Acute gastroenteritis (AG) affects several individuals and rotavirus (RV) still remains a very common cause of severe diarrhea in children under five years old. The RV has dsRNA, divided into eleven segments that encode six structural proteins (VP1-VP4, VP6 and VP7) and six non-structural proteins (NSP1-NSP6). The RV has nine species (RVA-RVI) and in RVA was frequently used the binary combination VP7 and VP4 genes that designate the respective G and P genotypes. In 2008, there was a proposed classification system that assigns a specific genotype for each of 11 genes, with genogroup constellations 1 (Wa-like) and 2 (DS1-like) more detected. Due to their relevance, two RVA vaccines are licensed and introduced in universal immunization, including Brazil where was adopted in 2006. With this, the monitoring type RVA current is important. Therefore, the aim of this study is to characterize the NSP4 gene RVA circulating in the Southeastern region of the state of Pará, Brazil, from 2006 to 2015. We analyzed 45 fecal specimens from children and adults with AG who were attended in Parauapebas, Pará, Brasil. Samples were submitted to Reverse Transcription Polymerase Chain Reaction (RT-PCR) using specific primers, were sequenced and analyzed phylogenetically. Analysis of NSP4 gene demonstrated two distinct genotypes, 3 samples G1P[8] and 1 sample G9P[8] belonging to the E1 genotype (Wa-like constellation) and 41 samples G2P[4] belonging to the E2 genotype (DS1-like constellation). In genogroup 2, 8 samples presented similarities of 99.94%, 99.96% and 99.97% with samples from cat (G3P[9]), cow (G6P[5]) and roe deer (G8P[14]), respectively. Such results suggest possible human/animal reassortment for NSP4 gene. The other samples showed similarity with strains of human origin, and all presented high similarity over the time studied, occurring the association of the binary classification to the respective constellations already described. The similarity observation of these human samples with strains of animal origin emphasizes the importance of the characterization of the RV genes to help the detection of possible genetic variants, derived from zoonotic transmission, which may represent a challenge to the immunizers currently used.

Palavras-chave: NSP4 gene, reassortment, rotavirus A