INVESTIGATING THE ORAL MICROBIOME AS A POSSIBLE BIOMARKER FOR DISORDERS OF GUT BRAIN INTERACTION

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Buccal microbiome analysis in 92 adults identified specific bacterial taxa that differentiate functional dyspepsia and irritable bowel syndrome subtypes, though overall microbial diversity did not differ between DGBI patients and healthy controls.

KEY POINTS

- Overall alpha and beta diversity of the buccal microbiome showed no significant differences between DGBI patients and healthy controls, between DGBI phenotypes, or between most subtype comparisons
- Individuals with overlapping functional dyspepsia and IBS had significantly lower microbial diversity compared to controls
- Candidatus Saccharibacteria was enriched in functional dyspepsia, particularly the epigastric pain subtype (LDA score 3.69, p=0.03), while genus Prevotella was increased in IBS with diarrhea compared to mixed IBS (LDA score 4.86, p=0.04)
- Several microbial species showed positive associations with higher anxiety and depression scores, though these did not remain significant after false discovery rate correction
- The authors conclude that the buccal microbiome may be a useful non-invasive tool for differentiating DGBI subtypes and potentially identifying targets for microbial modulation

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