Whole-Genome Sequences of Streptococcus tigurinus Type Strain AZ_3a and S. tigurinus 1366, a Strain Causing Prosthetic Joint Infection

GIZARD, Yann, et al.

Abstract
Streptococcus tigurinus, a novel member of the Streptococcus mitis group, was recently identified as a causative agent of invasive infections. We report the complete genome sequences of the S. tigurinus type strain AZ_3a and S. tigurinus strain 1366. The genome sequences assist in the characterization of virulence determinants of S. tigurinus.

Reference
GIZARD, Yann, et al. Whole-Genome Sequences of Streptococcus tigurinus Type Strain AZ_3a and S. tigurinus 1366, a Strain Causing Prosthetic Joint Infection. Genome Announcements, 2013, vol. 1, no. 2, p. e00210-12

DOI : 10.1128/genomeA.00210-12
PMID : 23640198
Streptococcus tigurinus, a novel member of the Streptococcus mitis group, was recently identified as a causative agent of invasive infections. We report the complete genome sequences of the S. tigurinus type strain AZ_3a and S. tigurinus strain 1366. The genome sequences assist in the characterization of virulence determinants of S. tigurinus.

Received 17 January 2013 Accepted 15 March 2013 Published 2 May 2013


Copyright © 2013 Gizard et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Patrice François, patrice.francois@genomic.ch.

S. tigurinus was recently described as a novel species within the Streptococcus mitis group and was demonstrated to cause invasive infections such as endocarditis, meningitis, and prosthetic joint infection (1, 2). Based on phenotypic and molecular analyses, S. tigurinus is most closely related to Streptococcus mitis, Streptococcus pneumoniae, Streptococcus pseudopneumoniae, Streptococcus oralis, and Streptococcus infantis. Accurate identification of S. tigurinus is facilitated by partial 16S rRNA gene analyses (1, 2).

To identify species-specific features and evaluate genome contents, the genomes of S. tigurinus type strain AZ_3a and S. tigurinus strain 1366 were sequenced. S. tigurinus 1366 was isolated from joint aspirate of a patient with prosthetic joint infection. Purified genomic DNA was subjected to whole-genome shotgun sequencing by using an HiSeq2000 system (Illumina, Inc.). Following fragmentation, end reparation, and sample tagging, the sequencer produced 3,297,278 and 2,647,247 reads for the strains AZ_3aT and 1366, respectively. The larger contigs showed sizes of 307,439 bp for strain AZ_3aT and 752,455 bp for strain 1366. Overall assembly values were satisfactory (for strain AZ_3aT, sum, 2.18 Mb; N₅₀, 162,462 bp; minimum, 407 bp; for strain 1366, sum, 1.87 Mb; N₅₀, 600,062 bp; minimum, 171 bp). In strains AZ_3aT and 1366, a total of 2,157 and 1,886 predicted coding sequences (CDS) were detected, respectively, by RAST (5). The majority of genes (n = 1,468) were common to both strains (E value, 1E−6; identity, >80%). More than 57% of the genes were assigned to specific subsystem categories by RAST (5). The chromosome of strain AZ_3aT contains 2,107 translated genes and 50 structural genes encoding 47 tRNAs and 3 rRNAs. The chromosome of strain 1366 contains 1,825 putative transcripts and 61 structural genes encoding 49 tRNAs and 12 rRNAs. Note that the two S. tigurinus strains are devoid of multicopy plasmids.

Dot plot analysis comparison of S. tigurinus with S. pneumoniae showed high similarity of ribosomal proteins. This may partially explain the misidentification of S. tigurinus strains as S. pneumoniae, which was observed by matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) (1, 2). When we performed whole-genome comparison, metabolic genes showed partial homology values of 80 to 90% with related species (e.g., S. oralis, S. pseudopneumoniae, and S. mitis) and >1,000 single-nucleotide polymorphisms (SNPs), with S. mitis strain NCTC 12261 considered to have the closest sequenced genome.

The S. tigurinus genomes contain genes for known virulence factors, such as exfoliative toxin and fibronectin-binding protein, as well as several prophages. Annotation allowed detection of three toxin-antitoxin systems as well as resistance determinants against heavy metals, aminoglycosides, and tetracycline; thus, numerous gene products are potentially involved in the expression of bacterial virulence. The annotated genes discriminating the two S. tigurinus strains AZ_3aT and 1366 relate mainly to features carried by mobile genetic elements, restriction systems, metabolic genes, and clustered regularly interspaced short palindromic repeat (CRISPR) sequences.

We conclude that S. tigurinus shows important virulence determinants potentially involved in the pathogenicity of S. tigurinus.

Nucleotide sequence accession numbers. The whole-genome sequences of S. tigurinus AZ_3aT and S. tigurinus 1366 were deposited in the DDBJ/EMBL/GenBank databases under the accession numbers AORU0000000 and AORX0000000, respectively.

ACKNOWLEDGMENTS

This study was supported by the University of Zurich and the Genomic Research Laboratory.

We thank the technicians for their dedicated help.

REFERENCES


March/April 2013 Volume 1 Issue 2 e00210-12 Genome Announcements genomea.asm.org 1

