First Draft Genome Sequence of Staphylococcus condimenti F-2T

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Received 20 April 2016 Accepted 21 April 2016 Published 2 June 2016

Citation Zheng B, Hu X, Jiang X, Li A, Yao J, Li L. 2016. First draft genome sequence of Staphylococcus condimenti F-2T. Genome Announc 4(3):e00499-16. doi:10.1128/genomeA.00499-16.

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This report describes the draft genome sequence of S. condimenti strain F-2T (DSM 11674), a potential starter culture. The genome assembly comprised 2,616,174 bp with 34.6% GC content. To the best of our knowledge, this is the first documentation that reports the whole-genome sequence of S. condimenti.

C oagulase-negative staphylococci (CoNS) are mainly found on the skin and mucosa of humans and are regarded as less pathogenic than coagulase positive staphylococci (1–3). However, the widespread use of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) has allowed an increasing detection rate of CoNS species from clinical samples (4). CoNS represent the most common cause of catheter-related bloodstream infections, prosthetic valve endocarditis, and prothrombotic joint infections (5). Staphylococcus condimenti is a member of the CoNS. S. condimenti strain F-2T (= DSM 11674) is the type strain, which was originally isolated from soy sauce mash (6). It is usually associated with food and used in starter cultures (7, 8). Although rare, S. condimenti also has been reported as a human pathogen causing catheter-related bacteremia (5). However, little is known about genetic determinants that contribute to its virulence and survival.

Here, we present the genome sequence of S. condimenti strain F-2T, as part of the CoNS whole-genome sequencing program initiated by our lab. Genomic DNA was prepared using the PureLink Genomic DNA minikit (Invitrogen, USA) (9). Libraries were prepared for sequencing with Nextera DNA kits (Illumina) and were sequenced on the Illumina HiSeq 2000 system, according to standard Illumina protocols. The raw reads were trimmed and assembled as previously described (10). Predicted genes were identified using Glimmer (11). tRNA genes, whereas ribosomal RNAs were found by using RNAmmer (13). The draft genome was annotated using the RAST server (14). All annotated genes were then classified based on their COG classes (15). Putative phage sequences were identified by PHAST (16). CRISPRFinder was used to screen for the presence of CRISPR arrays (17).

The draft genome sequence of S. condimenti strain F-2T comprises 80 contigs with a total length of 2,616,174 bp and a GC content of 34.6%. It is covered at a 165-fold depth with an N50 of 136,415 bp. The shotgun sequence encodes 2,547 predicted genes. These scaffolds also contain 60 tRNAs and 14 incomplete rRNAs. CRISPRFinder revealed 2 CRISPR arrays.

Coding sequences were analyzed to detect toxin genes by using VirulenceFinder (http://cge.cbs.dtu.dk/services/VirulenceFinder), which revealed that strain F-2T possesses a varying repertoire of putative virulence factors involved in adherence, such as extracellular fibronec tin binding protein, fibronec tin binding protein, elastin binding protein, and autolysin.

Prediction of putative phage elements revealed the presence of an intact prophage region together with one questionable prophage region. It is clear that prophages are directly associated with the virulence in Staphylococcus aureus (18). Proteins were also compared with the antibiotic resistance gene database (19), and we found two genes encoding proteins that belong to the β-lactamase family. Two putative CRISPR repeat regions were detected in the genome. The origin of the CRISPR systems in S. condimenti still remains unknown; however, the propagation of CRISPR has been proposed to occur through horizontal gene transfer by conjugation (20).

The genome sequence of S. condimenti F-2T will contribute to easier genetic manipulation of this strain and will enable further studies in the future.

Nucleotide sequence accession numbers. The whole-genome shotgun project of S. condimenti DSM 11674 has been deposited at DDBJ/EMBL/GenBank under the accession number LAQN00000000. The version described in this paper is the first version, LAQN00000000.1.

ACKNOWLEDGMENTS

This work was supported by the National Natural Science Foundation of China (grant nos. 81301461 and 41406140), and the National Basic Research Program of China (973 program, no. 2015CB554201).

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