V21. MOLECULAR AND EPIDEMIOLOGICAL PROSPECTIVE STUDY OF A COHORT OF CHILDREN UNDER TWO YEARS OF AGE (MANGUINHOS-RJ), VACCINATED WITH ROTAVIRUS VACCINE.

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INTRODUCTION Group A rotavirus (RVA) is a genetically diverse population of segmented double-stranded RNA (RNAds) viruses with 11 segments with a binary classification, G and P genotypes. Nowadays, 27G and 37P genotypes have been described. They are the main etiological agents of acute gastroenteritis (AG) affecting mainly children ≤ 5 years old worldwide. Annually, it is estimated that a third of total deaths in the world due to AG are caused by these viruses. Two vaccines were recommended by the Pan American Health Organization and World Health Organization (WHO): the monovalent Rotarix® (RV1) (transfer of technology GSK/ Bio-Manguinhos) and the pentavalent RotaTeq® (RV5). Brazil introduced the RV1 in its National Immunization Program (NIP) in March, 2006.

OBJECTIVE The main objective is to make molecular and epidemiological studies of RVA, from November 2014 to October 2017, in fecal samples from a cohort of newborns and infants in the Manguinhos, RJ, neighborhood, with medical assistancebefore, during and after receiving the RV1 in routine consultations and, as well as, during acute diarrhea disease (ADD) episodes.

METHODOLOGY RVA detection and molecular characterization have been done by protocols recommended by WHO as quantitative RT-PCR, multiplex RT-PCR for genotyping and nucleotide sequencing.

RESULTS 337 fecal samples have been analyzed, corresponding to 119 observed children. 18 (5,3%) out of 337 analyzed samples were positive for RVA and 13 were genotyped as G1P[8]. In 4 samples the genotype P[8] was characterized by multiplex RT-PCR and the G genotype was characterized as G1 by sequencing. One sample remain G and P untypeable, and sequencing analysis are in progress. Two samples characterized as G1P[8] the nucleotide sequencing of the entire genomic region coding for the NSP4 enterotoxin protein is being conducted, to investigate the occurrence of genetic events in this region that could affect the dynamic of infection in vaccinated children.

CONCLUSION The results obtained from this study support the surveillance of RVA genotypes after RV1 introduction, allowing detection and molecular characterization of emerging variants or new genotypes that could interfere with the NIP.

KEYWORDS acute gastroenteritis, group A rotavirus, genotypes, monovalent vaccine.