

Global Veterinary Microbiology and Veterinary Medicine Summit

October 17-18, 2016 Chicago, USA

Occurrence and evolutionary characterization of porcine *Deltacoronaviruses* in southern China

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Following the initial isolation of porcine *Deltacoronavirus* (PDCoV) from pigs with diarrheal disease in the United States in 2012, the virus has been detected on swine farms in some provinces of China. To date, little is known about the molecular epidemiology of PDCoV in southern China where major swine production is operated. To investigate the prevalence of PDCoV in this region and compare its activity to other enteric disease of swine caused by *Porcine epidemic diarrhea virus* (PEDV), transmissible *Gastroenteritis coronavirus* (TGEV) and *Porcine rotavirus group C* (Rota C), 90 fecal samples were collected from swine of various ages from three swine farms with diarrhea. Fecal samples were tested by reverse transcription-PCR (RT-PCR) that targeted PDCoV, PEDV, TGEV and Rota C, respectively. PDCoV was detected exclusively from nursing piglets with an overall prevalence of approximate 4.4%, not in suckling and fattening piglets. Despite a low detection rate, PDCoV was detected from all three farms. Interestingly, PDCoV-positive piglets were also tested positive for PEDV. PEDV was detected in approximate 18.8% of piglets with a similar distribution rate in both nursing and suckling piglets. None of tested fecal samples were positive for TGEV or PRV. Furthermore, phylogenetic analysis of spike (S) and nucleocapsid (N) gene sequences of PDCoVs revealed that currently circulating PDCoVs in southern China were more closely related to other Chinese strains of PDCoVs than to those reported in USA and Korea. This study demonstrated that PDCoV was present in southern China and supported an evolutionary theory of geographical clustering of PDCoVs.

Biography

Shao-Lun Zhai is an Epidemiologist and Assistant Researcher at Animal Disease Diagnostic Center, Institute of Animal Health, Guangdong Academy of Agricultural Sciences. His research interests focus on surveillance and rapid response research of emerging or reemerging animal pathogens.

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