




# 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  $\leq 96\%$  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 (GAllx, 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 A4 $\beta$  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 A4 $\alpha$  (based on L-Lys-D-Glu); *Paenisporosarcina* spp. had MK-7 and/or MK-8 as the major menaquinones, along with the A4 $\alpha$  type of peptidoglycan (L-Lys-D-Asp); and *Sporosarcina* spp. had MK-7 (>90%) with MK-6 (~2%) and the peptidoglycan type A4 $\alpha$  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)

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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](https://doi.org/10.1186/s13099-017-0187-8).

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