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Burden of Rotavirus (RV) Infection in Children Below Five Years of Age Having Acute Diarrhoea and Pattern of Circulating Genotypes in a Community in Indore City of Madhya Pradesh

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I N F O

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A B S T R A C T

Background: Determining the prevalence of rotavirus in a specific area can provide valuable insights regarding its seasonality, aid the healthcare system in effectively managing cases of acute diarrhoea, and contribute to the prevention of drug misuse.

Aim: To study the burden of rotavirus infection in children below five years of age having acute diarrhoea and pattern of circulating genotypes in a community in Indore city of Madhya Pradesh.

Methods: Children below five years of age with acute diarrhoea provided a total of 100 stool samples, which were then tested for the presence of rotavirus antigen using an enzyme immunoassay (EIA). After that, RT-PCR was used to genotype the EIA-positive samples' G and P types. Demographic and clinical information were recorded on a proforma.

Results: The prevalence of rotavirus infection in children below five years of age having acute diarrhoea was 17%. Nine typeable rotavirus strains out of a total of 17 were typed using RT-PCR. One strain (11.1%) was partially typed, two strains (22.2%) were not typeable, and six strains (66.7%) were fully genotyped for the G and P genotypes. The G1 genotype was found in the greatest number of strains (5, 71.4%), followed by G2 and G10 in 1 strain each (14.3% each). P8 and P4 were found in one strain each (50.0% each).

Conclusion: The majority of rotavirus strains were G1 genotyped. In order to boost the regional specificity of multivalent RV vaccines, this study emphasises the need to include new rotavirus strains.

Keywords: Rotavirus Strains, Under-Five Children, Acute Diarrhoea, Genotype

Introduction

A frequent cause of diarrhoea in children under the age of five is rotavirus (RV), which also contributes significantly to child mortality globally, particularly in low-income nations. Human rotavirus is the main reason of acute diarrhoea in children under the age of five years.[1] Infections with the rotavirus are common, with high rates of morbidity in industrialised nations and mortality in underdeveloped nations.[2] Around the world, rotavirus is responsible for 125 million cases of diarrhoea and more than 600,000 child fatalities each year. Direct contact or the faecal-oral route are the two main ways that rotaviruses are spread.[3]

The correct laboratory support can help children under the age of five who are particularly susceptible to severe diarrhoeal disease.[4] Also, identifying the enteric bacteria that are crucial in the development of paediatric diarrhoea's causes will help provide a precise and site-specific assessment of disease burden.[5] Unusual rotavirus strains that emerge have a direct impact on vaccine effectiveness and place a heavy cost burden on underdeveloped nations. Therefore, for successful vaccination, understanding the genetic diversity of this virus is essential.

Genotyping is crucial for evaluating rotavirus epidemiology, vaccine efficacy, and the effects of vaccine introduction when it does take place. Finding out how common rotavirus is in a certain nation can assist in determining seasonality, help medical professionals in the management of acute diarrhoea, and in the prevention of the misuse of drugs.[6] This study was conducted to analyse the burden of rotavirus (RV) infection among children aged less than five years having acute diarrhoea and the pattern of circulating genotypes in a community in the Indore city of Madhya Pradesh.

Materials and Methods

This one-year descriptive research was carried out among 100 study subjects in the Microbiology Department of the Index Medical College in Indore, Madhya Pradesh from August 2021 to July 2022. The study population consisted of children under the age of five years who had acute diarrhoea. One hundred faecal samples were collected from the study subjects with acute diarrhoea (diarrhoea, vomiting, and abdominal pain for less than 2 weeks) after being diagnosed with acute gastroenteritis.

Inclusion Criteria

1. Eligible study subjects who presented to the study site for the management of acute diarrhoea and received fluid therapy for at least 6 hours
2. Age less than 5 years
3. Able to comply with directions given for the collection of stool sample

Exclusion Criteria

1. Not able to provide informed consent/ assent
2. Cases with a history of chronic diarrhoea/ bloody diarrhoea/ dysentery

The parent or guardian was asked for pertinent demographic information as well as clinical history, such as loose stools, severity of diarrhoea (mucus, watery), vomiting, history of fever, and the length of presenting complaints. A history of breast milk and milk formula was also recorded. The grade of malnutrition was assessed by anthropometry. Children were examined for signs of dehydration and were categorised as having severe, some, or no dehydration.

In order to collect stool samples for laboratory examination, approximately 10 gm or ml of stool samples were acquired, placed in a sterile container, and transported to a virology laboratory while being kept at a temperature of -20 °C. Rotavirus antigen was found in the stool samples using an enzyme immunoassay (EIA). Reverse transcriptase-polymerase chain reaction semi-nested multiplex was used to genotype the G and P types of the EIA-positive samples (RT-PCR).

VP6-specific monoclonal antibodies in the antigen capture enzyme-linked immunosorbent assay were used to test for rotavirus antigen in the sample. RT-PCR was used to identify the rotavirus strains in the samples that tested positive for the disease.

The Institutional Ethics Committee gave its clearance before the study could be conducted. A Microsoft Excel spreadsheet was used to record the data which was analysed using statistical software. The data were expressed using descriptive statistics and were presented as frequencies and percentages.

Results

Data from 100 study subjects were analysed and have been presented here.

Rotavirus Antigen Detection & Prevalence of Rotavirus Infection of a total of 100 stool samples, the presence of rotavirus was confirmed in 17 (17%) samples. Thus the prevalence of rotavirus infection in children below five years of age having acute diarrhoea was 17%.

Genomic assessment of the rotavirus strains in circulation of a total of 17 rotavirus-confirmed samples, nine (52.9%) were typeable and the remaining eight (47.1%) were non-typeable (Table 1).

Table 1.Pattern of Rotavirus (Typed and Untyped) Strains among Study Subjects

Nature of Rotavirus Strain	Number of Strains n(%)
Typeable	9 (52.9)
Non-typeable	8 (47.1)
Total	17 (100.0)

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Nine typeable rotavirus strains out of a total of 17 were typed using RT-PCR. Six strains (66.7%) out of nine were fully typed for the G and P genotypes, one (11.1%) was partially typed, and the remaining two (22.2%) were not typeable (Table 2).

Table 2.Group A Rotavirus Types Detected by RT-PCR among Study Subjects (N = 9)

Variable	Number of Strains	Percentage
Strains typed by RT-PCR	9	100.0
Strains fully typed	6	66.7
Strains partially typed	1	11.1
Strains non-typeable	2	22.2

A total of 7 (77.3%) of G genotype and 2 (22.2%) of P genotype were found. The genotypes of two (25.0%) G genotype and six (75.0%) P genotype could not be identified (Table 3).

Table 3.Distribution of Typed and Untyped Rotavirus Strains as per G and P Types Among Study Subjects

Pattern of Rotavirus Strains	G Type n (%)	P Type n (%)	Total N (%)
Typeable	7 (77.3)	2 (22.2)	9 (100.0)
Non-typeable	2 (25.0)	6 (75.0)	8 (100.0)

The G1 genotype was identified in maximum i.e. 5 (71.4%) rotavirus strains, followed by G2 and G10 in 1 strain each (14.3% each). P8 and P4 were identified in 1 strain each (50.0% each) (Table 4).

Table 4.Patterns of Typeable G and P Genotype of Group A Rotavirus Detected among Study Subjects

Typeable Genotype		Number of Strains	Percentage
G type (n = 7)	G1	5	71.4
	G2	1	14.3
	G10	1	14.3
P type (n = 2)	P8	1	50.0
	P4	1	50.0

Discussion

Even though G1P8 is the most prevalent circulating rotavirus genotype globally, there are numerous intra-genotyping lineages and their sub-lineages that show genetic variation within G1P8 rotavirus strains.[7] In general, point mutations and gene rearrangements are two methods that contribute to the diversity of rotaviruses. Rotavirus vaccination is essential because the gastroenteritis it causes poses a threat to the healthcare system and places a heavy financial load on underdeveloped nations.

The rotavirus, which is a member of the Reoviridae family, is categorised into seven groups from A to G and is the most prevalent cause of gastroenteritis in children under the age of five years.[8]

Based on the group-specific antigens of the two main viral proteins, VP4 (P type) and VP7 (G type), there are currently at least 32 G types and 47 P types, and it is these types' combinations that infect humans. The most prevalent G types, G1–G4, G9 and G12, and the most prevalent P types, P[4], P[6], and P[8], combine to form the most widely circulating RV strains worldwide. The introduction of novel strains of the G and P types in India, Bangladesh, and the USA demonstrated the high antigenic and genomic diversity of the rotavirus, which led to the creation of new re-assortment or mutation in the RV genome.[9]

In combination with P[4], P[6], and P[8], the newly emerging strain known as G9 has exponentially expanded in prevalence globally. This has a large demographic impact and has become a significant strain in many nations. While G9 and G12 are re-emerging strains in the Indian subcontinent, G1 to G4 are the most common circulating strains there.[10]

According to the findings of the current study, the G1 genotype was identified in maximum strains i.e. 5 (71.4%) rotavirus strains, followed by G2 and G10 in 1 strain each (14.3% each). P8 and P4 were identified in 1 strain each (50.0% each). In contrast, the investigation of Mathew et al. found G1P8 (49.7%) to be the most frequently found strain, followed by G9P8 (26.4%), G2P4 (5.5%), G9P4 (2.6%), and G12P6 (1.3%).[11] An investigation by Forster et al. revealed G1P8 (40.3%), G9P8 (31.2%), G4P8 (13.5%), and G3P8 (7.1%) to be the most prevalent strains.[12]

A different investigation discovered an uncommon developing strain of G11P25.[13] In a different investigation, the genes G9P8, G12P6, and G12P8 from Pune were extracted.[14] According to the study, G2P4 predominated over G1P8 in 2007, and both G12P6 and G12P8 only appeared during that time.[15] The genetic variety of rotavirus is highlighted by the distinction between the detected strains in our study and those from previous studies.

Conclusion

The prevalence of rotavirus infection among under-five children with acute diarrhoea was 17% in the Indore region of Madhya Pradesh. The G1 genotype was identified in maximum strains of rotavirus. This study emphasised the significance of adding novel rotavirus strains in multivalent RV vaccines in the future to increase the vaccines' geographical specificity.

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