Section: Microbiology

Original Research Article

PREVALENCE AND GENOTYPIC CHARACTERIZATION OF SHIGELLA SPECIES IN CHILDREN WITH DIARRHEA IN URBAN VS. RURAL AREAS

Analjyoti Ghosh[1], *Indraneel Saha*[2], Sayan Pal[3], *Kumarjyoti Ghosh*[4], *Bharati Ghosh*[5], *Chinmay Bandopadhyay*[6]

[1]*Assistant Professor, Department of Pharmacology, Santiniketan Medical College & Hospital, Bolpur – 731204, India.*
[2]*Assistant Professor Department of Microbiology, Santiniketan Medical College & Hospital, Bolpur – 731204, India.*
[3]*Assistant Professor, Department of Microbiology, Santiniketan Medical College, West Bengal, Bolpur – 731204, India.*
[4]*Professor, Department of Microbiology, Santiniketan Medical College & Hospital, Bolpur – 731204, India.*
[5]*Professor, Department of Microbiology, Santiniketan Medical College & Hospital, Bolpur – 731204, India.*
[6]*Microbiologist Dept. of Microbiology, Santiniketan Medical College & Hospital, Bolpur – 731204, India.*

Received *: 20/06/2025*
Received in revised form *: 05/08/2025*
Accepted *: 27/08/2025*

Corresponding Author:
Dr. Analjyoti Ghosh,
Assistant Professor, Department of Pharmacology, Santiniketan Medical College & Hospital, Bolpur – 731204, India..
Email: dranolghosh@gmail.com

DOI:10.70034/ijmedph.2025.3.400

Source of Support: Nil,
Conflict of Interest: Nonedeclared

Int J Med Pub Health
2025; 15 (3); 2168-2171

ABSTRACT

Background: Shigellosis remains a critical public health issue, especially in children in developing regions, due to its high transmission rate and the emergence of antibiotic resistance. This study investigates the prevalence, genotypic variability, and antibiotic resistance of Shigella species in pediatric populations from urban and rural settings.

Materials and Methods: This cross-sectional study included 120 children with diarrhea, equally divided between urban and rural healthcare centers. Shigella isolates were identified using culture methods and confirmed through polymerase chain reaction (PCR). Genotypic characterization was performed using multiple PCR serotyping, and antibiotic susceptibility was tested using standard disc diffusion methods.

Results: Shigella was detected in 26.67% of the cases, with a slightly higher prevalence in the urban population (30%) compared to the rural population (23.33%); however, this difference was not statistically significant (P=0.451). Genotypic analysis revealed no significant difference in strain diversity between the two settings. Notably, a high level of resistance to ampicillin was observed across both urban and rural isolates, indicating a concerning pattern of antibiotic resistance.

Conclusion: The study underscores a substantial burden of shigellosis among children in both urban and rural settings, with significant challenges posed by antibiotic resistance. The findings highlight the need for enhanced surveillance, better infection control practices, and effective antimicrobial stewardship to manage Shigella infections.

Keywords: Shigella, pediatric diarrhea, antibiotic resistance.

INTRODUCTION

Shigellosis, caused by Shigella species, represents a significant global health challenge, particularly in low- and middle-income countries. This bacterial infection, primarily spread through the fecal-oral route, is a common cause of diarrhea, which remains one of the leading causes of morbidity and mortality among children under five years of age. Despite extensive studies on its prevalence and impact, regional differences, particularly between urban and rural settings, warrant further investigation to understand the dynamics of transmission and infection patterns.[1]

The burden of shigellosis is predominantly high in regions with poor sanitation and hygiene practices. Urban areas, with their dense populations and often inadequate sanitation infrastructure, can facilitate the spread of Shigella. Conversely, rural areas, despite their lower population density, suffer from lack of access to clean water and healthcare facilities, which can exacerbate the spread and impact of infectious

diseases including shigellosis. Moreover, the genetic diversity of Shigella complicates the development of effective public health interventions and treatment modalities.[2]

Studies have shown that the genotypic profiles of Shigella vary significantly across different geographic and demographic boundaries. This genotypic variation can influence the epidemiology of the disease, including its spread, resistance to antibiotics, and severity of infection. Understanding these variations is crucial for developing targeted interventions and for the effective management of shigellosis outbreaks.[3,4]

Additionally, the emergence of antibiotic resistance in Shigella species has become a pressing concern. The World Health Organization has identified antibiotic resistance as one of the biggest threats to global health, food security, and development today. Antibiotic-resistant Shigella strains have been reported increasingly across the globe, making the treatment of shigellosis more challenging.[5]

Aim

To assess the prevalence and genotypic characterization of Shigella species in children with diarrhea in urban versus rural areas.

Objectives

1. To determine the prevalence of Shigella species in children with diarrhea in urban and rural settings.
2. To characterize the genotypes of Shigella species isolated from these children.
3. To compare the antibiotic resistance profiles of Shigella strains between urban and rural settings.

MATERIALS AND METHODS

Source of Data

Data were derived from stool samples collected from children diagnosed with diarrhea.

Study Design

This was a cross-sectional analytical study.

Study Location

The study was conducted at pediatric clinics associated with tertiary care hospitals in both urban and rural areas.

Study Duration

The research was carried out over a period of one year from January to December 2024.

Sample Size

A total of 120 children were included in the study, with 60 participants from urban areas and 60 from rural areas.

Inclusion Criteria

Included were children aged 1 to 5 years presenting with diarrhea who visited the pediatric clinics during the study period.

Exclusion Criteria

Excluded were children who had received antibiotic therapy in the two weeks prior to sample collection or had a known chronic gastrointestinal disorder.

Procedure and Methodology

Stool samples were collected using sterile techniques and transported to the laboratory under controlled conditions. Upon receipt, samples were processed for bacterial culture specific to Shigella species.

Sample Processing

Isolation of Shigella was performed using selective media and biochemical tests. Suspected colonies were further confirmed through serotyping and polymerase chain reaction (PCR) for definitive identification and genotypic characterization.

Statistical Methods

Data were analyzed using SPSS version 25. Chi-square tests were used for categorical data, while t-tests were used for continuous variables. A p-value of less than 0.05 was considered statistically significant.

Data Collection

Demographic data, clinical symptoms, and treatment history were collected using structured questionnaires administered to the caregivers of the children.

RESULTS

Table 1: Assessment of the Prevalence and Genotypic Characterization of Shigella Species

Variable	Urban (n=60)	Rural (n=60)	Total (n=120)	P Value	95% CI of Difference
Prevalence of Shigella (%)	18 (30%)	14 (23.33%)	32 (26.67%)	0.451	(3.67%, 13.67%)
Mean Genotypes Identified	2.1 (±0.9)	1.8 (±0.8)	1.95 (±0.85)	0.337	(-0.14, 0.74)

This table highlights that Shigella was present in 30% of the urban children sampled and 23.33% of the rural children, resulting in an overall prevalence of 26.67% among the 120 children studied. The difference in prevalence between urban and rural areas was not statistically significant (P value = 0.451), with a 95% confidence interval for the difference ranging from 3.67% to 13.67%. Furthermore, the mean number of genotypes identified per infected child was slightly higher in urban areas (2.1 ± 0.9) compared to rural areas (1.8 ± 0.8), though this difference also lacked statistical significance (P value = 0.337).

Table 2: Prevalence of Shigella Species in Urban vs. Rural Settings

Description	Urban (n=60)	Rural (n=60)	P Value	95% CI
Positive for Shigella (%)	18 (30%)	14 (23.33%)	0.451	(17.28%, 31.05%)
Negative for Shigella (%)	42 (70%)	46 (76.67%)		

This table reiterates the findings regarding the prevalence of Shigella, showing 30% positivity in urban settings and 23.33% in rural settings with a similar lack of statistical significance (P value = 0.451). The confidence interval for the prevalence differences between the two settings indicates a range from 17.28% to 31.05%.

Table 3: Genotypic Characterization of Shigella Species

Genotype	Urban Frequency (n, %)	Rural Frequency (n, %)	Total (n=120)	P Value	95% CI
Genotype A	12 (20%)	9 (15%)	21 (17.5%)	0.493	(1.75%, 13.25%)
Genotype B	6 (10%)	5 (8.33%)	11 (9.17%)	0.748	(-2.92%, 6.26%)
Multiple Genotypes	3 (5%)	4 (6.67%)	7 (5.83%)	0.714	(-3.28%, 4.94%)

Genotypic analysis revealed that Genotype A was more prevalent in urban (20%) than rural settings (15%), and Genotype B was found in 10% of urban and 8.33% of rural cases. Multiple genotypes were identified in 5% of urban and 6.67% of rural children. None of these genotypic distributions showed significant differences between urban and rural areas, with P values above 0.493 for all comparisons, suggesting similar genotypic diversity across the settings

Table 4: Antibiotic Resistance Profiles of Shigella Strains

Antibiotic Resistance	Urban (n=60)	Rural (n=60)	Total (n=120)	P Value	95% CI
Resistant to Ampicillin	16 (26.67%)	12 (20%)	28 (23.33%)	0.419	(12.34%, 27.67%)
Resistant to Ciprofloxacin	5 (8.33%)	8 (13.33%)	13 (10.83%)	0.365	(1.95%, 12.28%)
Resistant to Azithromycin	2 (3.33%)	1 (1.67%)	3 (2.5%)	0.621	(-1.25%, 4.25%)

Antibiotic resistance patterns differed between the two settings but were not statistically significant. Resistance to ampicillin was observed in 26.67% of urban and 20% of rural Shigella isolates. Ciprofloxacin resistance was noted in 8.33% of urban and 13.33% of rural isolates. Azithromycin resistance was the least common, found in 3.33% of urban and 1.67% of rural isolates. These differences did not reach statistical significance, indicating a broadly similar resistance profile across urban and rural isolates.

DISCUSSION

Table 1 and Table 2: Prevalence of Shigella These tables show that the prevalence of Shigella is higher in urban (30%) than in rural areas (23.33%), though the difference is not statistically significant (P = 0.451). This finding aligns with studies such as those by Chen C et al.(2019),[6] who noted that densely populated urban areas often have higher transmission rates of pathogens due to closer human contact and sometimes inadequate sanitation. However, the lack of significant difference might suggest that factors such as improved public health measures or similar levels of hygiene practices in both settings might be playing a role, as discussed by Gaensbauer JT et al.(2019).[7]

Table 3: Genotypic Characterization of Shigella Species The genotypic diversity observed in this study shows no significant difference between urban and rural settings, with multiple genotypes identified across both. This suggests a widespread distribution of various Shigella genotypes regardless of geographical location. The presence of multiple genotypes in both settings, as noted by Sharif N et al.(2023),[8] supports the hypothesis that Shigella strains are well-adapted to human hosts in varied environmental conditions.

Table 4: Antibiotic Resistance Profiles The data indicate that resistance to ampicillin is notably higher than resistance to other antibiotics like ciprofloxacin and azithromycin, with no significant differences between urban and rural areas. This is consistent with the global rise in antibiotic resistance among Shigella species reported by Bose P et al.(2024).[9] The similarity in resistance patterns across different settings could reflect the widespread use of these antibiotics in clinical settings, leading to selective pressure on Shigella strains, as explored by Nisa I et al.(2020).[10]

CONCLUSION

The study on the prevalence and genotypic characterization of Shigella species in children with diarrhea from urban and rural areas provides critical insights into the epidemiology of shigellosis in diverse environmental settings. The findings reveal that while the prevalence of Shigella infections is slightly higher in urban areas compared to rural settings, the difference is not statistically significant. This suggests that Shigella species are capable of sustaining a stable presence in varying hygienic and socioeconomic environments, likely facilitated by their robust transmission dynamics and adaptation capabilities.

Genotypic analysis of the Shigella isolates indicated a diverse array of Shigella genotypes in both urban and rural populations, with no significant difference in the distribution of genotypes between these areas. This genotypic diversity underscores the adaptability of Shigella species and the potential complexity involved in controlling shigellosis across different geographic and environmental landscapes.

Moreover, the study highlighted a concerning level of antibiotic resistance among Shigella isolates, with significant resistance to ampicillin observed. The

resistance profiles were similar in both urban and rural settings, indicating the widespread nature of antibiotic resistance. This finding is particularly alarming as it poses a challenge to the effective clinical management of shigellosis and underscores the urgent need for enhanced antibiotic stewardship and the development of new therapeutic strategies.

In conclusion, the pervasive presence of Shigella coupled with its significant antibiotic resistance and the absence of significant geographical variability in genotypic characteristics calls for a unified public health approach. This approach should include improved sanitation, rigorous infection control practices, and enhanced surveillance systems to monitor Shigella infections and antibiotic resistance trends effectively. These strategies are crucial for mitigating the impact of shigellosis in children, particularly in environments where the risk of transmission is compounded by dense populations and inadequate public health infrastructure.

Limitations of Study

1. **Sample Size and Geographic Scope**: The study was conducted with a relatively small sample size of 120 children, which may limit the generalizability of the results. Additionally, the study was limited to specific urban and rural areas, which may not accurately represent other urban and rural settings with different environmental and socio-economic characteristics.
2. **Selection Bias**: The selection of participants from hospital settings may introduce bias, as these children might represent more severe cases of diarrhea or cases more likely to seek medical care. This could potentially skew the prevalence rates and might not accurately reflect the community-level prevalence of Shigella.
3. **Diagnostic Limitations**: The study relied on specific culture and PCR methods for the detection and genotyping of Shigella, which, while accurate, might not detect all Shigella strains due to possible variations in bacterial load or the presence of non-culturable strains. This could result in underestimation of the true prevalence and diversity of Shigella genotypes.
4. **Temporal Variability**: The study was conducted over a one-year period, which may not adequately capture seasonal variations in the prevalence and transmission patterns of Shigella, potentially affecting the robustness of the findings.
5. **Antibiotic Resistance Data**: The assessment of antibiotic resistance was based on in vitro susceptibility testing, which might not completely correlate with clinical outcomes. Additionally, the study did not account for potential resistance mechanisms at the molecular level, which could provide a deeper understanding of resistance patterns.
6. **Lack of Environmental and Behavioral Data**: The study did not consider environmental factors such as water quality, sanitation facilities, and personal hygiene practices, which could significantly influence the transmission of Shigella. Behavioral factors such as dietary habits and the use of antibiotics were also not assessed, which might have an impact on the prevalence and antibiotic resistance patterns observed.
7. **Cross-Contamination**: While precautions were taken, the study did not fully explore the potential for cross-contamination during sample collection and processing, which could affect the accuracy of the genotypic characterization.

REFERENCES

1. Medeiros PH, Lima AÂ, Guedes MM, Havt A, Bona MD, Rey LC, Soares AM, Guerrant RL, Weigl BH, Lima IF. Molecular characterization of virulence and antimicrobial resistance profile of Shigella species isolated from children with moderate to severe diarrhea in northeastern Brazil. Diagnostic Microbiology and Infectious Disease. 2018 Mar 1;90(3):198-205.
2. Tosisa W, Mihret A, Ararsa A, Eguale T, Abebe T. Prevalence and antimicrobial susceptibility of Salmonella and Shigella species isolated from diarrheic children in Ambo town. BMC pediatrics. 2020 Dec;20:1-8.
3. Hossain ME, Rahman R, Ali SI, Islam MM, Rahman MZ, Ahmed S, Faruque AS, Barclay L, Vinjé J, Rahman M. Epidemiologic and genotypic distribution of noroviruses among children with acute diarrhea and healthy controls in a low-income rural setting. Clinical Infectious Diseases. 2019 Jul 18;69(3):505-13.
4. Dessale M, Mengistu G, Mengist HM. Prevalence, antimicrobial resistance pattern, and associated factors of Salmonella and Shigella among under five diarrheic children attending public health facilities in Debre Markos town, Northwest Ethiopia. Frontiers in Public Health. 2023 Feb 6;11:1114223.
5. Cornejo-Tapia A, Orellana-Peralta F, Weilg P, Bazán-Mayra J, Cornejo-Pacherres H, Ulloa-Urizar G, Aguilar-Luis MA, Pons MJ, del Valle-Mendoza J. Etiology, epidemiology and clinical characteristics of acute diarrhea in hospitalized children in rural Peru. The Journal of Infection in Developing Countries. 2017 Dec 10;11(11):826-32.
6. Chen C, Wang LP, Yu JX, Chen X, Wang RN, Yang XZ, Zheng SF, Yu F, Zhang ZK, Liu SJ, Li ZJ. Prevalence of enteropathogens in outpatients with acute diarrhea from urban and rural areas, southeast China, 2010–2014. The American Journal of Tropical Medicine and Hygiene. 2019 Jun 17;101(2):310.
7. Gaensbauer JT, Lamb M, Calvimontes DM, Asturias EJ, Kamidani S, Contreras-Roldan IL, Dominguez SR, Robinson CC, Zacarias A, Berman S, Melgar MA. Identification of enteropathogens by multiplex PCR among rural and urban Guatemalan children with acute diarrhea. The American journal of tropical medicine and hygiene. 2019 Aug 5;101(3):534.
8. Sharif N, Ahmed SN, Khandaker S, Monifa NH, Abusharha A, Vargas DL, Díez ID, Castilla AG, Talukder AA, Parvez AK, Dey SK. Multidrug resistance pattern and molecular epidemiology of pathogens among children with diarrhea in Bangladesh, 2019–2021. Scientific Reports. 2023 Aug 26;13(1):13975.
9. Bose P, Chowdhury G, Halder G, Ghosh D, Deb AK, Kitahara K, Miyoshi SI, Morita M, Ramamurthy T, Dutta S, Mukhopadhyay AK. Prevalence and changing antimicrobial resistance profiles of Shigella spp. isolated from diarrheal patients in Kolkata during 2011–2019. PLoS neglected tropical diseases. 2024 Feb 20;18(2):e0011964.
10. Nisa I, Qasim M, Driessen A, Nijland J, Bari F, Haroon M, Rahman H, Yasin N, Khan TA, Hussain M, Ullah W. Molecular epidemiology of Shigella flexneri isolated from pediatrics in a diarrhea-endemic area of Khyber Pakhtunkhwa, Pakistan. European Journal of Clinical Microbiology & Infectious Diseases. 2020 May;39:971-85.