Differential oral, vaginal, and stool microbial signatures in patients with and without endometriosis

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Abstract

Objective To identify a diagnostic microbial signature for endometriosis. **Design** Prospective cohort study **Setting** Nepean Hospital and UNSW Microbiome Research Centre, St George Hospital, Australia **Population** 64 age- and sex-matched subjects (n=19 HC; n=24 N-ENDO and n=21 ENDO). All study participants, besides healthy controls, underwent laparoscopic surgical assessment for endometriosis, and histology was performed on excised lesions. **Methods** Oral, stool, and vaginal samples were self-collected at a single time point for healthy controls, and pre-operatively for patients undergoing laparoscopy. Samples underwent 16S rRNA amplicon sequencing, followed by bioinformatics analysis. **Main Outcome Measures** Compositional differences between cohorts as identified by diversity analyses, and differentially abundant microbial taxa, as identified by LEfSE analysis. **Results** The composition of the oral, stool, and vaginal microbiota is different between healthy controls and patients with and without endometriosis. Differentially abundant taxa are present within each cohort. Particularly , *Fusobacterium* was enriched in the oral samples from patients with moderate/severe endometriosis. **Conclusions** Distinct taxonomic and compositional differences were found between the microbiota in the mouth, gut and vagina of patients with and without endometriosis and healthy controls. *Fusobacterium* is noted as a key pathogen in periodontal disease, a common comorbidity in endometriosis. These findings support a role for the oral, vaginal, and stool microbiome in endometriosis, and present potential for microbial-based treatments and the design of a diagnostic swab.

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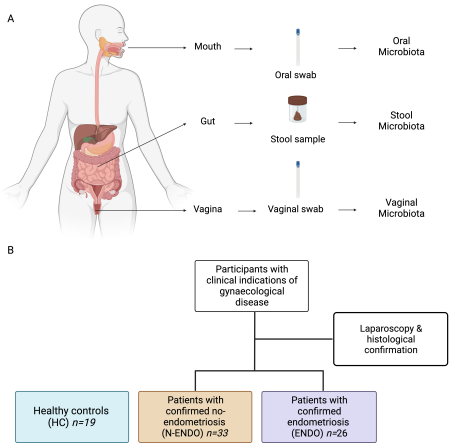
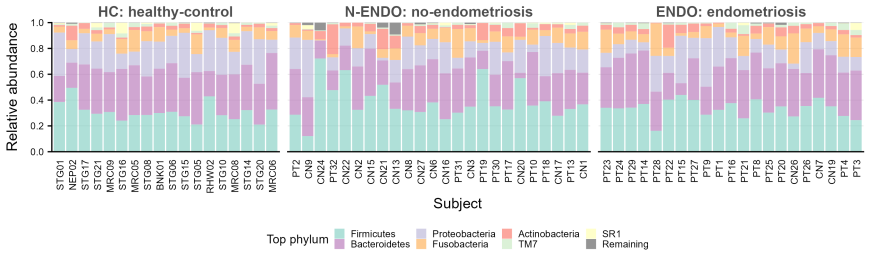


A) Oral



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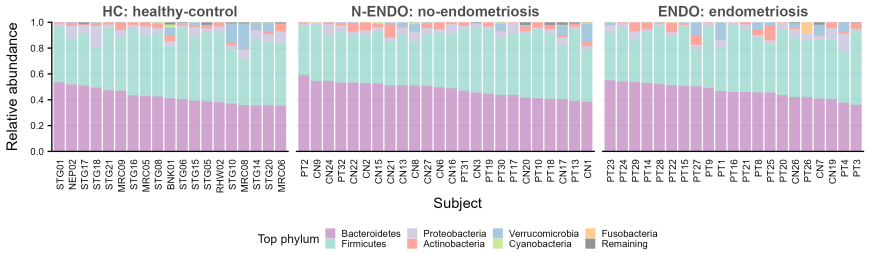

C) Vaginal