NOTES

Human Parechovirus Infection in Children Hospitalized with Acute Gastroenteritis in Sri Lanka

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Of 362 fecal specimens collected from infants and children hospitalized with acute gastroenteritis in Sri Lanka from September 2005 to August 2006, 30 (8.3%) were positive for human parechovirus (HPeV). Six different HPeV genotypes, including HPeV1, -3, -4, -5, -10, and -11, were identified, of these, HPeV11 was reported for the first time.

Human parechoviruses (HPeVs) are classified in the Parechovirus genus of the large family Picornaviridae, which is a highly diverse family of important pathogens of humans and animals (19). The previous findings reveal the genetic variability of HPeVs, and the number of newly identified HPeV genotypes has been on the increase. Based on VP1 sequence comparisons, the HPeVs have been divided into 14 genotypes (HPeV1 to -14) (http://www.picornaviridae.com/parechovirus/hpev/hpev.htm). Of these, 10 HPeV genotypes (HPeV1 to -8, -10, and -14) have been published to date (1, 3–8, 10–14, 20).

Little is known about the spectrum of viral agents causing acute gastroenteritis in Sri Lanka, except for recent studies mainly focused on rotavirus infection among infants and children less than 5 years old (2, 15). The present study aimed to screen stool samples collected from Sri Lankan children hospitalized with acute gastroenteritis due to infection with HPeV, one of the less-explored viral pathogens that has been reported to be associated with diarrhea recently, and to characterize the molecular properties of the HPeV strains detected.

Three hundred sixty-two fecal specimens collected from infants and children hospitalized with acute gastroenteritis in Kandy, Sri Lanka, from September 2005 to August 2006 were screened for HPeV. First, the viral genome was extracted from 140 μl of a 10% fecal suspension by using the QIAamp viral RNA Minikit (Qiagen GmbH, Hilden, Germany) according to the manufacturer’s instructions. Reverse transcription (RT)-PCR and sequence analysis were then performed as described in our earlier report (18). All fecal samples which were positive for HPeV were tested further for common viral pathogens that cause diarrhea, including rotavirus, adenovirus, norovirus, sapovirus, and astrovirus, by RT-PCR (22, 23) to see if there were coinfections with HPeV and these viruses.

Of the 362 samples tested, 30 were positive for HPeV and the HPeV detection rate was 8.3%. HPeV was detected nearly year round but not in May, with the peak incidence in October and November (data not shown). Among the 30 positive samples, 20 were coinfected with other viruses, such as rotavirus (14 samples, 46.7%), adenovirus (3 samples, 10%), norovirus GII (2 samples, 6.7%), and norovirus GII and adenovirus (1 sample, 3.3%), and 10 (33.3%) were infected with HPeV alone.

For genotyping, the VP1 region of 27 of 30 HPeV-positive samples was successfully amplified and sequenced. Phylogenetic analysis of the VP1 segments of reference HPeV strains and the strains studied showed that the strains studied could be identified as HPeV1 (11 strains), HPeV3 (1 strain), HPeV4 (5 strains), HPeV5 (3 strains), or HPeV10 (5 strains). Notably, the two remaining strains (LK-73 and LK-223) showed VP1 sequences that clustered together with none of the 10 known HPeV genotypes available in the GenBank databases was then performed. The results showed that the highest mean nucleotide and amino acid similarities with these two strains and global reference strains of the 10 known genotypes were 54.8 and 68.1% (Table 1). Therefore, these strains were expected to be classified into a new or previously unpublished HPeV genotype (HPeV9 and -11 to -13) on the basis of previous proposed criteria for the assignment of HPeV genotypes (16).

The VP1 sequences of the two strains studied were submitted to the International Committee on Taxonomy of Viruses.

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Picornavirus Study Group in order to identify their genotype (http://www.picornastudygroup.com/types/index.html). These two strains received the designation HPeV11, with nucleotide and amino acid sequence identities to the prototype HPeV11 strain of 90.5 and 99.1% (strain LK-73) and 90 and 98.6% (strain LK-223) (unpublished data).

The medical records of the 10 patients with samples positive for HPeV alone were reviewed. All 10 patients were children 2 to 26 months old. Of these, five patients (50%) were less than 12 months of age. Besides diarrhea, fever and vomiting were found in 30 and 40% of the patients, respectively. Respiratory tract symptoms such as wheezing, coughing, and coryza were present in 30% of the patients. According to the WHO guidelines for assessing dehydration, the majority of the patients (9 [90%] out of 10) suffered from dehydration and 1 of these patients experienced severe dehydration (21). Ten episodes of diarrhea per day along with vomiting were noted in both cases of HPeV11 infection.

This study is the first to evaluate HPeV infection among hospitalized infants and children with acute gastroenteritis in Sri Lanka. The percentage of HPeV-positive specimens (8.3%) was similar to that found in other studies of HPeV infection (4, 5). In addition, coinfections with HPeV and various types of common diarrheal viruses, such as rotavirus, norovirus, and adenovirus, were noted for the first time. The rate of coinfection with HPeV and these diarrheal viruses accounted for as many as 66.7% (20/30) of the HPeV-positive cases.

In this study, six different HPeV genotypes, HPeV1, -3, -4, -5, -10, and -11, were present among Sri Lankan infants and children with acute gastroenteritis. Obviously, the circulation of various HPeV genotypes was noted among Sri Lankan infants and children. Regarding HPeV1 infection, the finding was in good agreement with previous studies which reported that HPeV1 was predominant over other HPeVs found in patients with acute gastroenteritis (4, 5, 7, 11, 17, 18).

The alignment of deduced amino acid sequences of the strains studied and global HPeV reference strains of HPeV1 to -8, -10, and -14 revealed that the arginine-glycine-aspartic acid (RGD) motif, which is considered to be critical for HPeV1 entry (9), was not present in the two HPeV11 strains studied (data not shown). The lack of the RGD motif in HPeV11 may mean that HPeV11 has an RGD-independent entry pathway.

In conclusion, this is the first report of the circulation of HPeV in infants and children with acute gastroenteritis in Sri Lanka.
Lanka. In addition, this is the first report of HPeV11 infection in patients with acute gastroenteritis. With the identification of six different genotypes of HPeV in the samples tested, a diversity of Sri Lankan HPeVs was found. Taken together with the findings from previous studies, it is suggested that HPeV should be included in the spectrum of viruses which are routinely screened for among infants and children with acute gastroenteritis.

**Nucleotide sequence accession numbers.** The nucleotide sequences of the Sri Lankan HPeV strains studied here have been deposited in GenBank under accession numbers HQ163869 to HQ163881 and HQ163883 to HQ163894.

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**REFERENCES**


