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GENOME ANNOUNCEMENT

Genome Sequence of the Swine Pathogen *Streptococcus suis* Serotype 2 Strain S735

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***Streptococcus suis* is a major swine pathogen responsible for significant, worldwide economic losses in the swine industry, in addition to being an emerging zoonotic agent. Strains of serotype 2 are the most commonly associated with infections causing meningitis, endocarditis, and septicemia. Here we present the genome sequence of *S. suis* serotype 2 strain S735.**

Streptococcus suis is a major swine pathogen worldwide, endemic in all countries where intensive pig farming is practiced, causing meningitis, endocarditis, arthritis, pneumonia, and septicemia (3, 8). *S. suis* is also considered an emerging zoonotic agent, especially in Asian countries (6, 7). The massive use of antibiotics for growth promotion or for prophylaxis and therapy in the swine industry may contribute to the emergence and spread of antibiotic resistance in *S. suis* (10). Strains of serotype 2 are mostly responsible for severe infections in both swine and humans (3, 8). King et al. (9) developed a multilocus sequence typing (MLST) scheme and showed that *S. suis* serotype 2 isolates can be classified into at least 16 sequence types (STs), the most invasive strains belonging to the sequence type 1 (ST1) complex. Recently, Fittipaldi et al. (4) performed MLST on North American *S. suis* serotype 2 porcine isolates and reported that most strains can be classified into three major classes: ST1 (high virulence, low prevalence in North America), ST25 (intermediate virulence), and ST28 (low virulence). Here we report the genome sequence of *S. suis* serotype 2 strain S735 (NCTC 10234), an ST1 European (The Netherlands) reference strain isolated from a case of pneumonia in a pig (2).

The total genomic DNA of *S. suis* S735 was extracted using the method of Stuart et al. (11). Whole-genome shotgun DNA sequencing of *S. suis* S735 was performed using the Roche 454 pyrosequencing method on the Genome Sequencer FLX+ system at the Plateforme d'analyses génomiques of the Institut de Biologie Intégrative et des Systèmes (IBIS, Université Laval). In total, 70,238,071 bases were analyzed using the gsAssembler module of Newbler v2.5.3. A total of 37 contigs were produced, all of them larger than 500 bases. Contigs were merged using Consed (5). Two regions could not be resolved by 454 sequencing, and primers were designed to PCR amplify and Sanger sequence these regions. The DNA isolated from *S. suis* S735 was assembled into a single 1,980,887-nucleotide circular genome. Multiple, complete genome alignments using Mauve (1) and several published *S. suis* genomes (accession numbers AM946016.1, CP000408.1, CP000837.1, FM252031.1, and FM252032.1) identified a potential large inversion site bounded by a 1,529-nucleotide inverted repeat element. The orientation of this region was verified by PCR to ensure proper assembly. The genome of *S. suis* S735 was found to be in the same orientation as the majority of the published genomes in GenBank, leaving a single genome with the inversion.

The genome of *S. suis* S735 is slightly smaller than other sequences from the same species (27 kb smaller than *S. suis* strain P1/7). Three elements absent in *S. suis* S735 (totaling 28 kb) compared to P1/7 were previously identified as genomic islands or putative phage-related genomic islands. These elements are not present in all sequenced strains to date and could be potential pathogenicity determinants.

Nucleotide sequence accession number. The nucleotide sequence for the draft genome sequence of *S. suis* S735 has been deposited in DDBJ/EMBL/GenBank under the accession no. CP003736.

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