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Whole-Genome Sequence of *Streptococcus pseudopneumoniae* Isolate IS7493

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***Streptococcus pseudopneumoniae* is a member of the viridans group streptococci (VGS) whose pathogenic significance is unclear. We announce the complete genome sequence of *S. pseudopneumoniae* IS7493. The genome sequence will assist in the characterization of this new organism and facilitate the development of accurate diagnostic assays to distinguish it from *Streptococcus pneumoniae* and *Streptococcus mitis*.**

Streptococcus pseudopneumoniae is a recently designated species belonging to the viridans group streptococci (VGS) (1). Despite having >99% 16S rRNA gene identity with *Streptococcus pneumoniae* and *Streptococcus mitis*, it exhibits DNA-DNA hybridization values of <70% and is phenotypically distinct (1). Unlike *S. pneumoniae*, *S. pseudopneumoniae* is optochin resistant in the presence of 5% CO_2, is bile insoluble, and lacks the pneumococcal capsule. Its pathogenic potential and the underlying genetic identity are not well characterized in relation to those of *S. pneumoniae* or the commensal *S. mitis* (1, 6–8, 10).

To define genomic differences and establish genetic targets for clear identification of these closely related organisms, whole-genome shotgun sequencing (331,392 raw reads) of a representative *S. pseudopneumoniae* patient isolate, IS7493, and initial assembly were performed with the Genome Sequencer FLX (Roche, Basel, Switzerland). Isolate IS7493 was obtained from the sputum of a patient with human immunodeficiency virus (HIV) who had documented pneumonia. The contigs were sequentially arranged by comparison to all available genomes of *S. pneumoniae* in GenBank using MAUVE (4, 5). The remaining contigs were fitted *in silico* and by PCR amplification and Sanger sequencing (BigDye version 3.1 and the 3130*xl* genetic analyzer system; Applied Biosystems). In addition to a single circular (2,198,893 bp with 39.5% GC content) chromosomal genome, isolate IS7493 harbored a plasmid of 4.7 kb (pDRPIS7493). The genome was functionally annotated with the RAST server (2) and the NCBI Prokaryotic Genome Automatic Annotation Pipeline (PGAAP). The chromosome contains 2,237 coding sequences (CDS), 41 tRNA genes, and 3 rRNA genes. The plasmid, pDRPIS7493, contains 6 CDS of hypothetical proteins which include a putative recombination enzyme/mobilization protein and a putative replication protein.

Dot plot analysis comparison of *S. pseudopneumoniae* IS7493 with *S. pneumoniae* R6 and *S. mitis* NCTC 12261 genome sequences indicated differences in genetic content between the three species and implied that *S. pseudopneumoniae* is more closely related to *S. pneumoniae* R6. In comparison to *S. pneumoniae* R6, *S. pseudopneumoniae* lacks most of streptococcal pathogenicity island 1 (PAI1) (~200 kilobase pairs), the capsule biosynthesis genes, the bacteriocinlike peptide (Blp) cluster downstream of the competence locus, and pneumococcal iron acquisition operon *piaABCD* that is required for virulence in *S. pneumoniae*. The competence-stimulating peptide (CSP)-mediated induction of the *cibA-cibB*, *lytA*, and *cbpD* genes is required for allolysis in *S. pneumoniae* (3). The lack of the *comC* gene suggests that CSP-mediated induction of allolysis does not take place in *S. pseudopneumoniae* and may explain the observed bile insolubility. Optochin resistance has been previously linked to single point mutations in either the a-subunit (W206S) or the c-subunit (G20S, M23I, and A49T) of H^+-ATPase in *S. pneumoniae* (9). *S. pseudopneumoniae* only harbors an F5Y mutation in the c-subunit. Relative to *S. mitis* NCTC 12261, *S. pseudopneumoniae* IS7493 has acquired additional virulence factors and antibiotic tolerance and resistance genes. We conclude that *S. pseudopneumoniae* is a hybrid strain between *S. pneumoniae* and *S. mitis* lacking key virulence factors and therefore more akin to a commensal. However, due to the propensity for horizontal gene transfer, *S. pseudopneumoniae* may be able to acquire virulence genes and become pathogenic in humans.

Nucleotide sequence accession numbers. The whole-genome sequence and the plasmid sequence of *S. pseudopneumoniae* IS7493 were deposited in the DDBJ/EMBL/GenBank databases under the accession numbers CP002925 and CP002926, respectively.

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