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

Chloe HICKS<sup>1</sup>, Mathew Leonardi<sup>2</sup>, Xin-Yi CHUA<sup>1</sup>, Lisa MARI-BREEDT<sup>1</sup>, Mercedes Espada<sup>2</sup>, Emad El-Omar<sup>1</sup>, George CONDOUS<sup>2</sup>, and Fatima El-Assaad<sup>1</sup>

<sup>1</sup>University of New South Wales Saint George and Sutherland Clinical Campuses <sup>2</sup>The University of Sydney Nepean Clinical School

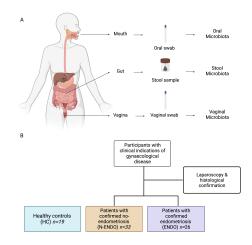
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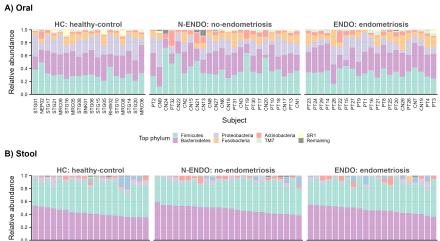
## Abstract

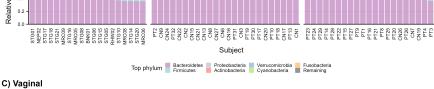
**Objective** To identify a diagnostic microbial signature for endometriosis. **Design** Prospective cohort study **Setting** Nepean Hospital and UNSW Microbiome Research Centre, St George Hospital, Australia **Population** 64 age- and sex-matched subjects (n=19 HC; n=24 N-ENDO and n=21 ENDO). All study 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. *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.

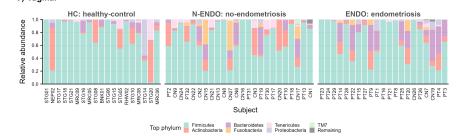
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11Dec\_BJOG\_Microbial signatures of endometriosis\_HICKS C et al., 2023.docx available at https://authorea.com/users/766041/articles/806043-differential-oral-vaginal-and-stool-microbial-signatures-in-patients-with-and-without-endometriosis

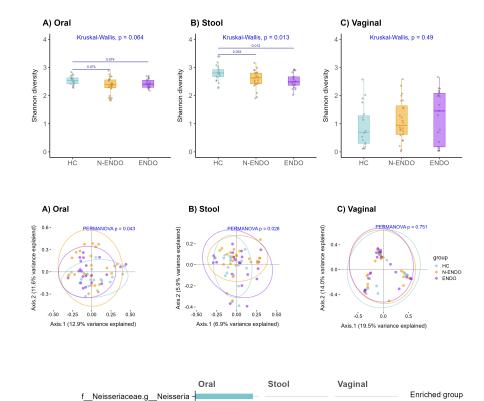








0.2 0.0



HC N-ENDO ENDO

Pasteurellaceae.g\_\_Actinobacillus f\_Burkholderiaceae.g\_Lautropia Neisseriaceae.g\_

F16.g\_

Actinomycetaceae.g\_ Clostridiales.f\_\_.g\_

f\_Streptococcaceae.g\_Lactococcus f\_Lachnospiraceae.g\_Butyrivibrio

f\_Veillonellaceae.g\_Veillonella f\_Veillonellaceae.g\_Bifidobacterium f\_Veillonellaceae.g\_Veillonella

f\_Lachnospiraceae.g\_Lachnospira RF32.f\_.g\_ f\_Ruminococcaceae.g\_Butyricicoccus Victivallaceae.g\_

Peptococcaceae.g\_\_\_\_ f\_Erysipelotrichaceae.g\_\_[Eubacterium] Bacteroidales.f\_\_.g\_\_\_ f\_Veillonellaceae.g\_Phascolarctobacterium f\_Lactobacillaceae.g\_Lactobacillus f\_Enterobacteriaceae.g\_Salmonella f\_Pseudomonadaceae.g\_Pseudomonas f\_Bacillaceae.g\_Bacillus f\_Listeriaceae.g\_Listeria f\_Leptotrichiaceae.g\_Sneathia f\_Pasteurellaceae.g\_Haemophilus [Weeksellaceae].g\_\_\_\_ f\_[Paraprevotellaceae].g\_Escherichia

f\_Enterobacteriaceae.g\_Escherichia f\_Enterococcaceae.g\_Enterococcus f\_Comamonadaceae.g\_Tepidimonas f\_Thermaceae.g\_Thermus

Bacteria.p\_\_.c\_\_.o\_\_.f\_\_.g\_ RF39.f\_\_.g\_ Peptococcaceae.g\_

f



0 1 2 3 4 50

1 2 3 4 50

LDA effect size

1 2 3 4

