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Complete Genome Sequence of the Pigmented *Streptococcus thermophilus* Strain JIM8232

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Streptococcus thermophilus **is a dairy species commonly used in the manufacture of cheese and yogurt. Here, we report the complete sequence of *S. thermophilus* strain JIM8232, isolated from milk and which produces a yellow pigment, an atypical trait for this bacterium.**

Streptococcus thermophilus is an important bacterium that is extensively used in starter cultures in the dairy industry. It is also found growing spontaneously in traditional products around the world, and it is believed to persist in the farm environment. Here, we have determined the genome of the nonstarter strain JIM8232, isolated from milk and previously specified *S. thermophilus* by multilocus sequence type analysis (5), since it produces a yellow pigment, which is atypical in streptococci except those belonging to the pathogenic species *Streptococcus agalactiae* (9). Lateral gene transfer events may play an important role in *S. thermophilus* genome plasticity, as described for the *eps* operon, integrative conjugative elements (ICEs), and genomic islands (1, 2, 6, 8). Recently, a genomic island containing the *prtS* gene and disseminating quickly in the *S. thermophilus* population was characterized in strain JIM8232 (4). The yellow atypical phenotype provides additional evidence of lateral gene transfers in *S. thermophilus* strain JIM8232.

The *S. thermophilus* JIM8232 sequence was determined by using Sanger and SOLiD sequencing technologies. Whole-genome assembly was performed from a short insert plasmid library, yielding 205 contigs with an average coverage of 3×. The contigs were ordered by using the PROJECTOR2 software (10). Gap closures were determined by primer walking on PCR products. Insertion sequence boundaries were systematically checked by PCR amplification and sequencing. Finally, mismatch and small insertion-deletion corrections were determined using the SOLiD sequencer (Applied Biosytems) with 95× coverage. Genome annotation was performed using the AGMIAL annotation platform (3).

The circular chromosome of *S. thermophilus* JIM8232 is composed of 1,929,905 bp with an overall G+C content of 38.9%. It includes 2,145 open reading frames that account for 85.1% of the genome, 1,745 of which (81.3%) were annotatable with known proteins with biological function or a functional domain and 400 of which (18.7%) were annotated as conserved hypothetical proteins. The genome also harbors 67 tRNA genes covering all amino acids and also 6 rRNA operons.

Comparative genomic analysis of *S. thermophilus* JIM8232 revealed strain-specific DNA of 129 kb compared to previously sequenced *S. thermophilus* strains. These sequences are present in 9 regions of 2.6 to 55 kb. Three of them correspond to hypervariable regions, such as the *eps* operon, genes encoding the restriction/modification system, and CRISPR sequences (7). Three regions, ranging from 2.5 to 7.5 kb, contain genes potentially involved in metabolism, such as oxidative stress, and are not flanked by mobile elements. Lastly, three regions may be ICE related and contain integrases. The two major islands are 53 kb and 40 kb long, and one of them contains an operon encoding proteins potentially involved in pigment synthesis. The complete genome sequence of *S. thermophilus* strain JIM8232 will promote studies to improve understanding of genomic plasticity and horizontal gene transfer within *S. thermophilus* populations.

Nucleotide sequence accession number. The complete genome sequence of *S. thermophilus* JIM8232 is accessible at GenBank under accession number FR875178.

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