ORT_07 - FUT2 gene profile of children with acute gastroenteritis, HBGA non-secretors living in the Northwest Amazon region, and association with rotavirus A and norovirus infection

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Introduction: In the infectious process, viruses take advantage of the host cellular receptors to invade human cells. Group A rotaviruses (RVA) and noroviruses, the main causes of acute gastroenteritis (AGE) of viral etiology, use the sugars that make up the histo-blood group antigens (HBGA) as receptors in this event. AGE is one of the main causes of morbidity and mortality of infectious origin and the second leading cause of mortality in children under five years of age. The genes FUT1, FUT2 and FUT3, which synthesize the enzymes of the metabolic pathway of such sugars/viral receptors, are the main ones involved in this process. The different HBGA profiles distributed differently among human populations reveal a susceptibility factor to RVA and norovirus infections.

Objectives: The objective of this study was to use the pyrosequencing technique to identify single nucleotide polymorphisms (SNP) in the FUT2 gene (385A>T and 428G>A) that confer HBGA non-secretory status and are related to the host susceptibility to infections by RVA and norovirus.

Methodology: Using Sanger sequencing, we detected in children treated at the Hospital da Criança de Santo Antônio in Roraima state, with AGE, mutations in the FUT2 gene that had never been previously described, population markers that may be related to susceptibility to AGE in populations with ancestry from people originally from the Amazon.

Results: Our results showed that the rs1047781 (385A>T) mutation was not detected in any of the previously phenotyped samples with a non-secretory profile analyzed (n = 49). On the other hand, none of the samples from children with a non-secretory profile presented the rs601338 (428G>A) mutation in homozygosity. The rs281377 mutation (357C>T) was predominant in children previously phenotyped with a non-secretory profile when the FUT2 gene sequences, analyzed by pyrosequencing, were sequenced using the Sanger method. Statistical association between positive RVA/norovirus samples, RVA vaccine profile and SNPs in the FUT2 gene was performed.

Conclusion: Our results reinforce the current knowledge that secretors are more susceptible to infection by both rotavirus and norovirus than non-secretors and the combination of SNPs, beyond the secretor status, may reflect the highly in amazonic population.

Keywords: Host susceptibility; FUT2 gene; Rotavirus A; Norovirus infection; HBGA