Acute gastroenteritis has been demonstrated to be a major cause of morbidity and mortality of children in both developed and developing countries (12, 13). It has been well established that virtually every child has become infected with a rotavirus at least once by 3 years of age (15, 17). The rotaviruses, which comprise a genus in the family Reoviridae, are spherical in appearance and measure about 70 nm in diameter. Rotaviruses contain 11 segments of double-stranded RNA. Rotaviruses are classified into seven groups (A to G) on the basis of their distinct antigenic and genetic properties. Human infection has been reported with group A, B, and C rotaviruses (4). Of these, group A rotavirus is the most important, being a significant cause of severe gastroenteritis in children worldwide (13, 15). The two outer capsid proteins, VP7 and VP4, allow the classification of rotaviruses into G and P genotypes, respectively. In rotavirus, at least 16 G and 27 P genotypes have been recognized (4, 7, 8). Of these, five rotavirus G-P combinations, G1P[8], G2P[4], G3P[8], G4P[8], and G9P[8], are the most common globally and are therefore the targets for current vaccine development strategies (16).

Recently Duan et al. identified a rotavirus strain, LL36755, in the fecal specimen collected from a female patient with acute gastroenteritis in China in 2003 by reverse transcription-PCR (3). By BLAST analysis, strain LL36755 shared high identities, from 92% to 95%, in the amino acid sequences of VP7 and VP4 to gastroenteritis in China in 2003 by reverse transcription-PCR (3). The targets for current vaccine development strategies (16).

Recent research has indicated that strain LL36755 was not a novel strain and was therefore the target for current vaccine development strategies (16).

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Author’s Reply

I thank Phan et al. for pointing out the previous description of a G5P[6] rotavirus in a single case of reinfection among children participating in a trial with rhesus-human reassortant tetravalent vaccine in Belem, Brazil, from 1990 to 1992, in a report published in 2002 (2). I sincerely apologize for the inadvertent omission of this Brazilian study in our case report. We had not read this paper at the time of submission of our manuscript due to limited circulation of the journal in China. Unfortunately, we had no access to either an electronic version or a print version of the full paper, while the description of the G5P[6] strain in the abstract was ambiguous.

Upon careful review of the Brazilian study, we found that the reported detection of the G5P[6] strain was based on PCR and hybridization. No nucleotide sequence information on that G5P[6] strain was determined in the study or deposited in the GenBank database. Thus, in our view, the data presented in the Brazilian study were insufficient in demonstrating the existence of a novel G5P[6] rotavirus at the nucleotide sequence level.

In this connection, our case report represents the first detection of a human G5 rotavirus in Asia and the first verification of the unusual combination of G5 and P[6] genotypes in humans (1). The nucleotide sequence information reported in our work provides a very critical piece of data in genotype analysis of this rotavirus and in the study of its origin. In this sense, our work does verify at the nucleotide sequence level that this is indeed a novel human rotavirus of the G5P[6] genotype.

I agree with Phan et al. that the striking sequence homology between the LL36755 strain and porcine rotaviruses is not surprising. However, our sequence data do implicate that interspecies transmission has occurred. Consistent with the importance of interspecies transmission, our continuing study has confirmed multiple sporadic cases of human infection with G5P[6] rotavirus in the local area.

REFERENCES


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