Microbiome profiling in peri-implantitis: comparative insights from implant sites and saliva

Lucinda J. Bessa[1], Conceição Egas[2], Carolina Pires[3], Luís Proença[1], Paulo Mascarenhas[1], Ricardo J. Pais[1], Helena Barroso[1], Vanessa Machado[1], João Botelho[1], Gil Alcoforado[1], José João Mendes[1] and Ricardo Alves[1]

[1] Egas Moniz Center for Interdisciplinary Research (CiiEM); Egas Moniz School of Health & Science, Caparica, Almada, Portugal

[2] Genoinseq – Next Generation Sequencing Unit, Biocant, BiocantPark, Núcleo 04, Lote 8, Cantanhede, Portugal

[3] Instituto Universitário Egas Moniz (IUEM), Egas Moniz School of Health & Science, Caparica, Almada, Portugal

lbessa@egasmoniz.edu.pt

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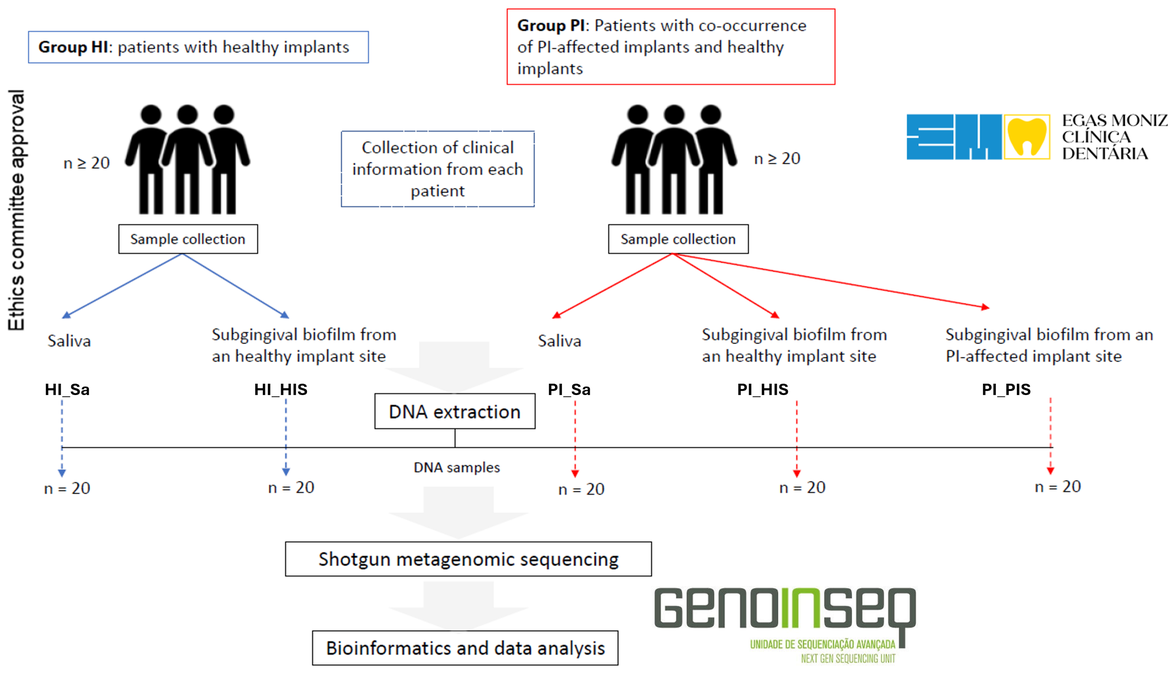
INTRODUCTION

The increasing use of dental implants as a preferred option for tooth replacement has been accompanied by a rising prevalence of peri-implant diseases, particularly **peri-implantitis (PI)** [1]. PI is a biofilm-mediated, chronic inflammatory condition marked by progressive peri-implant bone loss, ultimately leading to implant failure [2]. Despite its clinical importance, the microbial mechanisms underlying PI remain insufficiently understood. Clarifying the nature of microbial dysbiosis in PI is essential for advancing knowledge of its pathogenesis and informing the development of more effective diagnostic and management strategies. **AIMS:** This study aimed to characterise the composition, diversity, and functional potential of the subgingival microbiome in both healthy and PI-affected dental implants. Additionally, it explored the extent to which the salivary microbiome reflects subgingival microbial profiles, offering potential as a non-invasive indicator of peri-implant health.

MATERIALS AND METHODS



RESULTS

- Fifty-eight bacterial species were identified with relative abundance >1% in at least one group. The cumulative relative abundances were 78.95% (HI_Sa), 76.75% (HI_HIS), 79.07% (PI_Sa), 77.95% (PI_HIS), andb69.56% (PI_PIS) (Figure 1A)
- Alpha diversity, assessed by Hill diversity metrics (species richness, Shannon, Simpson indices), showed no significant differences between the saliva groups or among the subgingival groups ($p > 0.05$, Kruskal-Wallis) (Figure 1B)
- Beta diversity analysis (PERMANOVA based on Bray-Curtis and Jaccard indices) also revealed no significant differences in community structure between any two subgingival biofilm groups ($p > 0.1$) (data not shown)

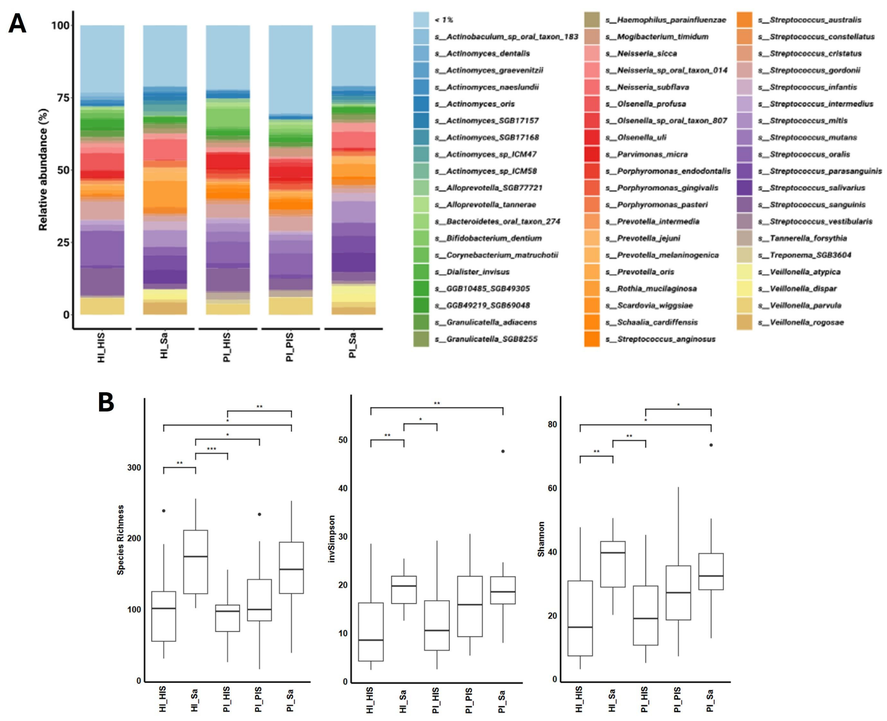


Figure 1. A) Relative abundances (>1%) of the bacterial composition at the species level in each study group. **B)** Hill diversity indices (Species richness, Shannon and Inverted Simpson) of the bacterial communities of the five study groups. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, based on the Kruskal-Wallis rank.

- High-quality Log-ratio abundance and differential ranking analysis identified key bacterial species distinguishing health from disease
- PI-associated species included *Mogibacterium timidum*, *Schaalia cardiffensis*, *Parvimonas micra*, *Filifactor alocis*, *Porphyromonas endodontalis*, *Porphyromonas gingivalis*, and *Olsenella uli*, suggesting their involvement in disease progression (Figure 2)
- In contrast, *Neisseria* spp., *Haemophilus parainfluenzae*, *Actinomyces naeslundii*, *Rothia mucilaginosa*, and *Rothia aeria* were more abundant in healthy implants, indicating possible protective roles (Figure 2)
- Notably, similar microbial shifts were observed in saliva (Figure 3)
- Functionally, PI-associated microbiomes were enriched in arginine and polyamine biosynthesis pathways, which are linked to microbial virulence and inflammation (data not shown)
- Healthy sites displayed higher activity in nucleotide biosynthesis, glucose metabolism, and tetrapyrrole biosynthesis, which support microbial stability and tissue homeostasis (data not shown)

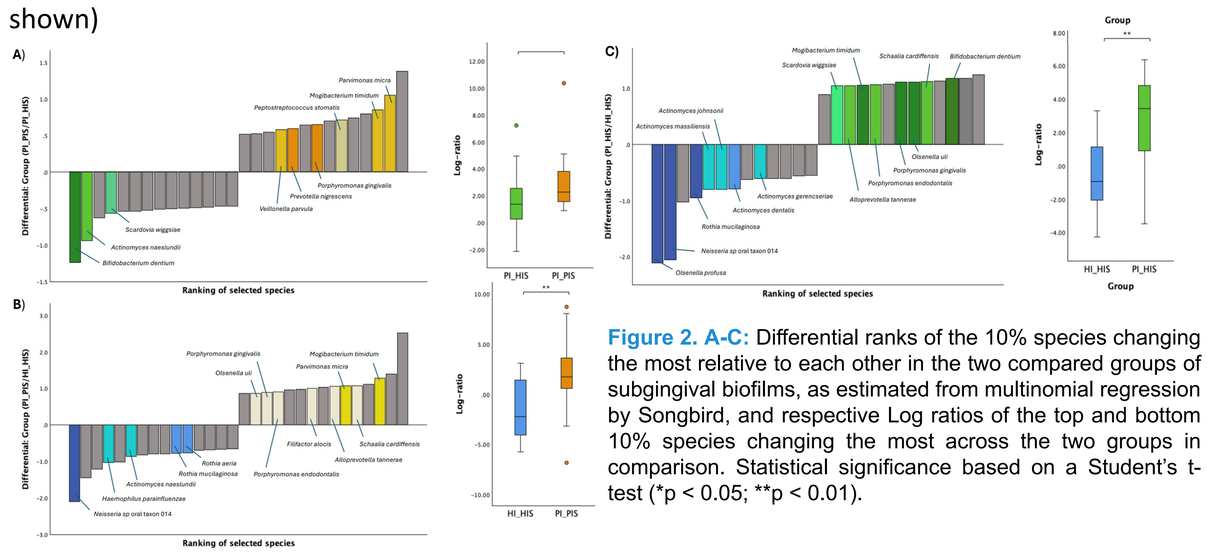


Figure 2. A-C: Differential ranks of the 10% species changing the most relative to each other in the two compared groups of subgingival biofilms, as estimated from multinomial regression by Songbird, and respective Log ratios of the top and bottom 10% species changing the most across the two groups in comparison. Statistical significance based on a Student's t-test (*$p < 0.05$; **$p < 0.01$).

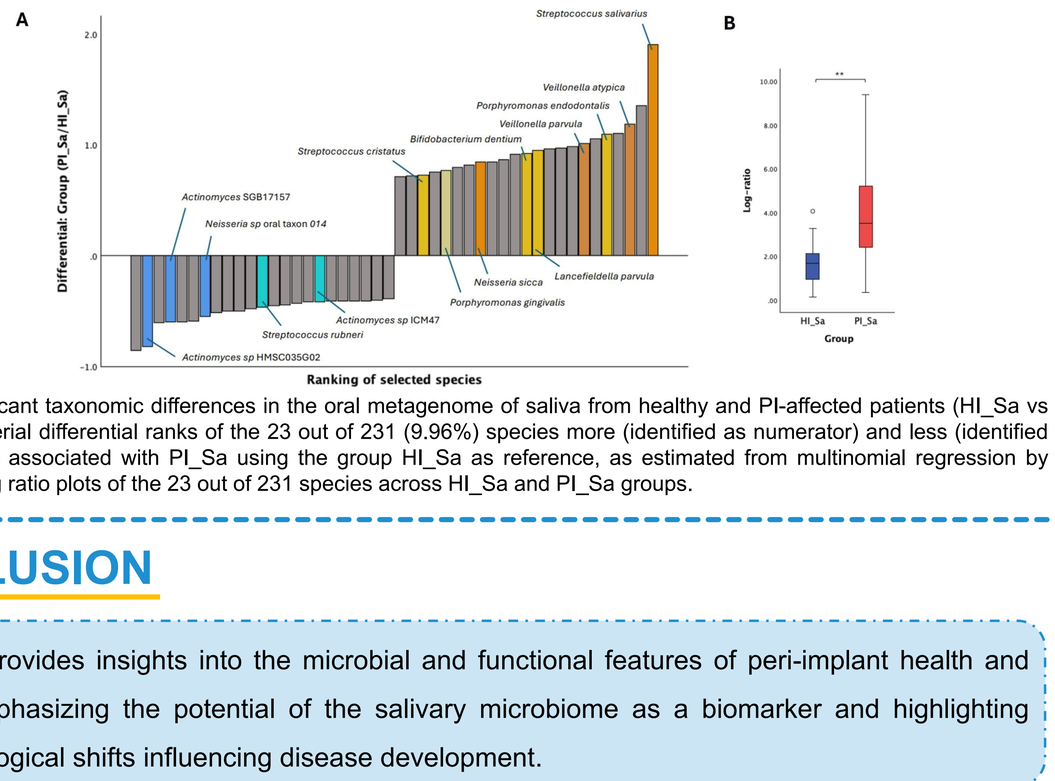


Figure 3. Significant taxonomic differences in the oral metagenome of saliva from healthy and PI-affected patients (HI_Sa vs PI_Sa). A) Bacterial differential ranks of the 23 out of 231 (9.96%) species more (identified as numerator) and less (identified as denominator) associated with PI_Sa using the group HI_Sa as reference, as estimated from multinomial regression by Songbird. B) Log ratio plots of the 23 out of 231 species across HI_Sa and PI_Sa groups.

CONCLUSION

This study provides insights into the microbial and functional features of peri-implant health and disease, emphasizing the potential of the salivary microbiome as a biomarker and highlighting broader ecological shifts influencing disease development.

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This study has been published. For furthter details go here

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