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Complete Genome Sequence of an Overattenuated Highly Pathogenic Porcine Reproductive and Respiratory Syndrome Virus

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JXA1-P170 is an overattenuated highly pathogenic porcine reproductive and respiratory syndrome virus (HP-PRRSV) that has been passaged in vitro 170 times. Vaccination with JXA1-P170 cannot protect pigs against JXA1 challenge. Compared with the parental virus JXA1, JXA1-P170 contains 1 nucleotide (nt) deletion and 113 nt mutations leading to 59 amino acid substitutions. Here we announce the first complete genome sequence of the overattenuated HP-PRRSV.

Porcine reproductive and respiratory syndrome virus (PRRSV) is an enveloped, positive-sense, single-stranded RNA virus belonging to the Arteriviridae genus, family Arteriviridae, order Nidovirales (2, 10). Highly pathogenic PRRSV (HP-PRRSV) is a mutant of PRRSV containing a novel discontinuous 30-amino-acid (30-aa) deletion in nonstructural protein 2 (Nsp2) (7, 12). HP-PRRSV is the etiological agent of HP-PRRS epidemics, which first emerged in southern China in 2006; the virus is currently widespread in China and several Southeast Asian countries, causing enormous economic losses (1, 3, 6, 9, 12). Live attenuated PRRSV vaccines based on serial in vitro passage are efficient tools that can be used to protect pigs against PRRSV infection (8, 13).

Here we announce the first complete genome sequence of the overattenuated HP-PRRSV. JXA1-P170 is a product that resulted from 170 continuous passages of strain JXA1 (GenBank accession no. EF112445) in Marc-145 cells, using the same assay as previously reported (5). Eighteen pairs of primers were used to amplify 18 overlapped fragments of the JXA1-P170 genome (5). PCR products were cloned into pGEM-T Easy vector (Promega), sequenced three times with an ABI Prism 3730 sequencer (Applied Biosystems), and assembled into the full-length sequence with SeqMan software (DNASTAR Inc.). The genome of JXA1-P170 is 15,319 bp, excluding the 3′ untranslated region (5′ UTR). Compared with JXA1-P170 for 28 days and then challenged with JXA1, they still showed high fever and clinical signs similar to those seen in pigs without vaccination. These results indicate that JXA1-P170 is overattenuated and cannot provide effective protection in pigs. It is generally believed that the 5′ UTR of PRRSV plays vital roles in viral replication, mRNA transcription, and protein translation (4); therefore, the guanine deletion in the 5′ UTR of JXA1-P170 might affect its infectivity in the pig. The substitutions in the 3′ UTR might also affect viral replication (11). The mutation differences between JXA1-P170 and JXA1 could help researchers to explore the virulence change, and the mutation differences between JXA1-P170 and JXA1-P80 should be crucial for understanding their differences in inducing host immune responses.

This is the first report of an overattenuated HP-PRRSV strain. The complete genome of JXA1-P170 should facilitate future research aimed at elucidation of the mechanisms of pathogenicity and immunogenicity changes from JXA1 to JXA1-P80 and then to JXA1-P170 and should also contribute to the production of a live-attenuated PRRSV vaccine with higher efficacy.

Nucleotide sequence accession number. The complete genome sequence of JXA1-P170 has been deposited in GenBank under accession number JQ804986.

ACKNOWLEDGMENTS

We thank Amy Galliher-Beckley of Kansas State University for her kind help in preparing this announcement.

This work was supported by grants from the National Scientific and Technical Supporting Programs (2006BAD06A07, 2008FY130100-2, and 2009BADB05-3) and the Scientific Achievement Transformation Program (2009GB23260435).

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