Draft Genome Sequence of *Tetzosporium hominis* VT-49 gen. nov., sp. nov., Isolated from the Dental Decay Plaque of a Patient with Periodontitis

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ABSTRACT

Here, we report the draft genome sequence of *Tetzosporium hominis* VT-49 gen. nov., sp. nov., isolated from the dental plaque of a patient with severe periodontal disease. The draft genome sequence was 2,780,751 bp in length with a 43.3% G+C content. We detected 3,001 genes, which are predicted to encode proteins that regulate both virulence and antibiotic resistance.

The novel *Tetzosporium* genus was isolated using previously described combined culture-based and gene-based methods (1–3) from the dental plaque of a patient with severe periodontitis. *T. hominis* VT-49 is a Gram-positive, aerobic, and rod-shaped bacterium.

The 16S rRNA gene of *T. hominis* VT-49 was found to possess ≥96% similarity with different members of the *Planococcaceae* family, namely, *Planococcus* spp., *Paenisporosarcina* spp., and *Sporosarcina* spp. The genome of *T. hominis* VT-49 was sequenced using a HiSeq 2500 platform (GAIIx, Illumina, USA) according to the manufacturer’s instructions, yielding 2,780,751 bp (43.4% G+C content) with a 120-fold coverage. The VT-49 genome sequence was assembled to 393 contigs using SPAdes version 3.5.0 and annotated using the NCBI Prokaryotic Genome Annotation Pipeline (4, 5). The VT-49 genome harbored 66 tRNAs, 15 rRNAs, 4 noncoding RNA operons, and 4,048 protein-coding sequences. Although *in silico* DNA-DNA hybridization (DDH) analysis is required to identify the species within the same order, we performed this analysis to double-check the 16S rRNA gene data. The DDH analysis performed using the genome-to-genome distance calculator algorithm confirmed that the genomes of *T. hominis* VT-49 and *Planococcus* spp., *Paenisporosarcina* spp., and *Sporosarcina* spp. belonged to two different species with a DDH value of less than 25%, which was well below the threshold value of 70% (6, 7).

Analysis of the fatty acids, quinolones, and polar lipids showed that MK-6 (17%), MK-7 (61%), and MK-8 (22%) were the major menaquinones of *T. hominis* VT-49, and the cell wall peptidoglycan belonged to the A4β type containing L-Orn-D-Glu. Simultaneously, *Planococcus* spp. had MK-6 (23.2%), MK-7 (46.4%), and MK-8 (30.3%), and the peptidoglycan type A4α (based on L-Lys-D-Glu); *Paenisporosarcina* spp. had MK-7 and/or MK-8 as the major menaquinones, along with the A4α type of peptidoglycan (L-Lys-D-Asp); and *Sporosarcina* spp. had MK-7 (>90%) with MK-6 (~2%) and the peptidoglycan type A4α L-Lys-Gly-D-Glu (8–10). Based on these characteristics, strain VT-49 was assigned to the novel genus and species *T. hominis*.

In the VT-49 genome, we identified the presence of protein-coding genes that confer resistance to antibiotics, such as the lactam utilization protein LamB, an organic hydroperoxide resistance protein, as well as multidrug-resistant transporters of the ATP-binding cassette (ABC) family, the multidrug and toxic compound extrusion (MATE)
family, and the major facilitator superfamily (MFS). Virulence factors, such as hemolysin D, metalloproteases, peptidases, deoxyribonucleases, ribonucleases, flagellar components, and adhesins, were identified in the VT-49 genome. Moreover, we identified the virulence factors that were typical to the collagenase-like protease and amine oxidase of other periodontal pathogens (11). Follow-up studies on T. hominis VT-49 and bacteriophages associated with this microorganism would enable us to understand explicitly its implications in human pathologies and its possible role in periodontal pathologies (12, 13).

**Accession number(s).** This complete genome sequence has been deposited in GenBank under the accession no. NOKQ00000000.

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