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GENOME ANNOUNCEMENT

Genome Sequence of Chinese Porcine Parvovirus Strain PPV2010

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Porcine parvovirus (PPV) isolate PPV2010 has recently emerged in China. Herein, we analyze the complete genome sequence of PPV2010. Our results indicate that the genome of PPV2010 bears mixed characteristics of virulent PPV and vaccine strains. Importantly, PPV2010 has the potential to be a naturally attenuated candidate vaccine strain.

Porcine parvovirus (PPV) is a member of the genus *Parvovirus* and the family *Parvoviridae* (8). PPV is a negative-oriented, single-stranded DNA virus that causes porcine reproductive failure characterized by infertility, embryonic and fetal death, mummified fetuses, and stillbirth in swine (5). Currently, three complete genome sequences of attenuated PPVs, including the prototype strain NADL-2 (USA, 1976) and the N (China, 1989) and China (China) strains, are available in GenBank. The role of attenuated PPV in disease is not fully understood.

In March of 2010, a PPV with low virulence, named PPV2010, was isolated from a disease outbreak in a hoggery in Jilin Province, northeastern China. Tissue samples tested positive for PPV by PCR using primers targeting viral VP2. Sequence alignment was performed using MUSCLE software (2, 3).

The whole genome of PPV2010 was sequenced with an ABI 3730xl genetic analyzer using the Sanger method, based on five overlapping DNA fragments amplified by PCR. The genome is comprised of 5,076 bp with a GC content of 37.9%, which is similar to that of the other sequenced PPV strains. The 5′ nontranslated region (NTR) has 291 nucleotides (nt) and the 3′ NTR 527 nt; the complete coding sequence contains 4,258 nt. The PPV genome includes two open reading frames (ORFs) (6); ORF1 locates at the 5′ end and ORF2 at the 3′ end. ORF1 encodes the nonstructural proteins NS1 (663 amino acids [aa]), NS2 (162 aa), and NS3 (108 aa); ORF2 encodes the structural proteins VP1 (730 aa) and VP2 (580 aa). PPV2010 has 99.6% and 99.9% sequence homology with the BQ strain (China), a virulent Chinese PPV, at the amino acid and nucleotide levels, respectively. The NADL-2 and Kresse strains differ in the VP2 protein by six amino acids, which have been demonstrated to be responsible for the replication efficiency of PPV in cell culture (4). The six amino acids are the same in PPV strain PPV2010 and the virulent Kresse strain; however, they are different from the amino acid sequences at the same location in PPV vaccine strains N and NADL-2. Even more interesting, by comparing the 3′ NTRs, we found that PPV2010 has two complete repeat units that are the same as those of the attenuated strains NADL-2 and N; however, the highly virulent Kresse strain has only one repeat unit and the moderately virulent BQ strain, which is very similar to PPV2010 in the coding regions, lacks 63 nt in the first repeat unit (7). PPV virulence is related to a 127-bp repeat in the 3′ NTR (1). PPV2010 shares the highest similarity with BQ in complete ORFs; however, in the 3′ NTR, PPV2010 has 99.9% homology with vaccine strain NADL-2. These data indicate that PPV2010 bears the characteristics of virulent and vaccine PPV strains. PPV2010 can replicate in cell culture (unpublished data) and has the potential to be a vaccine strain with low attenuation. The question of whether PPV2010 is a recombinant strain of BQ and NADL-2 needs to be investigated in the future. The genome data of PPV2010 will be helpful for analyses of molecular epidemiology and the pathogenesis of PPV.

Nucleotide sequence accession number. The GenBank accession number of PPV2010 is JN872448.

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X.R. is the sole owner of PPV strain PPV2010.

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