Complete Genome Sequence of *Streptococcus equi* subsp. *zooepidemicus* Strain ATCC 35246

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***Streptococcus equi* subsp. *zooepidemicus* is an opportunistic pathogen. It has caused a very large economic loss in the swine industry of China and has become a threat to human health. We announce the complete genome sequence of *S. equi* subsp. *zooepidemicus* strain ATCC 35246, which provides opportunities to understand its pathogenesis mechanism and genetic basis.**

Streptococcus equi subsp. *zooepidemicus* is classified in Lancefield's group C and is a primarily opportunistic pathogen of a wide variety of domesticated species (11). It is a rare cause of human invasive infections, such as septicemia and meningitis, usually originating from zoonotic transmission from domesticated animals to humans (1, 4, 6). In China, it is the main pathogen causing disease in swine (5, 8). For a further understanding of the genetic background of the pathogenic potential and mechanism of the bacterium, *S. equi* subsp. *zooepidemicus* strain ATCC 35246, isolated from a dead pig in Sichuan province, China, was chosen for genome sequencing.

Whole-genome sequencing was performed by using a Roche 454 genome sequencer FLX system. A total of 303,103 raw reads were assembled into 649 contigs with 51-fold sequence coverage. Gap filling was based on the conservation of gene order between the *S. equi* subsp. *zooepidemicus* strain ATCC 35246 and strain MGCS 10565 (CP001129.1) chromosomes. The gap-spanning PCR products were sequenced with an ABI 3730 DNA analyzer, and the resulting sequences were added into contigs by using Phred/Phrap/Consed software (http://www.phrap.org/phredphrapconsed.html). Protein-coding genes were predicted with the Glimmer 3.02 program (3), and the functions of these genes were determined by homology searches in the NCBI nonredundant protein database, cluster of orthologous groups (COGs), and InterProScan (10). The tRNA genes and rRNA genes were identified by using the tRNAScan-SE tool and RNAmmer1.2 (7, 9), respectively.

The complete genome of *S. equi* subsp. *zooepidemicus* ATCC 35246 is composed of a 2,167,264-bp single circular chromosome with a GC content of 41.65%. A total of 2,087 protein-encoding genes, 57 tRNA genes, and 5 5S-16S-23S rRNA operons are found to be located in this chromosome. Genome annotation analysis revealed that previously identified virulence-associated genes, such as the *szm* (SeseC_02415) gene, *fbpZ* (SeseC_02469) gene, *skc* (SeseC_02411) gene, *has* operon (SeseC_00231 to SeseC_00233), and *scl* gene family were also found in strain ATCC 35246, suggesting that it is a invasive and virulent strain. Comparative genomic analysis of the ATCC 35246 and MGCS 10565 (CP001129.1) and H70 (FM204884.1) genomes revealed that one prophage-associated gene cluster (SeseC_00875 to SeseC_00918) was unique in ATCC 35246, which contributed to the diversification of the bacterial genome architecture and enhanced the virulence of the bacterial host (2). In conclusion, knowledge of this genome sequence provides a key genetic framework for assessing our understanding of the molecular events contributing to *S. equi* subsp. *zooepidemicus* pathogenesis.

Nucleotide sequence accession number. Genome information for *S. equi* subsp. *zooepidemicus* strain ATCC 35246 has been deposited in GenBank under accession number CP002904.

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