

Microbial Signatures of Peri-implantitis: 16S rRNA Sequencing Reveals Fusobacteria Enrichment

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Introduction

Peri-implantitis is a biofilm-mediated inflammatory disease characterized by dysbiosis of the peri-implant microbiome. Understanding microbial community differences between healthy implants and diseased sites may provide insights into disease pathogenesis and therapeutic targets. This study employed 16S rRNA gene sequencing to characterize the microbial composition associated with peri-implantitis compared to healthy implant sites.

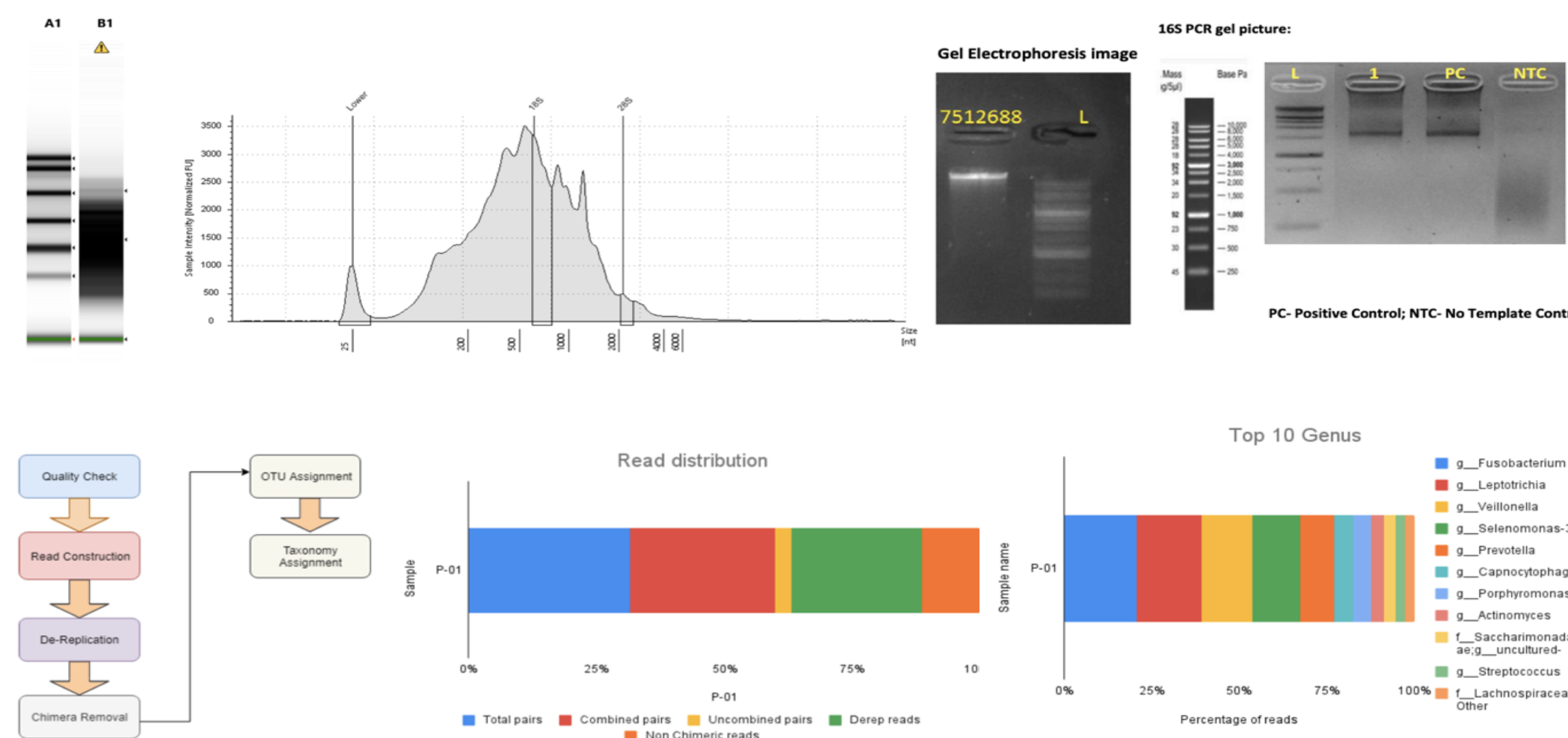
Aim

To study the microbial composition in peri-implant plaque samples using 16s rRNA sequencing

Materials & Methods

Dental plaque samples were collected from peri-implantitis and healthy implant sites. DNA was extracted and amplified for the V3–V4 region of the 16S rRNA gene, followed by sequencing on the Illumina platform. Quality control was performed using FASTQC, chimeric reads were removed with VSEARCH, and operational taxonomic units (OTUs) were clustered at 97% similarity. Taxonomic classification was performed against the SILVA-132 database. Alpha diversity (Chao1, Shannon indices) and relative abundance at the phylum and genus levels were analyzed.

Experimental Results



Conclusion

The peri-implantitis microbiome is characterized by enrichment of Fusobacteria, particularly *Fusobacterium* spp., highlighting its role in disease progression. 16S rRNA sequencing provides valuable insights into microbial shifts associated with peri-implant disease and underscores the importance of microbial surveillance for early detection and management.

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