

Whole genome characterization of porcine rotavirus a collected in southern Mozambique, reveals G9P[13] and G4P[6] strains with a wa-like backbone

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Introduction

Group A rotavirus (RVA) is an important cause of diarrhea in the young of many species, including pigs and humans. The presence of RVA in pigs has been poorly investigated in Mozambique. The aim of this study was to determine the prevalence of porcine RVA in two districts in Mozambique and determine their constellations.

Methodology

Between August and September 2016, 135 stool samples of pigs up to 3 months of age, from rural and commercial herds in Manhiça and Moamba districts were collected. The samples were tested for the RVA antigen using ELISA kit (ProSpecT™ Rotavirus, Oxoid, UK). Total RNA was extracted from 8 ELISA positive samples with TRI-reagent (Sigma) followed by precipitation of ssRNA with LiCl. cDNA was synthesized using the Maxima H Minus double-stranded cDNA kit (Thermo Scientific) and sequencing was performed using an Illumina platform. Sequences were assembled using CLC Bio Genomics Workbench (9.0) and ViPR was used to determine genotype constellation.

Results

Of the 135 samples tested by ELISA, 21,5% (29/135) were positive for RVA antigen: 69,0% (20/29) from Manhiça and 31,0% (9/29) from Moamba. Of eight characterized porcine rotavirus strains, seven had genotype combination G9P[13] and presented Wa-like genome constellation with the exception of (I5) and (A8) genes (-I5-R1-C1-M1-A8-N1-T1-E1-H1). One strain had a G4P[6] genotype and presented Wa-like genome constellation with the exception of (A8) and (T7) genes (-I1-R1-C1-M1-A8-N1-T7-E1-H1).

Conclusion

The G/P genotypes and the constellation identified in the present study are typical porcine and were reported previously. Further analysis will indicate if these strains are also related to human rotavirus strains, since genotypes G9, G4 and P6 can also occur in human.

Keywords: Rotavirus A; Porcine; Wa-like; Mozambique