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PROKARYOTES

Draft Genome Sequence of *Tannerella forsythia* Clinical Isolate 9610

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ABSTRACT We present here the draft genome sequence of *Tannerella forsythia* 9610, a clinical isolate obtained from a periodontitis patient. The genome is composed of 79 scaffolds with 82 contigs, for a length of 3,201,941 bp and a G+C of 47.3%.

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Tannerella forsythia is a Gram-negative, asaccharolytic, and oral anaerobe (1, 2). *T. forsythia* is a member of the "red complex," a trio of periopathogens associated with the development of periodontal disease and inflammation (3). *T. forsythia* is strongly associated with the onset of both severe (4) and refractory periodontitis (5, 6). In comparison to its red complex fellows *Poryphyromona gingivalis* and *Treponema denticola*, little is known of the intermicrobial relationships formed and virulence mechanisms utilized by *T. forsythia* due to its fastidious growth requirements. To fully understand the role *T. forsythia* plays in the initiation and progression of periodontitis, it is vital that there is increased availability of genomic sequences. Here, we report the identification and phylogenetic placement of a draft genome sequence of *T. forsythia* clinical isolate 9610.

Isolate 9610 was collected between 1988 and 1991 at the University of Washington Graduate Periodontics Clinic from patients with various forms of periodontal disease, 5- to 10-mm pocket depths, and bleeding upon probing ($n = 4$ per patient). Samples were pooled and stored at -80°C.

In this study, 9610 was serially diluted on blood agar medium for bacterial isolation for a total of three passages, anaerobically incubated at 37°C for 3 days, then anaerobically incubated in SHI liquid medium (7) at 37°C for 3 days prior to generation of a final 20% glycerol stock solution. Genomic DNA extraction was performed utilizing the Qiagen DNeasy blood and tissue kit. The Illumina MiSeq platform was used to produce paired-end 300-bp reads, which were then assembled using SPAdes 3.9.0 (8, 9).

The draft genome consists of 79 scaffolds with 82 contigs, for a total length of 3,201,941 bp and a G+C content of 47.3%. Annotation performed by the National Center for Biotechnology Information (NCBI) Prokaryotic Genome Annotation Pipeline (PGAP) found a total of 2,620 genes, composed of 2,488 coding genes, 44 tRNAs, five rRNAs, and one clustered regularly interspaced short palindromic repeat (CRISPR).

Relatives of 9610 identified by creating a 16S rRNA gene phylogenetic tree were *T. forsythia* 8563 (10, 11), 8464 (11, 12), and Ko3 (13). When the genomic sequence of 9610 was compared to the finite available sequenced genomes of the species, composed of *T. forsythia* KS16, 92A2, and ATCC 43037, 9610 has an average amino acid identities (AAI) of 98.26%, 97.93%, and 97.77%, respectively. These results support the identification of 9610 as a novel genome to the *Tannerella forsythia* species.

When 9610 was compared to KS16, 92A2, and ATCC 43037 via Rapid Annotations using Subsystems Technology (RAST) SEED-based comparison (14), 9610 was found to possess the unique gene valine-glycine repeat protein G (VgrG). VgrG, a puncturing

component (15) of the type VI secretion system (T6SS), is used by Gram-negative bacteria to deliver effectors into target cells via direct cell-cell contact (16). Further study is required to determine if 9610 possesses other distinct components of the T6SS and how the T6SS is used for microbial competition or pathogenesis.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. MEHX00000000. The version described in this paper is version MEHX01000000.

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We declare no conflicts of interest.

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