IVD_22 - Molecular epidemiology of human adenoviruses in children living in the Northwest Amazon region hospitalized with acute gastroenteritis

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Introduction: Adenoviruses are among the primary viral agents responsible for acute gastroenteritis in humans, peaking in children under 5 years old. Gastrointestinal infections are often attributed to subgroups *A*, *D*, and *F*, with serotypes *40* and *41* of subgroup *F*, and serotype *31* of subgroup *A*, primarily associated with acute gastroenteritis (AGE).

Objectives: Due to the scarcity of studies addressing the detection of circulating strains of human adenovirus (HAdV) in children from the Amazon region, this study aimed to determine the molecular prevalence and genotypic distribution of HAdV among children up to five years old with AGE living in the Amazon region.

Methodology: Previously, an epidemiological investigation study in the Amazon region was conducted to identify viral etiological agents causing AGE in humans and their association with host HBGA susceptibility in 734 children ≤ 5 years over one year (October 2016 to October 2017). In this study, all HAdV-positive fecal samples by real-time qPCR (n = 126; 71 AGE/55 control/non-AGE) showing crossing of the threshold line in both replicates up to a Ct value of 35 and displaying a characteristic sigmoid curve were used. Positive samples were PCR amplified and genotyped for HAdV *hexon*, *polymerase*, and *penton* genes through Sanger sequencing.

Results: Considering the three genes studied, genotype *F41* was the most prevalent, accounting for 17.36% (29/167) of cases. *F41* had a frequency of 17.85% (15/84) for the *hexon* gene, with 7 AGE (n=50) and 8 non- AGE (n=34) cases, followed by genotypes *C2* (12/84) and *B3* (8/84); for the *polymerase* gene, *F41* had a frequency of 15.55% (7/45), with 3 AGE (n=23) and 4 non-AGE (n=22) cases, followed by genotypes *F40* (6/45), *C2*, *B7*, and *A31* (5/45 each). In the penton gene, *F41* had a frequency of 18.42% (7/38), with 2 AGE (n=18) and 5 non-AGE (n=20) cases, followed by genotypes *B7* (6/38); *A31* (5/38), and *F40* (4/38). Additionally, various very rare genotypes such as *C57* and *D60* were identified in this study.

Conclusion: This study provided crucial information regarding the molecular and clinical epidemiological surveillance of HAdV in children from the Amazon region in the years 2016 and 2017.

Keywords: Human adenoviruses; Northwest Amazon region; Acute gastroenteritis