Complete Genome Sequence of Porcine Parvovirus 2 Recovered from Swine Sera

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A complete genomic sequence of porcine parvovirus 2 (PPV-2) was detected by viral metagenome analysis on swine sera. A phylogenetic analysis of this genome reveals that it is highly similar to previously reported North American PPV-2 genomes. The complete PPV-2 sequence is 5,426 nucleotides long.

Porcine parvovirus (PPV) is a small nonenveloped virus associated with reproductive problems and is endemic in virtually all swine-producing regions worldwide (1). The viral genome is a single-stranded DNA molecule of approximately 5 kb (2). Porcine parvovirus 2 (PPV-2) was first detected in 2001 and is probably distributed worldwide; however, links between PPV-2 and disease remain unclear (3).

Here, the complete sequence of a PPV-2 genome, identified in sera of Brazilian sows, is reported. Sera from ten clinically healthy, 5-months-old gilts (Sus scrofa) of the Large White breed were collected in Senador Canedo, Goiás, Brazil. Samples were pooled and viral particles were pelleted by centrifugation. The pellet was resuspended in Tris-EDTA and treated with DNase I (Roche) and RNase (Invitrogen). Viral genomes were extracted with a commercial kit (PureLink Viral RNA/DNA minikit) and amplified by random PCR (4). The products were purified and sequenced on an Ion Torrent platform with a 316 Ion chip. A total of 261,836 raw reads were generated and reduced to 126,661 after trimming with the Geneious version 8.0.2. From these, 18,862 reads were filtered by closest matching, where 95% of those fit within the family Parvoviridae. The reads were de novo assembled, with a mean coverage of at least 347X. A contig of 5,426 nucleotides (nt) comprised the full Brazilian PPV-2 (BrPPV-2) genome. Phylogenetic analyses performed with MEGA version 6.0 revealed that BrPPV-2 is closely related to genomes of North American PPV-2, with an overall 98.3 to 98.7% nt identity. The complete sequence of BrPPV-2 reveals two putative open reading frames (ORF): ORF1 (1,985 nt) and ORF2 (3,098 nt). In addition, two 14 nt-long palindromic sequences were identified, one at each extremity of the genome.

Nucleotide sequence accession number. The GenBank accession number is KM926355.

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REFERENCES