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

Chloe HICKS¹, Mathew Leonardi², Xin-Yi CHUA¹, Lisa MARI-BREEDT¹, Mercedes Espada², Emad El-Omar¹, George CONDOUS², and Fatima El-Assaad¹

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

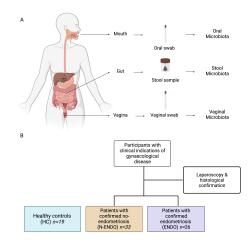
April 10, 2024

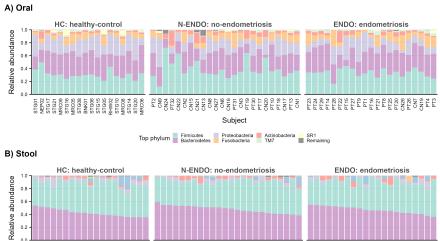
Abstract

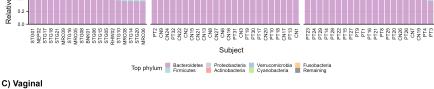
Objective To identify a diagnostic microbial signature for endometriosis. **Design** Prospective cohort study **Setting** Nepean Hospital and UNSW Microbiome Research Centre, St George Hospital, Australia **Population** 64 age- and sex-matched subjects (n=19 HC; n=24 N-ENDO and n=21 ENDO). All study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

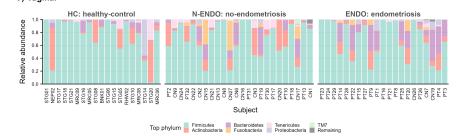
Hosted file

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

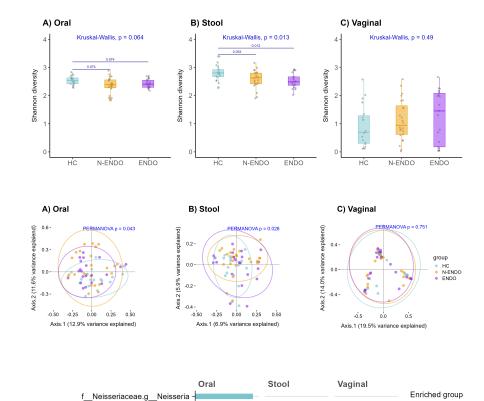








0.2 0.0



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

