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Detection and genetic characterization of porcine sapovirus from pigs with diarrhea

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Abstract

Porcine Sapovirus (SaV) was first identified by electron microscopy in the United States in 1980 and has since been reported from both asymptomatic and diarrheic pigs usually in mixed infection with other enteric pathogens. SaV as the sole etiological agent of diarrhea in naturally infected pigs has not previously been reported in the United States. Here, we used four independent lines of evidence including metagenomics analysis, real-time RT-PCR (rRT-PCR), histopathology, and in situ hybridization to confirm porcine SaV genogroup III (GIII) as the sole cause of enteritis and diarrhea in pigs. A highly sensitive and specific rRT-PCR was established to detect porcine SaV GIII. Examination of 184 fecal samples from the outbreak farm showed that pigs with clinical diarrhea had significantly lower Ct values (15.9 ± 0.59) compared to clinically unaffected pigs (35.8 ± 0.71). Further survey of 336 fecal samples from different states in the United States demonstrated that samples from pigs with clinical diarrhea had a comparable positive rate (45.3%) with those from non-clinical pigs (43.1%). However, the SaV-positive pigs with clinical diarrhea had significantly higher viral loads (Ct = 26.0 ± 0.5) than those positive but clinically healthy pigs (Ct = 33.2 ± 0.9). Phylogenetic analysis of 20 field SaVs revealed that all belonged to SaV GIII and recombination analysis indicated that intra-genogroup recombination occurred within the field isolates of SaV GIII. These results suggest that porcine SaV GIII plays an important etiologic role in swine enteritis and diarrhea and rRT-PCR is a reliable method to detect porcine SaV. Our findings provide significant insights to better understand the epidemiology and pathogenicity of porcine SaV.

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