29].

The fourth point is related to the diagnostic method, since the ability of most commercial identification systems to accurately identify *Aeromonas* species to the species level is limited and uncertain, and some kits have trouble separating *Aeromonas* species from *Vibrio* species[30,31]. The fifth point is due to the unrecognized short-duration diarrhoea which is caused by *Aeromonas* species, and the quick recovery without antibiotics[32,33].

Furthermore, the global clinical burden of *Aeromonas* in human gastroenteritis remains undefined. Nevertheless, its prevalence fluctuates geographically, peaking in areas with poor sanitation[34-36]. Diverse global literature reports *Aeromonas* species isolation rates ranging from 0.6% to 7.2% among diarrheal patients, with the highest frequency observed in pediatric populations[37,38]. Meanwhile, in North America and Europe, the bacterium is implicated in approximately 2% of traveler's diarrhea cases[39,40]. By comparison, *Aeromonas* species represent the third most common cause of bacterial gastroenteritis among Spanish children, comprising 2.5 to 4% of diagnosed cases[41-43]. A similar incidence rate of 2.5% has been

documented in American children suffering from diarrhea[43]. In the current study, *Aeromonas* spp. was detected in 0.61% of diarrheal stool samples. This finding aligns with earlier literature and reinforces the established understanding that in industrialized nations, *Campylobacter* species remain the dominant bacterial pathogens, accounting for 1.32% of the cases in this cohort[44].

Aeromonas species were unexpectedly the second most frequent intestinal pathogen found in stool samples within our study, outnumbering *Salmonella enterica* (which stood at 0.46%)**.** This highlights that *Aeromonas* species should be recognized as significant human intestinal pathogens, much like *Campylobacter* and *Salmonella* species. Furthermore, relying on traditional stool culture techniques without specific selective media may cause health professionals to underestimate how often this pathogen actually occurs, even in developed nations[45]. *Aeromonas* spp. infection was monomicrobial in most of our cases (93%). This contrasts with previous studies on traveler's or children's diarrhoea, which reported a higher prevalence of co-infections[46] a discrepancy likely driven by differences in study populations. Because our survey avoids patient recruitment bias, it reveals a bimodal distribution: one peak in children under 15 years old and a second, substantial peak in individuals over 45. Consistent with prior literature, 30% of the patients in our cohort were infants and children[40].

The findings of this study outline a highly concerning antibiotic susceptibility profile among the 38 *Aeromonas* species isolates retrieved from diarrheic patients in Sana'a, Yemen. The absolute resistance (100%) observed against ampicillin, ampicillin-sulbactam, oxacillin, and penicillin G aligns closely with established microbiological paradigms. Virtually all *Aeromonas* species naturally harbor chromosomal beta-lactamase genes, including classical penicillinases and cephalosporinases, which render standard and inhibitor-assisted penicillins therapeutically useless[47].

A critical concern raised by these results is the high level of resistance to nalidixic acid (84.2%) and ofloxacin (76.3%), alongside an unstable split in susceptibility to ciprofloxacin (42.1% sensitive, 28.9% intermediate, 28.9% resistant**)**. Fluoroquinolones have historically served as the cornerstone empirical therapy for severe, persistent gastroenteritis caused by Gram-negative pathogens like *Aeromonas*. The severe drop in ciprofloxacin efficacy, alongside the failure of earlier-generation quinolones, signals a profound shift. This shift points to the rapid acquisition of target-site mutations (such as in the *gyrA* or *parC* genes) or plasmid-mediated quinolone resistance (PMQR) factors. This alarming pattern restricts oral outpatient treatment choices for severe cases in the region[47].

The 57.9% resistance rate observed for both trimethoprim and gentamicin further highlights a multidrug-resistance (MDR) crisis in Yemen[49-51]. In Yemen, public health infrastructure challenges combined with easy, unregulated access to over-the-counter medications have historically driven the overuse of broad-spectrum agents like trimethoprim, sulfamethoxazole. While aminoglycosides like gentamicin are normally reserved for systemic or severe infections, the 0% full sensitivity noted in this cohort where the remaining 42.1% of isolates fell entirely into the intermediate range suggests widespread adaptation to aminoglycoside-modifying enzymes[49,50-54]. Conversely, chloramphenicol (60.5% sensitive), nitrofurantoin (57.9% sensitive), and cefotaxime (57.9% sensitive) achieved the highest rates of bacterial inhibition. The relative efficacy of chloramphenicol and nitrofurantoin may stem from their less frequent use in routine diarrheal management due to toxicity concerns and localized prescription habits[54]. The 57.9% sensitivity to cefotaxime indicates that a narrow majority of strains remain vulnerable to third-generation cephalosporins. However, the remaining resistant fraction indicates the encroaching presence of extended-spectrum beta-lactamases (ESBLs) or AmpC overproduction within the local microbial reservoir[54]. Ultimately, the diverse responses seen across antibiotics like clindamycin (31.6% sensitive, 26.3% intermediate, 42.1% resistant) reflect an increasingly unpredictable resistance landscape. These dynamics necessitate rapid diagnostic profiling and stringent antibiotic stewardship policies across clinical centers in Sana'a to preserve the few remaining viable therapies[53,54].

Limitations of the study

First, there is a geographical bias; although the study claims to address the situation in Yemen comprehend-sively, the selection of patients was limited exclusively to major hospitals in Sana'a. A second limitation stems from the study's "cross-sectional" design and its reliance on a single center as sample collection was confined to one urban hub or specific medical facility which may fail to account for seasonal variations or population dynamics in rural regions across Yemen.

CONCLUSIONS

In conclusion, diarrheal disease primarily affects young children (aged two months to nine years), although it impacts a broad age range, extending up to 75 years. Non-typhoidal *Salmonella* and *Shigella* serogroups are the most significant bacterial causes of diarrhea identified in this study, followed by *V. cholerae*. *Aeromonas* species, while less frequent, exhibit high levels of drug resistance; they show complete (100%) resistance to common antibiotics such as penicillin, ampicillin-sulbactam, oxacillin, and ampicillin as well as high resistance to nalidixic acid. The use of beta-lactam antibiotics and fluoroquinolones (e.g., ciprofloxacin) should be avoided in treating *Aeromonas* infections, given their variable susceptibility profiles.

ACKNOWLEDGEMENTS

The authors express their gratitude to The National Centre of Public Health Laboratories (NCPHL), Sana'a, Yemen for their kind assistance.

AUTHOR'S CONTRIBUTIONS

Abdu SSA: formal analysis, conceptualisation, data organisation, writing original draft. **Hassan SMA:** data analysis, manuscript writing. **Al-Shamahy HA:** data analysis, manuscript writing. **Nahshal IMA:** literature survey. **Al-Arashi IA:** critical review. **Aljabri AAS:** data analysis, manuscript writing. **Al-Haddad AM:** critical review, editing. **Al-Haidary NM:** literature survey, editing. Final manuscript was checked and approved by all authors.

DATA AVILIABILITY

The data will be available to anyone upon request from the corresponding author.

CONFLICT OF INTEREST

None to declare.

REFERENCES

1. Bhowmick UD, Bhattacharjee S. Bacteriological, clinical and virulence aspects of *Aeromonas*-associated diseases in humans. Pol J Microbiol 2018; 67: 137–149. *https://doi.org/10.21307/pjm-2018-020*
2. Fernández BA, Figueras MJ. An update on the genus *Aeromonas*: Taxonomy, epidemiology, and pathogenicity. Microorganisms 2020; 8: 129. *https://doi.org/10.3390/microorganisms8010129*
3. Yuwono C, Wehrhahn MC, Liu F, *et al*. The isolation of *Aeromonas* species and other common enteric bacterial pathogens from patients with gastroenteritis in an Australian population. Microorganisms 2021; 9: 1440. *https://doi.org/10.3390/microorganisms9071440*
4. García VC, García VM, Del CAG, *et al*. Acute bacterial gastroenteritis: 729 cases recruited by a primary care national network. An Pediatr (Barc) 2017; 87:128–134. *https://doi.org/10.1016/j.anpedi.2016.04.020*
5. Persson S, Al-Shuweli S, Yapici S, *et al*. Identification of clinical *Aeromonas* species by rpoB and gyrB sequencing and development of a Multiplex PCR method for detection of *Aeromonas* Hydrophila. J Clin Microbiol 2015; 53: 653–656. *https://doi.org/10.1128/JCM.01963-14*
6. Burr SE, Stuber K, Wahli T, *et al*. Evidence for a type 111 secretion system in *Aeromonas* salmonicida subsp *Salmonicida*. J Bacterio 2002; 184: 5966-5970. *https://doi.org/10.1128/JB.184.21.5966-5970.2002*
7. Kirov SM. The public health significance of *Aeromonas* species in foods. Int J Food Microbiol 1993; 20: 179-198. *https://doi.org/10.1016/0168-1605(93)90164-C*
8. Altwegg M. *Aeromonas* and *Plesiomonas* in manual of clinical microbiology. ASM Press, Washington DC 1999: 507-516.
9. Abdul MGTA, Al-Moyed KA, Al-gunaid EA, *et al*. Diarrhea causing *Enterobacteriaceae* and their antibiotic resistance patterns among diarrhea patients from Sana'a city, Yemen. Universal J Pharm Res, 2024; 9(2): 15-20. *http://doi.org/10.22270/ujpr.v9i2.1083*
10. Al-Mohanadi EMA, Moharem ASS, Al-Moyed KAKA, *et al*. Cholera in Sana'a, Yemen: Clinical features, risk factors and antibiotic sensitivity of *Vibrio cholerae*. Universal J Pharm Res 2022; 7(2): 1-8. *https://doi.org/10.22270/ujpr.v7i3.772*
11. AL-Mekhlafi AM, Al-Moyed KA, Al-Haddad AM, *et al*. Prevalence of intestinal protozoa, Helminthes, and coccidian infections among primary school children in Thala 'a district at Amran governorate, Yemen. Universal J Pharm Res 2023; 8 (3):1-8. *https://doi.org/10.22270/ujpr.v8i3.943*
12. Sheiban AA, Al-Shamahy HA, Alattab NM, *et al*. Epidemicity of *Vibrio cholera* in Sana'a city, Yemen: Prevalence and potential determinants. Universal J Pharm Res 2018; 2(6):1-6. *https://doi.org/10.22270/ujpr.v2i6.R1*
13. Shamsan ENA, De-ping C, Al-Shamahy HA, *et al*. Coccidian intestinal parasites among children in Al-torbah city in Yemen: In country with high incidence of malnutrition. Universal J Pharm Res 2019; 4(4): 1-8. *https://doi.org/10.22270/ujpr.v4i4.301*
14. Al-Ghaithi GAAA, Al-Moyed KA, Al-Shamahy HA, *et al*. Prevalence of salmonella and intestinal parasites among food handlers predispose consumers to significant health risks. Universal J Pharm Res, 2023; 8(1): 1-8. *https://doi.org/10.22270/ujpr.v8i1.890*
15. World Health Organization (WHO). Diarrhoeal disease fact sheet. WHO Global Reports. Available at: WHO Diarrhoeal Disease.
16. GBD. Enteric Infectious Diseases Collaborators. Global burden of enteric infectious diseases, diarrhoeal diseases, and corresponding aetiologies, 1990–2023: A systematic analysis for the Global Burden of Disease Study 2023. The Lancet Infectious Diseases.
17. Forbes B, Sahm D, Weissfeld A. Baily and Scotts Diagnostic Microbiology. London, Madried, Mexico, Singapore, Tokyo, Mosby 1998; 10: 511-513.
18. Janda JM, Abbott SL, Carnahan AM. *Aeromonas* and Plesiomonas, in Manual of Clinical Microbiology 1995; 6: 477-482.
19. Obi CL, Potgieter N, Bessong PO, *et al*. Scope of potential bacterial agents of diarrhoea and microbial assessment of quality of river water sources in rural Venda communities in South Africa. Water Sci Technol 2003; 47(3):59-64. *https://doi.org/10.2166/wst.2003.0161*
20. Kotloff KL. The Global Enteric Multicenter Study (GEMS) of diarrheal disease in infants and young children in developing countries: Use of molecular diagnostics for pathogen attribution. The Lancet.
21. Fletcher SM. Intestinal parasitic infections: A review of global prevalence, clinical transmission, and diagnostic strategies. Journal of Parasitology Research.
22. Kaakoush NO, Castaño-Rodríguez N, Mitchell HM, *et al*. Global epidemiology of campylobacter infection. Clin Microbiol Rev 2015; 28:687–720. *https://doi.org/10.1128/CMR.00006-15*
23. Sinha S, Shimada T, Ramaurthy T, *et al*. Prevalence, serotype distribution, antibiotic susceptibility and genetic profiles of mesophilic *Aeromonas* species isolated from hospitalized diarrhoeal cases in Kolkata, India. J Medical Microbiol 2004, 53: 527-534. *https://doi.org/10.1099/jmm.0.05269-0*
24. Albert MJ, Ansaruzzaman M, Talukder KA, *et al*. Prevalence of enterotoxin genes in *Aeromonas* species. Isolated from children with diarrhea, healthy controls, and the environment. J Clin Microbiol 2000; 38:3785-90. *https://doi.org/10.1128/JCM.38.10.3785-3790.2000*
25. Kirov SM. *Aeromonas* and *Plesiomonas* species. In Doyle M P, Beuchat L R, and Montville T J (ed), Food microbiology: Fundamentals and frontiers. American Society for Microbiology Press, Washington, D C 2001; 301-327.
26. Jiang ZD, Nelson AC, Mathewson JJ, *et al*. Intestinal secretory immune response to infection with *Aeromonas* species and Plesiomonas shigelloides among students from the United States in Mexico. J Infect Dis 1991; 164(5): 979-82. *https://doi.org/10.1093/infdis/164.5.979*
27. Gonçalves PRB, de Oliveira WF, Marques DSC, *et al*. The genus *Aeromonas*: A general approach. Microb Pathog 130:81-94. *https://doi.org/10.1016/j.micpath.2019.02.036*
28. Thornley JP, Shaw JG, Gryllos IA, *et al*. Virulence properties of clinically significant *Aeromonas* species: Evidence for pathogenicity. Rev Med Microbiol 1997; 8: 61-72. *https://doi.org/10.1097/00013542-199704000-00002*
29. Zhou Y, Yu L, Nan Z, *et al*. Taxonomy, virulence genes and antimicrobial resistance of *Aeromonas* isolated from extra-intestinal and intestinal infections 11 medical and health sciences 1108 medical microbiology Laith Yakob. BMC Infect Dis 2019; 19. *https://doi.org/10.1186/s12879-019-3766-0*
30. Tison DLV, Murray PR, Baron EJ, *et al*. Mannual of Clinical Microbiology, 7th ed. Washington DC 1999. American Society for Microbiology.
31. Yuwono C, Wehrhahn MC, Liu F, *et al*. The isolation of *Aeromonas* species and other common enteric bacterial pathogens from patients with gastroenteritis in an Australian population. Microorganisms 2021; 9: 1440.

https://doi.org/10.3390/microorganisms9071440

32. Namdari H, Bottone EJ. Cytotoxin and enterotoxin production as factors delineating entero-pathogenicity of *Aeromonas* caviae. J Clin Microbiol 1990; 28:1796-1798.
33. Zhou Y, Yu L, Nan Z, *et al*. Taxonomy, virulence genes and antimicrobial resistance of *Aeromonas* isolated from extra-intestinal and intestinal infections 11 medical and health sciences 1108 medical microbiology Laith Yakob. BMC Infect Dis 2019; 19. *https://doi.org/10.1186/s12879-019-3766-0*
34. von Graevenitz A. The role of *Aeromonas* in diarrhea: A review. Infection 2007; 35:59–64. *https://doi.org/10.1007/s15010-007-6243-4*
35. Gracey M, Burke V, Robinson J. *Aeromonas*-associated gastroenteritis. Lancet 1982; 2:1304–1306. *https://doi.org/10.1016/s0140-6736(82)91510-0*
36. Pessoa RBG, de Oliveira WF, Correia M, *et al*. *Aeromonas* and human health disorders: Clinical approaches. Front Microbiol 2022; 13:868890. *https://doi.org/10.3389/fmicb.2022.868890*
37. Borchardt MA, Stemper ME, Standridge JH. *Aeromonas* isolates from human diarrheic stool and groundwater compared by pulsed-fieldgel electrophoresis. Emerg Infect Dis 2003; 9:224–228. *https://doi.org/10.3201/eid0902.020031*
38. Yuwono C, Wehrhahn MC, Liu F, *et al*. The isolation of *Aeromonas* species and other common enteric bacterial pathogens from patients with gastroenteritis in an Australian population. Microorganisms 2021; 9:1440. *https://doi.org/10.3390/microorganisms9071440*
39. Keskimäki M, Mattila L, Peltola H, *et al*. Prevalence of diarrheagenic Escherichia coli in finnswith or without diarrhea during a round-the-world trip. J Clin Microbiol 2000; 38:4425–4429. *https://doi.org/10.1128/JCM.38.12.4425-4429.2000*
40. Senderovich Y, Ken-Dror S, Vainblat I, *et al*. A molecular study on the prevalence and virulence potential of *Aeromonas* spp. recovered from patients suffering from diarrhea in Israel. PLoS One 2012; 7:e30070. *https://doi.org/10.1371/journal.pone.0030070*
41. Pablos M, Remacha MA, Rodríguez-CJM, *et al*. Identity, virulence genes, and clonal relatedness of *Aeromonas* isolates from patients with diarrhea and drinking water. Eur J Clin Microbiol Infect Dis 2010; 29:1163–1172. *https://doi.org/10.1007/s10096-010-0982-3*
42. García VC, García VM, Del CAG, *et al*. Acute bacterial gastroenteritis: 729 cases recruited by a primary care national network. An Pediatr (Barc) 2017; 87:128–134. *https://doi.org/10.1016/j.anpedi.2016.04.020*
43. San JVH, Pickett DA. *Aeromonas*-associated gastroenteritis in children. Pediatr Infect Dis J 1988; 7: 53–57. *https://doi.org/10.1097/00006454-198801000-00013*
44. Kaakoush NO, Castaño RN, Mitchell HM, *et al*. Global epidemiology of campylobacter infection. Clin Microbiol Rev 2015; 28: 687–720. *https://doi.org/10.1128/CMR.00006-15*
45. Valledor S, Valledor I, Gil RMC, *et al*. Comparison of several real-time PCR kits versus a culture-dependent algorithm to identify enteropathogens in stool samples. Sci Rep 2020; 10: 4301. *https://doi.org/10.1038/s41598-020-61202-z*
46. Kitagawa D, Suzuki Y, Abe N, *et al*. Comparison of MALDI-TOF mass Spectrometry and rpoB gene sequencing for the identi fication of clinical isolates of *Aeromonas* spp. Heliyon 2022; 8: e11585. *https://doi.org/10.1016/j.heliyon.2022.e11585*
47. Vila J, Marco F, Soler L, *et al*. *Aeromonas* spp. and Traveler's Diarrhea: Clinical Features and Antimicrobial Resistance. Emerging Infect Dis 2003; 9(5), 552–555
48. Ishak AA, Alhadi AM, Al-Moyed KAA, *et al*. Childhood urinary tract infection: Clinical signs, bacterial causes and antibiotic susceptibility. Universal J Pharm Res 2021; 6(4): 1-6. *https://doi.org/10.22270/ujpr.v6i4.643*.
49. Al-Haifi AY, Al Makdad ASM, Salah MK, *et al*. Epidemiology, bacterial profile, and antibiotic sensitivity of lower respiratory tract infections in Sana'a and Dhamar City, Yemen. Universal J Pharm Res 2020; 5(2):1-8, *https://doi.org/10.22270/ujpr.v5i2.386*.
50. Al-Shami HZM, Al-Haimi A, Al-Dossary OAE, *et al*. Patterns of antimicrobial resistance among major bacterial pathogens isolated from clinical samples in two tertiary hospitals in Sana'a, Yemen. Universal J Pharm Res 2021; 6(5):1-8. *https://doi.org/10.22270/ujpr.v6i5.674*
51. Lateef A, Oloke JK, Kana GE. Antibiotic Susceptibility Profile of *Aeromonas* Species Isolated from Wastewater and Clinical Samples. J Environ Health Sci Eng 2012; 9(1), 19. *https://doi.org/10.1100/2012/764563*
52. Bisi-Johnson MA, Obi CL, Hattori T. Antibiotic susceptibility patterns of *Aeromonas* species isolated from environmental and clinical sources. Afr J Microbio Res 2016; 10(47): 1992–1999.
53. Fernández-Bravo A, Figueras MJ. *Aeromonas* infections in humans antibiotic resistance and treatment options. Antibiotics 2020; 9(11): 788.
54. Al-Yosaffi EA, Al-Shamahy HA, Othman AM, *et al*. Antibiotic sensitivity of bacterial bloodstream infections in the intensive care unit patients of university hospitals in Sana'a City, Yemen. Universal J Pharm Res 2023; 8 (5): 1-8. *https://doi.org/10.22270/ujpr.v8i5.1004*