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Published in:
Genome Announcements

Link to article, DOI:
10.1128/genomeA.00483-14

Publication date:
2014

Document Version
Publisher’s PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):
Complete Genome Sequence of Classical Swine Fever Virus Genotype 2.2 Strain Bergen

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The complete genome sequence of the genotype 2.2 classical swine fever virus strain Bergen has been determined; this strain was originally isolated from persistently infected domestic pigs in the Netherlands and is characterized to be of low virulence.

Classical swine fever virus (CSFV) belongs to the genus Pestivirus within the family Flaviviridae. CSFV is an important animal pathogen that causes disease in pig species and has low-, moderate-, and high-virulence characteristics (1). The CSFV genome consists of a positive-sense RNA, approximately 12,3 kb in length, which encodes a single polyprotein that is co- and posttranslationally cleaved to form the mature structural and nonstructural proteins. The CSFV strains can be divided into genotypes 1, 2, and 3, each comprising three to four subgenotypes (2, 3). CSFV strain Bergen represents a low-virulence strain that originally was isolated from persistently infected pigs in the Netherlands (4). The low-virulence phenotype of the Bergen strain was confirmed in a recent pathogenicity study (5). The Bergen strain has been grouped together with genotype 2.2 strains based on partial 5′-untranslated region (UTR) and E2 sequences (2, 3). Complete genomic sequences have been described for most CSFV genotypes. However, complete genome sequences from genotype 2.2 are lacking in the public sequence databases.

Here, we describe the complete genome sequence of the CSFV genotype 2.2 strain Bergen (isolate CSF0906) obtained from the CSFV collection at the EU Reference Laboratory (EURL). Viral RNA was extracted from infected PK15 cells, and full-length viral cDNAs were amplified by long reverse transcription-PCR (RT-PCR), as previously described (6), using cDNA primer 5′-GGGCGGTAGGAAATTACCTTATGAT-TGAGGTTAGTCTCGTGACACTATGGCTAACCTTAC-3′ and PCR primers 5′-TCTATATGGCGCCGCTTAATACGACTGATAGGTTAGTCTCGTGACACTATGGCTAACCTTAC-3′ and 5′-ATTACCTGTTAGGAAATTACCTTATGAT-TGAGGTTAGTCTCGTGACACTATGGCTAACCTTAC-3′. The sequencing library was generated from the RT-PCR product using the Ion Plus fragment library kit and sequenced using an Ion Torrent PGM (Life Technologies). Newbler (Roche) was used for de novo assembly and the Burrows-Wheeler Aligner (BWA) (7) for mapping of the reads using the de novo assembly as the reference sequence. Finally, consensus sequences were aligned using MAFFT in the Geneious software platform (Biomatters).

The final 12,295-nucleotide (nt)-long consensus sequence for the CSFV strain Bergen genome was obtained from a de novo assembly consisting of 16,318 sequence reads, with an average sequence depth of 268 reads per nt. The polyprotein-coding sequence is 11,697 nt long and contains 3,899 codons.

Acknowledgment
This study was supported by DTU National Veterinary Institute.

REFERENCES

