Classical swine fever (CSF), listed with the Office International des Epizooties (OIE), is one of the most highly contagious and fatal diseases of swine. Classical swine fever virus (CSFV), the causative agent of CSF, is a member of the genus Flavivirus, which also contains bovine viral diarrhea virus (BVDV) and border disease virus (BDV). CSFV is a single positive-stranded RNA virus, whose genome is approximately 12.3 kb in length, and it comprises a single long open reading frame (ORF) that encodes a polyprotein composed of 3,898 amino acids, flanked by two noncoding regions at the 5' UTR and 3' UTR. Based on the E2 gene and a partial nonstructural region of 3,898 amino acids, 10 subgenotypes (1.1, 1.2, 1.3, 2.1b, 2.1c, 2.1d, 2.2, 2.3, 3.1, 3.2, and 3.3) have been classified. The complete genome sequence of JSZL is 12,297 nucleotides (nt) in length, with a 5' UTR of 373 nt and 3' UTR of 227 nt. A single large ORF is 11,697 nt, coding for a polyprotein of 3,898 amino acids.

In a comparison of the full-length E2 gene of JSZL with 119 reference strains, phylogenetic analysis indicated that strain JSZL belongs to the new subgenotype 2.1d. Furthermore, the new subgenotype has new molecular characteristics. Compared with the genome of subgenotype 2.1a, 2.1b, 2.1c, 2.1d, 2.2, 2.3, 3.1, 3.2, 3.3, and 3.4 (4), JSZL shares 84.6 to 85.4%, 85.2%, 93.1 to 94.4%, 94.6 to 95.6%, 92.2 to 92.4%, 96.6 to 97.4%, 87.6 to 91.8%, 88.8 to 89.9%, 84.0%, and 83.2 to 83.5%, respectively. Since late 2014, a large number of wild new CSFVs have been detected or isolated in many immune pig farms in China. Furthermore, most of the new CSFV isolates belong to the new subgenotype 2.1d. Therefore, these new strains and the representative strain JSZL should be worthy of high attention.

**Nucleotide sequence accession number.** The complete genome sequence of CSFV strain JSZL has been deposited in GenBank under the accession no. KT119352.

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