DETECTION OF ROTAVIRUS G6 FROM CHILDREN HOSPITALIZED WITH ACUTE GASTROENTERITIS IN THE AMAZON REGION FROM BRAZIL

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Acute gastroenteritis (AG) accounted for 525,000 deaths of children under 5 years old in worldwide and it may be caused by Rotavirus A (RVA), which has importance in public health. Rotavirus are classified into 41 G (VP7) and 57 P (VP4) genotypes based on binary classification. Due to segmented genome of RVA allow the emergence of new genotypes through the human-animal genetic rearrangement. The unusual G6 genotype with bovine origin has been detected in Brazil, studies have reported infections in children, demonstrating the strong zoonotic potential. This study aims to detect the RVA G6 and establish the phylogenetic relationships of the VP7 and VP4 genes. Nine fecal specimens from children hospitalized with AG in 2021 were collected. Subsequently, the viral genome was subjected to polymerase chain reaction preceded by reverse transcription (RT-PCR) for target genes and conducted Sanger sequencing. Phylogenetic analysis was performed by maximum-likelihood method. VP7 gene of nine strains clustered in lineage I of G6 genotype together with Brazilians strains circulating in 2019 (bootstrap value ranging of 76.1 to 90.3%). Eight samples were grouped in lineage III of P[8] genotype, three strains clustered with G3P[8] Brazilians strains detected in 2015-2016 (bootstrap value of 85.4%) and five samples clustered with G3P[8] strain that circulated during 2013-2014 worldwide. One strain classified by P[9] type was clustered with a Italy strain (100%). No evidence of zoonotic transmission was observed in VP7 and VP4 genes. Our observations provide important insights into the diversity of RVA G6 circulating in Brazil, and demonstrated the importance of continuous epidemiological surveillance of RVA cases.

Keywords: Group A rotavirus; Human G6 strain rotavirus; Acute gastroenteritis.

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