MOLECULAR CHARACTERIZATION OF BOVINE ROTAVIRUS SEROGROUP A VARIANT UK STRAIN IN VACCINATED BRAZILIAN CATTLE HERD

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The most frequent combination of G (VP7) and P (VP4) genotypes of group A bovine rotavirus (BoRV-A) are G6P[1] (NCDV-Lincoln) and G10P[11] (B223). Therefore, these BoRV-A strains are present in commercial vaccines. The G6 genotype is divided in five lineages, being that BoRV-A strains are included in the lineages III, IV, and V. The P[5] genotype until the now is not divided in lineages and include strains of animal (bovine and porcine) and human origins. This study had the aim of molecular characterization of G and P genotypes of BoRV-A identified in stool samples of calves in an outbreak of neonatal diarrhea in a beef cattle herd with extensive management in the state of Mato Grosso Sul, Brazil. The VP7 (G) and VP4 (P) genes of 12 wild-type BoRV-A strains were amplified by RT-PCR assays using consensus primers. The amplified products with 1062 bp and 876 bp respectively, were sequenced in MegaBACE™ 1000. Phylogenetic tree were realized using MEGA 4.1 and sequence identity matrix in BioEdit. The nucleotide (nt) analysis revealed that the 12 BoRV-A strains belonged to the genotype G6P[5]. In the phylogenetic analysis carried out in the 953 bp amplicon (nt 49-1001) of the VP7 gene the G6 genotype clustered in the lineage IV. This lineage include rotavirus strains of bovine origin as the prototypes strains NCDV-Lincoln (G6P[1]) and UK (G6P[5]). However the Brazilian wild type G6P[5] strains formed a different cluster in the phylogenetic tree. The 631 bp amplicon (nt 112-742) of the VP4 gene the Brazilian BoRV-A strains were classified in the P[5] genotype with similarity of 85.8 - 86.6% with the prototype UK strain. The higher similarity was observed with the VMRI strain of bovine origin. G6P[5] is the third genotype more frequently identified in BoRV-A strains worldwide. However, the G6P[5] Brazilian wild type BoRV-A strains formed a distinct cluster of the G6P[5] prototype strains in the phylogenetic tree. These results can suggest the evidence of virus evolution in field infection. The vaccine failure identified in this neonatal diarrhea outbreak might have been occurred due the molecular differences in the G6 genotype identified in the wild strains and the lack of heterologous immunity for the P[5] genotype. The results also evidenced the occurrence of genetic lineages in the P[5] genotype still not demonstrated in BoRV-A.

Keywords: Calves, BoRV-A, genotype G6P[5], vaccine failed.

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