

Genetic diversity of group a rotavirus strains circulating in porcine from five provinces in South Africa during 2007, 2008 and 2015

Thenjiwe Ngomane, Mapaseka Seheri , Ina peenze

Sefako Makgatho health science university

Background and objectives

Rotavirus (RV) is the major cause of diarrhea in humans and animals worldwide. Group A rotavirus (RVA) has been credited to have an economic impact through loss in pig breeding and pork production. ProSystem, the porcine RVA vaccine has not been introduced to South African farmers, therefore practice of good biosecurity majors is the only method used to prevent RV infection. In this study the prevalence, migration patterns and genotypes were determined and compared to worldwide strains from the NCBI GenBank.

Methods

from 238 samples collected from South African pigs during 2007, 2008 and 2015, RVA antigen was detected using EIA and EIA positive samples were subjected to PAGE and RT-PCR, where migration patterns and genotypes were identified. RT-PCR product was subjected to Sanger sequencing and Chromatograms were used to draw phylogenetic trees.

Results

RVA was detected in 27.3% (65/238), 64.6% (42/65) of which presented with a long migration pattern. There was 17 genotype combinations, where G3 and G4 combined with P[6] to P[8] and P[23], G5 with P[6] to P[8], P[13] and P[23] and G9 with P[8] and P[13].

Conclusion

The RVA prevalence in South Africa (27.3%) is within a common range when compared with Kenya (27.2%) and Uganda (25.1%).Introduction of the ProSystem vaccine would be protective to South African pigs, since it includes Five of the nine genotypes detected in this study