

TITLE: VIRAL GASTROENTERITIS IN TOCANTINS, BRAZIL: CHARACTERIZING THE DIVERSITY OF CLASSIC HUMAN ASTROVIRUS FROM 2010 TO 2016

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ABSTRACT:

Classical human astroviruses (HAstVs) are recognized as a common cause of acute gastroenteritis in children worldwide. Classical HAstV strains have been investigated in Brazil since the mid-90's; however, molecular investigation of classic HAstV strains had never been conducted in the state of Tocantins, a north-central state. The aim of the present study was to monitor the genotypic diversity of classic HAstV strains circulating in Tocantins during a 6-year period, 2010-2016. A total of 232 stool samples collected from children under 5 years of age experiencing gastroenteritis symptoms were screened by next generation sequencing (NGS) and conventional RT-PCR targeting ORF2 region. Phylogenetic analysis was performed for comparison with other previously reported strains, and for determination of HAstV lineages. HAstV infection was detected in 6.9% of samples (16/232). The mean and median ages of HAstV-positive patients were 1.5 years (2 days to 4 years) and 1 year, respectively. Seven specimens (43.7%;7/16) were positive by NGS and RT-PCR. NGS revealed six additional positive samples (37.5%;6/16), while RT-PCR recognized three (18.8%;3/16). A total of 13 full-genome HAstV sequences could be obtained from NGS positive samples, and partial ORF2 HAstV sequences were obtained from the three RT-PCR positive specimens. The Brazilian HAstV belonging to lineages HAstV-1a (9/16), HAstV-4c (3/16) and HAstV-5c (3/16) and displayed close genetic relation with strains detected worldwide. HAstV-5 is rare in Brazil, and this is the first report of the HAstV-5 genotype in more than 15 years of acute gastroenteritis virus surveillance in the country. Knowledge of whole genome genetic characteristics of HAstV strains in Brazil is limited. The 13 nearly full length HAstV genome sequences reported here, expanded the scanty HAstV whole-genome sequences availability from Brazil and described for the first time the complete sequence of Brazilian HAstV-1 strains. The data generated in the present investigation contributes to the growing database of the molecular diversity of HAstV circulating in Brazil, especially in rarely surveyed low-income areas in north-central region. Conventional RT-PCR surveillance coupled with NGS could be a powerful tool to study the molecular epidemiology of enteric viruses.

Keywords: Complete genome sequencing; Gastroenteritis; classic human astrovirus; Genotyping; surveillance

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