



Original Research Article

MICROBIOLOGICAL PROFILE OF ACUTE PEDIATRIC DIARRHEA AND ITS ASSOCIATION WITH DEMOGRAPHIC AND SOCIOECONOMIC FACTORS IN PAKISTAN

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Received : 05/08/2026
Received in revised form : 01/09/2026
Accepted : 13/09/2026

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DOI: 10.70034/ijmedph.2026.3.786

Source of Support: Nil,

Conflict of Interest: None declared

Int J Med Pub Health

2026; 16 (3); 5096-5102

ABSTRACT

Background: Acute diarrheal disease remains one of the leading causes of childhood morbidity and mortality in low- and middle-income countries, with bacterial enteropathogens accounting for a substantial share of cases in resource-limited settings. Despite the recognized burden of diarrheal illness in Pakistan, robust local data on the microbiological etiology of acute pediatric diarrhea remain scarce a gap that limits evidence-based empirical treatment, rational antimicrobial stewardship, and targeted public health surveillance in the province.

Materials and Methods: We conducted a cross-sectional study at the Pediatric Department of Lady Reading Hospital, Peshawar, over six months (May 2025 to November 2025). Using non-probability consecutive sampling, 292 children aged 1–15 years presenting with acute diarrhea were enrolled. Fresh stool specimens were cultured, and bacterial isolates were identified by colonial morphology, Gram staining, and biochemical testing. The frequency of bacterial diarrhea was stratified by age, sex, illness duration, parental education, household socioeconomic status, and residence, with between-group differences assessed by chi-square test (significance threshold $p \leq 0.05$).

Results: The 292 children had a mean age of 8.0 ± 5.94 years; most were aged 1–7 years (61.0%), male (56.8%), urban residents (72.9%), and from low- or middle-income households (89.0%). Bacterial pathogens were confirmed in 53 children, an overall frequency of 18.2% (95% CI: 13.8–22.6%). This frequency was strikingly uniform across subgroups: 18.0% in children aged 1–7 years versus 18.4% in those 8–15 years ($p=0.923$); 18.1% in males versus 18.3% in females ($p=0.968$); and 18.1% with illness ≤ 30 days versus 18.2% with longer duration ($p=0.992$). No significant associations were found with parental education ($p=0.981$), socioeconomic status ($p=0.902$), or urban versus rural residence ($p=0.821$).

Conclusions: Confirmed bacterial enteropathogens accounted for 18.2% of acute diarrheal episodes among children at a major tertiary referral center in Peshawar a prevalence consistent with other developing-country settings and considerably higher than reported in high-income populations. The near-identical distribution of bacterial infection across all demographic and socioeconomic subgroups suggests broad, undifferentiated endemic exposure across this catchment population rather than concentration in any particular risk group. The results of this study support the inclusion of systematic stool culture in the routine management of acute diarrhea in children to inform targeted rather than empirical antimicrobial prescribing and highlight the importance of continued investment in water, sanitation and hygiene (WASH) infrastructure and childhood immunization coverage in KPK.

INTRODUCTION

Diarrheal disease is one of the most important but preventable causes of child mortality globally.^[1] In 2019, the Global Burden of Disease Study estimated that diarrheal illness caused about 1.5 million deaths worldwide, with children in low- and middle-income countries (LMICs) accounting for a disproportionate share of these deaths nearly 480,000 children.^[1,2] Although decades of investment in oral rehydration therapy and rotavirus vaccination, diarrhea is still one of the leading causes of under-5 mortality in LMICs, highlighting the need for more equitable population-level impact of interventions.^[3]

Acute gastroenteritis sudden-onset loose or watery stools lasting under 14 days, often with vomiting, fever, and dehydration is usually self-limiting, but its consequences extend well beyond the acute episode.^[4] The consequences of acute gastroenteritis are not limited to the acute illness itself, but also include chronic environmental enteric dysfunction, which is a reduction in nutrient absorption between episodes of diarrheal illness, and is a major contributor to stunting, wasting and developmental delay, the "impoverished gut" cycle now recognized as a major driver of intergenerational poverty in high-burden settings.^[4,5]

Acute diarrhea is caused by different factors in different settings. Viral pathogens cause 70-80% of episodes in high-income countries with good sanitation and immunization coverage.^[6] Rotavirus was historically the leading cause, responsible for an estimated 37% of under-five diarrheal deaths before widespread vaccination; norovirus has since emerged as the dominant cause of medically attended gastroenteritis in vaccinated populations, alongside adenovirus, arbovirus, and sapovirus.^[6,7]

In low-resource settings, bacterial enteropathogens dominate, accounting for an estimated 50–60% of episodes driven by unsafe water and sanitation, high background pathogen carriage, and the immunological toll of undernutrition.^[8] The Global Enteric Multicenter Study (GEMS), the largest case-control study of its kind across sub-Saharan Africa and South Asia, identified *Shigella*, enterotoxigenic *E. coli* (ETEC), *Cryptosporidium*, and rotavirus as the leading contributors to attributable diarrheal burden in children under five.^[9] A molecular reanalysis of the GEMS data later showed that culture-based methods substantially underestimate bacterial co-infection, particularly for *Shigella* and ETEC. Among older children, *Shigella*, non-typhoidal *Salmonella*, and *Campylobacter jejuni* predominate, while enteropathogenic *E. coli* remains a major cause of prolonged watery diarrhea in infants, with disproportionate mortality risk among the malnourished.^[10]

Pakistan carries a substantial share of this regional burden: South and Southeast Asia together account for an estimated 150,000–200,000 diarrhea-

attributable child deaths annually, with Pakistan, Bangladesh, and India contributing the largest totals.^[11] Structural drivers here are well established food insecurity, high rates of stunting and wasting, inadequate access to safe water and sanitation, and primary care systems with limited capacity for point-of-care microbiology.^[12] These conditions sustain bacterial transmission through contaminated water and food, while widespread indiscriminate antibiotic use has progressively eroded first-line efficacy against common enteric pathogens, making empirical prescribing increasingly unreliable.^[12,13]

Khyber Pakhtunkhwa (KPK) exemplifies these challenges. The largest public tertiary center in Peshawar, Lady Reading Hospital (LRH) has an unusually diverse catchment, including urban residents, IDPs, and rural and border-adjacent communities, which is compounded by limited healthcare infrastructure and high poverty. However, published information on the microbiological etiology of childhood diarrhea in KPK is limited, with few studies having recruited non-consecutive samples, or having included only a small age range, or not having performed systematic stool culture, and so the distribution of confirmed bacterial infection by demographic and socioeconomic groups is poorly defined.^[14-16]

The study is significant because of the high burden of childhood diarrheal disease in the region, the lack of local evidence on the bacterial etiology of diarrheal disease and the increasing concern about antimicrobial resistance of enteric pathogens. Local information on the prevalence and distribution of bacterial pathogens is crucial to inform clinical management, as most children with acute diarrhea do not need antimicrobial treatment, and those with confirmed bacterial infection may benefit from targeted treatment. Moreover, knowledge of the local bacterial profile can help in provincial disease surveillance and in making evidence-based decisions on vaccination strategies, antimicrobial stewardship and investments in water, sanitation and hygiene (WASH) intervention.^[17] Therefore this study aimed to find out the prevalence of confirmed bacterial infection in children aged 1-15 years attending LRH, Peshawar with acute diarrhea and to see if there was any significant difference in the prevalence of confirmed bacterial infection by age, sex, duration of illness, parental education, socioeconomic status of the household and place of residence.

MATERIALS AND METHODS

Study design and setting

This was a cross sectional descriptive study carried out in the Pediatric Department of Lady Reading Hospital, Peshawar during a period of six months from May 2025 to November 2025. The study was conducted to find out the prevalence of bacterial infection in children with acute diarrhea.

Study population and sample size

A total of 292 children aged 1-15 years with acute diarrhea were included in the study. Both boys and girls were eligible to participate. The sample size was determined using the World Health Organization sample size calculator with an expected frequency of bacterial infection of 5%, a 95% confidence level and a margin of error of 2.5%. Non-probability consecutive sampling was used to recruit participants.

Participant recruitment and data collection

After obtaining approval from the hospital ethical and research committee, children who met the criteria were recruited once the purpose and potential benefits of the study were explained to their parents/guardians. Informed consent was obtained in writing prior to enrollment. All participants had a clinical evaluation with a relevant history and physical examination. A predesigned data-collection proforma was used to record demographic and clinical data such as age, sex, duration of diarrhea, place of residence, socioeconomic status, and parental educational level.

Stool specimen collection and microbiological investigation

Each participant had a stool sample taken in a clean, sterile container and sent to the microbiology lab for bacteriological analysis. Stool samples were enriched in alkaline peptone water and incubated at 37°C for 6–8 hours in the laboratory. The samples were then enriched and then subcultured by streaking on MacConkey agar and blood agar plates. The inoculated plates were incubated aerobically at 37°C for overnight. Bacterial growth was evaluated after incubation based on the colony morphology. Suspected isolates were further examined by Gram staining and biochemical testing. Bacterial identification was done by the combination of characteristic colonial morphology, Gram-staining characteristics and biochemical properties. The main outcome of the primary study was the presence of bacterial infection in the stool sample. Children with a bacterial pathogen identified were classified as having bacterial diarrhea, and children with no bacterial pathogen identified were classified as having no bacterial infection detected. Children with negative bacterial results were not considered to have viral diarrhea as viral pathogens were not investigated.

Statistical Analysis

The data were entered and analyzed in SPSS version 20. Continuous variables such as age and duration of diarrhea were summarized as mean and standard deviation, while categorical variables were summarized as frequencies and percentages. The frequency of bacterial diarrhea was examined across age, sex, duration of diarrhea, place of residence, socioeconomic status, and parental educational level. Associations between categorical variables were assessed using the chi-square test. A P value of ≤ 0.05 was considered statistically significant.

RESULTS

Study population and participant characteristics

A total of 292 children presenting with acute diarrhea were included in the study. The mean age of the participants was 8 ± 5.94 years. Children aged 1–7 years accounted for 178 (61.0%) participants, while 114 (39.0%) were aged 8–15 years. There was a slight male predominance, with 166 (56.8%) boys and 126 (43.2%) girls.

With regard to the duration of diarrhea, 193 (66.1%) children had diarrhea for ≤ 30 days, whereas 99 (33.9%) had a duration of >30 days. Regarding parental educational status, 114 (39.0%) parents were illiterate, 137 (46.9%) had primary to secondary education, and 41 (14.0%) had graduate or postgraduate education. Nearly half of the children belonged to middle-class families (137, 46.9%), while 123 (42.1%) were from poor socioeconomic backgrounds and 32 (11.0%) were from rich families. Most participants were from urban areas (213, 72.9%), compared with 79 (27.1%) from rural areas.

Frequency of bacterial diarrhea

Among the 292 children investigated, bacterial infection was detected in 53 (18.2%), whereas no bacterial infection was detected in the remaining 239 (81.8%). Thus, bacterial infection accounted for a substantial minority of acute diarrhea presentations in this study. The children in whom bacterial infection was not detected were not classified as having viral diarrhea, because viral pathogens were not investigated in the present study.

Association of bacterial diarrhea with demographic and clinical characteristics

The distribution of bacterial diarrhea was subsequently examined across age, sex, duration of diarrhea, parental education, socioeconomic status, and place of residence. The proportion of children with bacterial diarrhea was remarkably similar across the examined groups, and none of the evaluated characteristics showed a statistically significant association with bacterial infection.

Bacterial diarrhea was detected in 32 of 178 (18.0%) children aged 1–7 years and 21 of 114 (18.4%) children aged 8–15 years (*P* = 0.9235). Similarly, bacterial infection was identified in 30 of 166 (18.1%) boys and 23 of 126 (18.3%) girls (*P* = 0.9681). Duration of diarrhea was also not associated with bacterial infection: 35 of 193 (18.1%) children with diarrhea lasting ≤ 30 days and 18 of 99 (18.2%) children with diarrhea lasting >30 days had bacterial infection (*P* = 0.9921).

No significant association was observed with parental education. Bacterial diarrhea occurred in 21 of 114 (18.4%) children whose parents were illiterate, 25 of 137 (18.2%) among those whose parents had primary-to-secondary education, and 7 of 41 (17.1%) among those whose parents had graduate or postgraduate education (*P* = 0.9809).

Likewise, bacterial infection was detected in 22 of 123 (17.9%) children from poor socioeconomic backgrounds, 26 of 137 (19.0%) from middle-class families, and 5 of 32 (15.6%) from rich families (*P* = 0.9020). Finally, bacterial diarrhea was

identified in 15 of 79 (19.0%) children from rural areas and 38 of 213 (17.8%) from urban areas, with no significant association with residence (*P* = 0.8212). [Table 1]

Table 1: Frequency of bacterial diarrhea according to demographic and clinical characteristics. Percentages are based on the total sample of 292 children. Categorical variables were analyzed using chi-square testing, with $P \leq 0.05$ considered statistically significant

Characteristic	Bacterial diarrhea, n/N (%)	No bacterial infection detected, n/N (%)	P value
Age			0.9235
1–7 years	32/178 (18.0)	146/178 (82.0)	
8–15 years	21/114 (18.4)	93/114 (81.6)	
Sex			0.9681
Male	30/166 (18.1)	136/166 (81.9)	
Female	23/126 (18.3)	103/126 (81.7)	
Duration			0.9921
≤30 days	35/193 (18.1)	158/193 (81.9)	
>30 days	18/99 (18.2)	81/99 (81.8)	
Parental education			0.9809
Illiterate	21/114 (18.4)	93/114 (81.6)	
Primary–secondary	25/137 (18.2)	112/137 (81.8)	
Graduate–postgraduate	7/41 (17.1)	34/41 (82.9)	
Socioeconomic status			0.9020
Poor	22/123 (17.9)	101/123 (82.1)	
Middle class	26/137 (19.0)	111/137 (81.0)	
Rich	5/32 (15.6)	27/32 (84.4)	
Residence			0.8212
Rural	15/79 (19.0)	64/79 (81.0)	
Urban	38/213 (17.8)	175/213 (82.2)	

DISCUSSION

In this study, bacterial pathogens were confirmed by stool culture in 53 of 292 children (18.2%, 95% CI 13.8–22.6%) presenting with acute diarrhea to a tertiary care hospital in Peshawar. This frequency is lower than the 50–60% bacterial contribution reported in some aggregate estimates from high-burden low- and middle-income settings, but considerably higher than the figures typically reported from high-income countries, where viral pathogens account for most paediatric diarrheal illness.^[18] This discrepancy is likely attributable to a combination of diagnostic and epidemiological factors.

From a diagnostic standpoint, conventional stool culture has well-recognized limitations in sensitivity. It requires the survival of viable organisms during transport and subculture, favors rapidly growing genera, and does not detect diarrheagenic *E. coli* pathotypes that are identified routinely by molecular methods. Studies comparing culture with multiplex PCR in paediatric diarrheal stool have reported similar findings: in one study from India, *Shigella* was detected in only 2% of samples by culture compared with 16% by multiplex PCR,^[19] while a study using cycle-threshold analysis in Israel found that only approximately half of PCR-positive *Shigella*, *Salmonella*, and *Campylobacter* samples yielded growth on culture, with the discrepancy most pronounced at low bacterial loads.^[20] If a comparable pattern applies to the present cohort, the true frequency of bacterial

diarrhea in this population may be underestimated, and the reported figure of 18.2% should be interpreted as a conservative estimate. Nonetheless, culture remains the most feasible pathogen-identification method available in most public-sector laboratories in Khyber Pakhtunkhwa (KP), and it offers the additional advantage of a viable isolate for antimicrobial susceptibility testing.

Differences in study design and population selection may also contribute to the observed frequency. Unlike case-control studies such as the Global Enteric Multicenter Study, which enrolled children with moderate-to-severe diarrhea and compared them with asymptomatic community controls, the present study enrolled an unselected hospital population spanning the full spectrum of clinical severity.^[18] Inclusion of milder, potentially self-limiting and viral cases would be expected to lower the observed proportion of bacterial infection relative to studies restricted to more severe disease.

The frequency reported here is consistent with findings from an earlier study conducted in the same department approximately six years prior, which enrolled a similarly sized cohort ($n = 292$) over a comparable enrolment period and reported a bacterial diarrhea frequency of 18%, with an age and sex distribution similar to that of the present cohort.^[21] This consistency across two independent samples separated by several years suggests that the observed frequency may reflect a relatively stable local baseline rather than seasonal or sampling variation. This interpretation is further supported by regional environmental data: a study sampling

municipal drinking water, market milk, and raw produce in Peshawar over an 18-month period isolated *Shigella flexneri* from more than 6% of drinking-water samples, with contamination concentrated at sites where sewage or hospital waste intersected the water supply.^[22] A subsequent molecular analysis of clinical *S. flexneri* isolates from the same region reported extensive plasmid-mediated multidrug resistance. These findings suggest that bacterial enteropathogens are established within the local water and food supply chain in this setting, rather than representing sporadic contamination events.^[23]

No statistically significant association was observed between bacterial infection and age, sex, illness duration, parental education, socioeconomic status, or urban versus rural residence. This finding may be explained by relatively diffuse environmental exposure across the study catchment, which would be expected to limit the extent to which sociodemographic factors modulate infection risk. This interpretation is broadly consistent with provincial surveillance data describing a rise in acute diarrhea reporting across Punjab, Sindh, and KP as a widespread rather than localized phenomenon,^[14] and with the broader literature identifying unsafe drinking water, rather than household wealth or maternal literacy, as the principal driver of Pakistan's paediatric diarrheal burden.^[11] These null findings should, however, be interpreted with caution: with only 53 culture-positive children distributed across several socioeconomic and educational categories, the study had limited statistical power to detect modest differences between subgroups, and a true association of a few percentage points could plausibly have gone undetected.

These findings have practical implications for clinical management. Approximately one in five children presenting with acute diarrhea at this hospital had a bacterial cause identifiable by routine culture, and this proportion did not appear to be concentrated within any readily identifiable demographic subgroup. This suggests that stool culture may be more appropriately incorporated into the routine initial assessment of children hospitalised with diarrhea, rather than reserved for those considered at elevated risk on demographic grounds, with antimicrobial therapy adjusted once culture and susceptibility results are available. This consideration is particularly relevant in light of regional antimicrobial resistance trends: a systematic review of community-acquired enteric pathogens among children in low- and middle-income countries reported rising resistance to first-line agents among *Shigella*, *Salmonella*, *Campylobacter*, and *E. coli* isolates,^[24] and Pakistan-specific data have documented high, and in some instances rising, resistance among *Salmonella* Typhi and Paratyphi isolates, including emerging extensively drug-resistant strains. Empirical antimicrobial prescribing without culture

confirmation may therefore result in both undertreatment of children requiring targeted therapy and unnecessary antibiotic exposure among children with self-limiting, non-bacterial illness.^[25]

Two additional contextual factors, although not directly assessed in this study, warrant consideration. First, rotavirus vaccine was introduced into Pakistan's national immunization schedule in 2017, and coverage in KP has increased since; independent effectiveness studies estimate that the vaccine prevents approximately three in ten rotavirus-attributable hospitalizations.^[26] As viral pathogens were not assessed in this study, its potential influence on the relative contribution of bacterial versus viral etiology in this population could not be evaluated, and documented disparities in vaccine uptake associated with maternal literacy and distance from immunization centers suggest that coverage may not be uniform across this population.^[27] Second, water, sanitation, and hygiene (WASH) infrastructure remains the most consistently cited structural determinant of diarrheal disease burden in the literature reviewed here; although access to safely managed drinking water has expanded across South Asia in recent years, progress remains insufficient to meet universal access targets on current trajectories. In this context, stool culture and antimicrobial stewardship represent downstream clinical interventions rather than substitutes for upstream structural prevention.^[28]

Finally, these findings should be considered against the broader trajectory of child mortality, which recent global reporting indicates has slowed since 2015.^[29] The most recent United Nations inter-agency estimates identify Pakistan among the countries with the highest numbers of malnutrition-attributable child deaths, and diarrheal disease continues to be among the leading infectious causes of under-five mortality worldwide.^[11] Within this context, a culture-confirmed, KP-specific estimate of bacterial diarrheal burden provides evidence relevant to guiding diagnostic and therapeutic resource allocation within a constrained health system.

CONCLUSION

Confirmed bacterial pathogens accounted for 18.2% of acute diarrheal illness among children aged 1–15 years presenting to this tertiary hospital in Peshawar, a figure that closely matched an earlier survey from the same department and sits within the range reported from other high-burden settings. Bacterial infection was distributed evenly across age, sex, illness duration, parental education, socioeconomic status, and residence, consistent with shared, catchment-wide exposure rather than concentration in any identifiable risk group.

Read alongside regional data on environmental *Shigella* circulation and antimicrobial resistance,

these findings support two concrete actions: incorporating stool culture into the routine assessment of children hospitalized with acute diarrhea, regardless of demographic background, so that antimicrobial therapy can be targeted rather than assumed; and treating WASH investment as the primary long-term lever for reducing this burden, since no demographic subgroup in this catchment appears exempt from exposure. Responses built around universal diagnostic access and structural WASH investment are more likely to move the needle than ones built around demographic risk stratification.

Limitations

This study has several limitations. It was single-center and hospital-based, drawing on a non-probability consecutive sample, so findings reflect children reaching LRH rather than the full community burden of paediatric diarrhea across KP. Bacterial identification relied on conventional culture without molecular, viral, or parasitic testing, so the 18.2% frequency should be read as a conservative, floor-level estimate and etiology of culture-negative cases remains undetermined; isolates were also not identified to species level or tested for antimicrobial susceptibility. The six-month enrolment window did not capture a full seasonal cycle, the sample offered limited power to detect modest subgroup differences, and clinical severity, outcome data, and socioeconomic status (assessed via a non-standardized categorical scheme rather than a validated asset index) were not captured with enough granularity to support finer-grained analysis.

Future Recommendations

Building on these findings, future work should priorities multi-center, full-year surveillance across KP's urban, rural, and IDP-settlement catchments to test whether 18.2% generalizes provincially and to characterize seasonal variation, pairing conventional culture with multiplex PCR to quantify the diagnostic gap and characterize viral, parasitic, and mixed infections. Reporting species-level identification and antimicrobial susceptibility for every isolate would strengthen local AMR surveillance, while linking clinical severity and outcome data to microbiological findings, paired environmental (water and food) sampling, tracking rotavirus vaccine uptake alongside bacterial and viral diagnostics, a cost-effectiveness analysis of routine versus selective culture, and adoption of a validated asset-based socioeconomic index would together help translate these findings into actionable clinical and policy guidance.

REFERENCES

- Hartman RM, Cohen AL, Antoni S, Mwenda J, Weldegebril G, Biey J, et al. Risk factors for mortality among children younger than age 5 years with severe diarrhea in low-and middle-income countries: findings from the World Health Organization-coordinated Global Rotavirus and Pediatric Diarrhea Surveillance Networks. 2023;76(3):e1047-e53.
- Ayoade O, Yeo S, Ehiri JE. Childhood Diarrhea in a Global Context: Epidemiology, Determinants, and Evidence-Based Interventions. *Maternal and Child Health, Vol 2: Global Challenges, Programs, and Policies*: Springer; 2026. p. 15-33.
- Xie M, Song Y, Tao J, Jiang M, Liu Y, Cheong IH, et al. Global trends, age-period-cohort analysis, and future projections of diarrhea burden: Findings from the Global Burden of Disease Study 2021. 2025;7(05):295-305.
- Rahman MM, Ghoshal UC, Sultana S, Kibria MG, Sultana N, Khan ZA, et al. Long-Term Gastrointestinal Consequences are Frequent Following Sporadic Acute Infectious Diarrhea in a Tropical Country: A Prospective Cohort Study. *The American journal of gastroenterology*. 2018;113(9):1363-75.
- Cocciolillo S, Collins SM. The long-term functional consequences of acute infectious diarrhea. *Current opinion in gastroenterology*. 2016;32(1):1-6.
- Wang LP, Zhou SX, Wang X, Lu QB, Shi LS, Ren X, et al. Etiological, epidemiological, and clinical features of acute diarrhea in China. *Nature communications*. 2021;12(1):2464.
- Jain P, Jain A. Waterborne Viral Gastroenteritis: An Introduction to Common Agents. *Water and Health*. 2013:53-74.
- Ezioma DA, Omosigbo PO, Sulaiman G, Bridget OO, Eze GO, Omoruyi Ec, et al. Molecular epidemiology of bacterial enteric pathogens associated with diarrhea in children under 5 years of age in Lagos State, Nigeria. 2025;46(4):165-77.
- Siddiqui FJ, Belayneh G, Bhutta ZA. Nutrition and diarrheal disease and enteric pathogens. *Nutrition and infectious diseases: Shifting the clinical paradigm*: Springer; 2020. p. 219-41.
- Derakhshan-Sefidi M, Eidy F, Nadi-Ravandi S, Bagheri-Josheghani S, Mirfakhraei MJBg. Prevalence of common diarrheagenic enterobacteriaceae in Iran (2000–2023): a systematic review and meta-analysis. 2025;25(1):43.
- Rahmat ZS, Zubair A, Abdi I, Humayun N, Arshad F, Essar MY. The rise of diarrheal illnesses in the children of Pakistan amidst COVID-19: A narrative review. *Health science reports*. 2023;6(1):e1043.
- Patlán-Hernández AR, Stobaugh HC, Cumming O, Angioletti A, Pantchova D, Lapègue J, et al. Water, sanitation and hygiene interventions and the prevention and treatment of childhood acute malnutrition: A systematic review. *Maternal & child nutrition*. 2022;18(1):e13257.
- McClelland PH, Kenney CT, Palacardo F, Roberts NL, Luhende N, Chua J, et al. Improved water and waste management practices reduce diarrhea risk in children under age five in rural Tanzania: a community-based, cross-sectional analysis. 2022;19(7):4218.
- Ali A, Khan M, Khan TA, Ahmad S, Rahman N, Waheed A, et al. Whole genome sequencing of drug-resistant *Vibrio cholerae* serotype Ogawa from an outbreak in Khyber Pakhtunkhwa. 2025;15(1):39.
- Atif M, Ayub G, Shakoor F, Farooq M, Iqbal M, Zaman Q, et al. Evolution of waterborne diseases: A case study of Khyber Pakhtunkhwa, Pakistan. 2024;12:20503121241263032.
- Javed N, Baig MZ, Nisar N, Naz S, Bettani MA, Anjum J, et al. Epidemiological Trends and Burden of Acute Watery Diarrhea during 2022 in Khyber Pakhtunkhwa, Pakistan. 2026;65(1):18-23.
- Ali Z, Rehman AU, Rafiq MJJoB, Sciences M. Assessing Drinking Water Quality, Accessibility, and Public Perception: Evidence from Khyber Pakhtunkhwa. 2025;6(2):85-95.
- Kotloff KL, Nataro JP, Blackwelder WC, Nasrin D, Farag TH, Panchalingam S, et al. Burden and aetiology of diarrhoeal disease in infants and young children in developing countries (the Global Enteric Multicenter Study, GEMS): a prospective, case-control study. *Lancet (London, England)*. 2013;382(9888):209-22.
- Bhat A, Rao SS, Bhat S, Vidyalakshmi K, Dhanashree B. Molecular diagnosis of bacterial and viral diarrhoea using

- multiplex-PCR assays: An observational prospective study among paediatric patients from India. *Indian journal of medical microbiology*. 2023;41:64-70.
20. Karam R, Kechker P, Ken-Dror S, Peretz A, Azrad M. Diagnosing gastrointestinal infections based on cycle threshold cut-offs of PCR. *Microbiology spectrum*. 2025;13(2):e0123424.
 21. Hayat M, Hussain M, Irshad M, Adeeb H, Ullah I, Aftab MJRJoHS. FREQUENCY OF BACTERIAL AND NON-BACTERIAL ACUTE GASTROENTERITIS IN CHILDREN ADMITTED AT A TERTIARY CARE SETTING. 2022;4(2):71-6.
 22. Nisa I, Qasim M, Driessen A, Nijland J, Rafiullah, Ali A, et al. Prevalence and associated risk factors of *Shigella flexneri* isolated from drinking water and retail raw foods in Peshawar, Pakistan. *Journal of food science*. 2021;86(6):2579-89.
 23. Nisa I, Driessen A, Nijland J, Rahman H, Mattner J, Qasim M. Novel plasmids in multidrug-resistant *Shigella flexneri* serotypes from Pakistan. *Archives of microbiology*. 2023;205(5):175.
 24. Okumu NO, Muloi DM, Moodley A, Watson J, Kiarie A, Ochieng L, et al. Antimicrobial resistance in community-acquired enteric pathogens among children aged ≤ 10 -years in low-and middle-income countries: a systematic review and meta-analysis. *Frontiers in microbiology*. 2025;16:1539160.
 25. Ullah A, Shabil M, Abdulsamad SA, Jan A, Naeem AA, Ullah H, et al. Prevalence of the Antibiotic Resistance of *Salmonella typhi* and *Salmonella paratyphi* in Pakistan: A Systematic Review and Meta-analysis. *Open forum infectious diseases*. 2025;12(4):ofaf131.
 26. Hussain A. Rotavirus Vaccine Demand in Pakistan. *Iranian journal of public health*. 2016;45(12):1658-9.
 27. Huda M, Ali T, Hasnani FB, Sayani S, Zaidi S. Predictors of Uptake of Rotavirus Vaccination Amongst Disadvantaged Communities in Pakistan. *Global pediatric health*. 2024;11:2333794x241235746.
 28. Rakotomanana H, Komakech JJ, Walters CN, Stoecker BJ. The WHO and UNICEF Joint Monitoring Programme (JMP) Indicators for Water Supply, Sanitation and Hygiene and Their Association with Linear Growth in Children 6 to 23 Months in East Africa. *International journal of environmental research and public health*. 2020;17(17).
 29. Sharrow D, Hug L, You D, Alkema L, Black R, Cousens S, et al. Global, regional, and national trends in under-5 mortality between 1990 and 2019 with scenario-based projections until 2030: a systematic analysis by the UN Inter-agency Group for Child Mortality Estimation. 2022;10(2):e195-e206.