

BACKGROUND

More than 75 species/species-level phylotypes of spirochetes belonging to the genus *Treponema* inhabit the human oral cavity. The phylogroup 2 species *T. denticola* is associated with periodontitis, a serious oral infectious-inflammatory disease. *T. putidum* is a closely related species (originally isolated from human periodontitis lesion) whose clinical relevance and physiology remain largely unknown. We have sequenced the whole genome of 4 human oral *T. putidum* isolates and compared them with 17 human *T. denticola* strains.

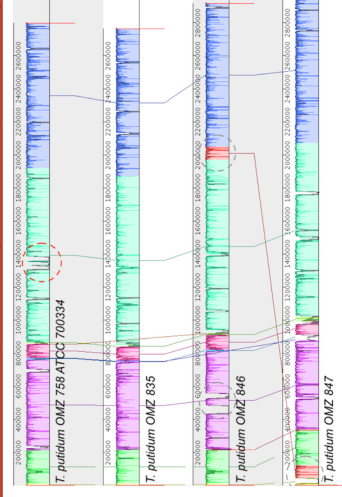
METHODS

T. putidum strains (supplied by Dr. Chris Wyss) were cultivated anaerobically in TYGVS medium and their genomic DNA was purified (Promega, Wizard genomic DNA purification kit). Whole genomes were sequenced using both the Oxford Nanopore Technology MinION (R9.4) and Illumina Hi-Seq (PE150) platforms. Hybrid *de novo* assembly was performed using canu and pilon. The complete genome sequences were annotated using prokka and NCBI PGAP, and compared using roary and KEGG tools.

RESULTS

The average genome size for the human oral *T. putidum* strains was 2.86 Mbp, with a GC content of 37.24%. There were ca. 2,700 predicted coding sequences (CDs) in each strain. Two sets of the 16S-23S-5S rRNA operon were observed in all *T. putidum* genomes. We detected the trNA-Gly-CCC in all 4 *T. putidum* strains but not in any *T. denticola* strain ($n = 17$). The average nucleotide identities (ANI) within the *T. putidum* genomes ($n = 4$) was 98.4%. ANI between *T. putidum* and *T. denticola* strains was 88.3%. Pan-genome analysis of these 21 oral treponeme genomes revealed a core gene set of 602 genes. *T. putidum* and *T. denticola* species carried 2,324 and 4,837 specific genes, respectively. They shared 1,369 genes (16% of pan-genome size) in common. Prophage regions were predicted in all *T. putidum* strains. The lack of dentilisin and sialidase genes in the *T. putidum* genomes is consistent with their reported phenotypic characteristics. *T. putidum* possess unique sets of genes absent in *T. denticola* species such as the altronate dehydratase (EC:4.2.1.7) and 2-keto-3-deoxygluconate permease (K02526) involved in D-Galacturonate degradation and proton symporter activity, respectively.

T. putidum genome sequences alignment



All the chromosomal sequences are fully complete and circular. Sequences are linearized to start at the *dnaA* gene. *T. putidum* strains were aligned with the type strain ATCC 700334^T by MAUVE (left) and MUMMER (right). Minimal genome rearrangements were detected in this species. Red circles indicate insertion in the reference strain ATCC 700334^T at ca. 1.3 Mbp. Grey circles indicate insertions in OMZ 846 at ca. 500 kbp and 2 Mbp, and insertion in OMZ 847 at the start.

T. putidum predicted genomic islands

