

## VP6 gene diversity in Brazilian strains of porcine group C rotavirus

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Genet. Mol. Res. 9 (1): 506-513 (2010)  
Received November 19, 2009  
Accepted January 4, 2010  
Published March 23, 2010

**ABSTRACT.** Group C rotavirus (RV-C) has been found in Brazilian pig herds; however, wild-type strains have not yet been characterized. We made a molecular analysis of a region of gene 5 in Brazilian RV-C strains. Stool samples from 11 piglets (diarrheic and with normal consistency) positive for the RV-C VP6 gene in an RT-PCR assay were sequenced. A 270-bp amplicon of nine sequences was analyzed. All sequences showed high identity to the Cowden strain of the porcine RV-C prototype and 81.3 to 94.3% to each other (230 nucleotide fragment). Three Brazilian strains were classified in the Cowden group, while the other six showed higher heterogeneity (84.3 to 87.3%) with the prototype strain. Four clusters were formed in the dendrogram, including one human, one bovine, and two porcine clusters; one of these was formed by the six Brazilian strains described in this study. The Brazilian RV-C strains described here did not show any association with the year of collection, the presence of diarrhea, the age of the pig, or the geographical region of herd origin. This strongly suggests that these heterogeneous strains are widely spread in Brazilian pig herds. We conclude that there is genetic polymorphism in the VP6 gene of porcine RV-C strains in Brazil.

**Key words:** Piglets; Diarrhea; Porcine group C rotavirus; VP6 gene; Phylogenetic analysis