

In-depth sequence analysis of highly-conserved *pyrH* gene to study distributions of oral treponemes in periodontal disease versus health

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ABSTRACT

Background: More than 75 species/species-level phylotypes of oral treponeme bacteria inhabit the oral cavity. However, their respective genomic compositions and clinical distributions remain poorly understood.

Objectives: To compare distributions of phylogroup 1 and 2 oral treponemes in subjects with various periodontal health conditions, via sequence analysis of a highly-conserved treponeme 'housekeeping' gene.

Methods: Subgingival plaque samples were collected from Chinese subjects with chronic periodontitis (n=5), aggressive periodontitis (n=4), gingivitis (n=5), and healthy controls (n=4). Samples were analyzed by a PCR/plasmid clone sequencing-based approach, using primer sets targeting the *pyrH* gene. Data was analyzed using various computational/bioinformatic approaches.

Results: 1,227 quality-filtered *pyrH* gene sequences were obtained (mean 66.2±9.6 sequences per subject), which were assigned to 33 '*pyrH* genotypes' (97% identity cut-off). 538 *pyrH* sequences (17 *pyrH* genotypes) corresponded to phylogroup 1 treponemes (including '*T. vincentii*', *Treponema medium*, and '*Treponema sinensis*' taxa). 689 *pyrH* sequences (16 *pyrH* genotypes) corresponded to phylogroup 2 taxa. Correlations between *pyrH* genotype distributions and disease status were complex. One *pyrH* genotype, which was phylogenetically-related to *T. denticola* GM-1/MS25 strains, was highly prevalent: being detected in 17/18 subjects.

Conclusions: Both healthy and periodontally-diseased subjects harbor multiple genetic lineages corresponding to the same treponeme species/phylotype within their subgingival niches.