

Review

Novel human astroviruses (HAstVs) identified recently

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Received 26 February, 2014; Accepted 27 June, 2014

Human astrovirus (HAstV) plays an important role in human viral gastroenteritis, especially in young children and the elderly. In recent years, some novel astrovirus strains different from HAstV were reported previously and new subtypes or lineages of HAstV were found. These new strains might be responsible for the acute gastroenteritis in hospital or community, thus should be paid more attention in HAstV surveillance. This study reviewed the novel HAstVs identified recently.

Key words: Human astrovirus (HAstV), diarrhea, genotype, lineage.

INTRODUCTION

Human astrovirus (HAstVs), first detected in 1975 by electron microscopy (Madeley and Cosgrove, 1975; Guix et al., 2002), constituted the only *genus* in the family *Astroviridae* (Oh and Schreier, 2001). Its importance was determined as the second most common cause of viral gastroenteritis in young children (Ulloa et al., 2005). The complete genome of HAstV contains three open reading frames (ORFs): ORF1a, ORF1b, ORF2, which encoded the viral non-structural protein, the viral RNA-dependent RNA polymerase, and the capsid protein respectively (Moser et al., 2007). Because the structural protein encoded by ORF2 was associated with the genome packaging and virus particle release (van Hemert et al., 2007), ORF2 was thought to be most important region, and the type-specific reverse transcription-polymerase chain reaction (RT-PCR) and sequence analysis were performed mostly in the ORF2 region (Jakab et al., 2003; Liu et al., 2007, 2008; Wang et al., 2011). Based on the sequence analysis of ORF2, HAstV can be divided into eight genotypes (Oh and Schreier, 2001), and the genotype classification is in agreement with serotypes

(Noel et al., 1995). Recently, some novel HAstV strains different from known eight genotypes/serotypes (such as AstV-MLB and HMOAstV/AstV-VA) and subtypes/lineages belong the eight genotypes/serotypes were reported.

AstV-MLB and HMOAstV/AstV-VA

AstV-MLB1 was first reported in 2008 when an epidemiologic study was conducted in North America (Finkbeiner et al., 2008, 2009a, 2009b), and AstV-MLB2 was identified from pediatric patients with diarrhea in two continents (Finkbeiner et al., 2009). Based on the complete genome sequence of AstV-MLB1, it showed high diversity from all previously described animal and human astroviruses (Finkbeiner et al., 2008). However, both AstV-MLB1 and AstV-MLB2 was thought to be globally widespread (Finkbeiner et al., 2009c; Banyai et al., 2010) and may not cause diarrhea (Holtz et al., 2011). The clades of these new distinct strains might be deduced by the selective pressure many years ago.

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HMOAstV/AstV-VA was another novel astrovirus species identified from human stool (Kapoor et al., 2009; Burbelo et al., 2011). HMOAstV consisted of three subgroups (Burbelo et al., 2011), HMOAstV-A, HMOAstV-B, and HMOAstV-C, while HMOAstV-C was also named AstV-VA1. Another two novel astroviruses named AstV-VA2/3 were identified, which showed high homology to AstV-VA1 (Finkbeiner et al., 2009c). Both AstV-MLB and HMOAstV/AstV-VA were most closely related to ovine and mink astroviruses (Finkbeiner et al., 2009a; Kapoor et al., 2009), Xiao et al. (2011) also found AstV-VA1/2/3 were detected from bat species. Because of their closest phylogenetic relatives in animals, AstV-MLB and HMOAstV/AstV-VA may suggest the possibility of cross-species transmissions (Kapoor et al., 2009). Interestingly, further studies of human humoral responses showed the novel astrovirus HMOAstV-C was a highly prevalent human infectious agent (Burbelo et al., 2011).

HAsV SUBTYPES/LINEAGES

As suggested by Jakab et al. (2003) and Walter et al. (2001), a strain with an identity of less than 95% and a distance of >0.05 can be considered as a new subtype. Thus, based on the sequence analysis of the complete ORF2 region, a new HAsV-3 subtype was identified from an infant with diarrhea in China (Liu et al., 2008). However, the identification of a new HAsV subtype would be reliable only when the sequence analysis was performed on a long genome, because the evolutionary relationships among HAsV genotypes based on a long genome was found to be different from the results from analyses of short genetic regions (Lukashov and Goudsmit, 2002; Liu et al., 2008).

Nowadays, lineage is more popularly used for the genetic diversity analysis within the HAsV genotypes. A new lineage can be defined when a strain has the sequence diversity of at least 7% (Medina et al., 2000; Guix et al., 2002; Gabbay et al., 2007). Thus, based on the 348-bp sequence analysis in HAsV ORF2, there were six lineages for HAsV-1 (Gabbay et al., 2007; Wang et al., 2011), four lineages for HAsV-2 (De Grazia et al., 2011; Malasao et al., 2012), and two lineages for HAsV-4 (Gabbay et al., 2007), respectively. Importantly, some lineages were responsible for the outbreak of HAsV infection among the children (Li et al., 2010). Although, there were no new lineages reported for other HAsV genotypes, more and more lineages would be found, as well as the recent-reported lineages of HAsV-1 (Gabbay et al., 2007) and HAsV-2 (De Grazia et al., 2011). Interestingly, lineages can be further divided into numerous groups (Gabbay et al., 2007; Wang et al., 2011) and the emergence of new groups may be related to selection and spread of specific HAsV variants for the several years interval (Wang et al., 2011).

Complete genomic sequence analysis indicated that HAsV has high evolutionary rate of 3.7×10^{-3} nucleotide

substitutions per site per year, and 2.8×10^{-3} nucleotide substitutions per site per year for the synonymous changes (Babkin et al., 2012), which is similar to those of other RNA viruses, but significantly higher than that of rotavirus (Yang et al., 2004), a leading cause of viral gastroenteritis in humans. Thus, based on high genetic evolutionary and cross-species recombinant, more and more novel HAsV strains will be found in the future, which may be responsible for the outbreaks of acute gastroenteritis and become the dominant epidemic strains.

Conflict of Interests

The author has not declared any conflict of interest.

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