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P0069 Spread of the ermerging equine-like G3P[8] DS-1-like genetic backbone rotavirus strain in Brazil

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Background: In 2013, a novel equine-like G3P[8] DS-1 like rotavirus (RVA) emerged as dominant strain worldwide. In 2016, this strain was reported in Brazil. The aims of the present study were to conduct a genetic retrospective investigation since 2013 in order to identify the possible entry of this novel G3P[8] strain in Brazil, describe its distribution across the country, help the understanding of evolutionary dynamics and potential implications in RVA vaccine programs.

Materials/methods: Between January/2013 and October/2017, a total of 4025 fecal specimens were collected from Southern, Southeastern and Midwest regions, and likely to be representative of Brazilian population. Specimens were screened for RVA using ELISA, and genotyped by RT-PCR. VP7 amplicons of positive G3P[8] samples were submitted to sequencing in order to identify the equine-like G3P[8] strains by nucleotide similarity search. Six equine-like G3P[8] representative samples were selected for investigation of the whole genome.

Results: G3P[8] represented 16.7% (123/736) of all RVA-positive samples, and further divided as equine-like G3 (6.4%; 47/736) and wild-type G3 (11.5%; 85/736). During 2013-2014, wild-type G3P[8] was the dominant strain across Brazil, and no equine-like G3P[8] was detected. Equine-like G3P[8] strain was first identified in March/2015 in Paraná State, suggesting that the strain stepped into Brazil through Southern region. The equine-like G3P[8] circulated only in Paraná till February/2016, but rapidly spread across the country after that, reaching Amazonas in March, Goiás in July and the Federal District in September. Equine-like G3P[8] strain reached São Paulo in August/2017. No wild-type G3 was detected since March/2015, therefore, it could be speculated that the atypical G3P[8] genotype was able to completely replace wild-type G3P[8] strains. Whole genome analysis revealed a DS-1 like genotype constellation (G3-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2), and segments shared the highest nucleotide sequence identity with strains isolated in Brazil and Spain.

Conclusions: This study highlights the emergence of the atypical equine-like G3P[8] genotype circulating in Brazil, and reinforces the potential for novel human/animal reassortant to arise within human population. Equine-like G3P[8] DS-1-like strains pose a challenge for the RVA surveillance, once G/P typing characterization by RT-PCR is unable to identify this intergenogroup reassortant without inclusion of sequencing analysis.