

Genome Sequencing and Analysis of a Porcine Delta Coronavirus from Eastern China

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Abstract

Porcine delta coronavirus (PDCoV) has been reported in many countries, including the United States, Canada, South Korea, China, Thailand, Vietnam and Laos. In December 2016, clinical diarrhea similar to that caused by porcine epidemic diarrhea virus (PEDV), but with a lower mortality rate, was reported on a swine farm in Shanghai, China. 6 Intestine samples were collected from dead suckling piglets (<3 weeks old) with clinical diarrhea, and they were assayed for the presence of swine enteric coronaviruses. Polymerase chain reaction results were positive for PDCoV (6/6), but negative for PEDV (0/6), transmissible gastroenteritis virus (TGEV) (0/6) and porcine rotavirus group A (Rota A) (0/6). The full-length genome sequence of the PDCoV strain SHJS/SL/2016 was determined. Phylogenetic trees demonstrated that PDCoV strain SHJS/SL/2016 belongs to the Chinese clade, which might share a common evolutionary ancestor with United States and South Korean clades, but it clustered separately from Thai and Laotian PDCoV strains. This report describes the complete genome sequence of SHJS/SL/2016, and the data will promote a better understanding of the molecular epidemiology and genetic diversity of PDCoV isolates in China.

Keywords: Porcine deltacoronavirus; Full-length genome; Phylogenetics

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Biography

Zhou J and Liu P is a University Instructor and PhD candidate in Sports Biomechanics and Strength and Conditioning at Canterbury Christ Church University. Tom completed his BSc in Sport Science (Advanced Strength and Conditioning) at The University of Salford in 2016, attaining a first-class degree with honours. During this time he developed a deep interest in biomechanics,

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