Surveillance and characterization of porcine rotavirus in the Western Cape Province, South Africa

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Background

Rotavirus is a major cause of acute gastroenteritis in young mammalian species. Rotaviruses are classified into eight groups (RVA-RVH) with RVA classified into three genogroups, namely Wa-like, DS-1-like and AU-like. Zoonotic transmission of RVA has been reported and there is evidence for a common origin of human Wa-like and porcine rotavirus strains. Surveillance of animal reservoirs is important because it inform on interspecies transmission which can contribute to strain diversity in humans. The aim of this study was to identify and characterize rotavirus strains circulating on a pig farm in the Western Cape, South Africa.

Methods

Rotavirus surveillance was initiated on a farm in George, Western Cape, South Africa from January 2018 to February 2019. Stool samples were collected on three separate occasions from asymptomatic and diarrheal piglets and sows. Total RNA was extracted from stool samples using TRIzol reagent (Sigma). Single stranded RNA was precipitated with lithium chloride (2 M) and dsRNA was purified with MinElute gel extraction kit (Qiagen). Rotavirus screening was carried out using polyacrylamide gel (PAGE) analysis followed by silver staining. An anchor-primer was ligated to the dsRNA, and cDNA synthesis was prepared using Maxima H Minus Double stranded cDNA kit (ThermoFisher). The purified cDNA was submitted for next generation sequencing (NGS) on an Illumina Miseq platform at the NGS Unit, University of the Free State.

Results

A total of 41 stool samples were collected during three visits in a 14-month period. A rotavirus type A strain was detected in piglets during each of the trips, i.e. a detection rate of 7.3%. The three strains showed an identical long electropherotype profile of 4:2:3:2 during PAGE analysis. Whole-genome constellations will be presented for the three rotaviruses.

Conclusion

Although symptomatic rotavirus A strains were detected, further analysis will reveal if these strains are the result of multiple infections or rather a single circulating strain causing infection.