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Complete Genome Sequence of a Highly Prevalent Porcine Circovirus 2 Isolated from Piglet Stool Samples in China

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Porcine circovirus type 2 (PCV2) is the etiologic agent of porcine circovirus-associated disease. Here, we first report the complete genome sequence of PCV2 strain JSTZ, which was isolated from piglet stool samples and is highly prevalent in China. It will help in understanding the epidemiology and molecular characteristics of PCV2.

Porcine circovirus type 2 (PCV2), a member of the *Circoviridae* family, is a small nonenveloped single-stranded circular DNA virus with a 1.76-kb ambisense genome (9). PCV2 was demonstrated to be a causative agent for porcine circovirus-associated disease (PCVAD), which includes porcine multisystemic wasting syndrome (PMWS), porcine dermatitis and nephropathy syndrome (PDNS), porcine respiratory disease complex (PRDC), congenital tremor (CT), and reproductive failure (1, 10). Since its emergence in the early 1990s, PCVAD has continuously been a threat to the global swine industry, causing high economic losses.

In the autumn of 2010, severe diarrhea in piglets emerged in China, affecting more than 1,000,000 piglets. Different pathogens have been detected in the stool sample, which included the porcine epidemic diarrhea virus (PEDV), transmissible gastroenteritis virus (TGEV), porcine rotavirus (PRV), porcine bocavirus (PBoV), porcine kobuvirus, porcine parvovirus (PtV), and others (2, 4–7, 11).

In this study, a PCV2 strain, JSTZ, was detected and identified in stool samples of a piglet with severe diarrhea in China. More importantly, there was a 67.2% infection rate in the stool samples of piglets with different degrees of diarrhea. It is thus necessary to analyze the genome sequence of PCV2 strain JSTZ and understand its molecular characteristics.

The complete genome of PCV2 strain JSTZ was sequenced with an ABI 3730xl genetic analyzer using the Sanger method, based on DNA fragments amplified by PCR with a previous primer (12). The genome of PCV2 strain JSTZ is a single-stranded DNA molecule comprising 1,767 bp, with a GC content of 48.33%. It contained at least three open reading frames (ORFs), encoding 2 major proteins. ORF1 encodes the replicase protein Rep; ORF2 encodes the viral capsid (cap) protein. The comparison of genome sequence revealed that PCV2 strain JSTZ exhibited 94.8 to 99.8% nucleotide identity to other Chinese PCV2 strains and shared 94.2 to 97.6% nucleotide identity with other PCV2 genomes from stool samples in other countries (3, 8). Furthermore, the Rep and cap proteins shared 97.8 to 100% and 93.8 to 100% amino acid identity with those proteins of all Chinese PCV2 strains, respectively. Phylogenetic analyses based on the genome and the ORFs of all Chinese PCV2 strains indicated that PCV2 strain JSTZ belonged to a novel genotype in China (12, 13), PCV-2d.

The genome sequence of JSTZ is the first genomic information on PCV2 from stool samples in China and will facilitate future investigations of the etiology of the diarrhea; furthermore, these data will be helpful for analyses of the evolutionary characteristics and molecular pathogenesis of PCV2.

Nucleotide sequence accession number. The genome sequence of PCV2 strain JSTZ was deposited in GenBank under accession no. [JQ413808](https://doi.org/10.1093/jvi/0000000000000000).

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