

Human Endometrial Microbiota at Term of Normal Pregnancies

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Background:

The endometrium poses challenges for metagenomic analysis due to low prokaryotic load and sample contamination. The relationship between the bacterial composition and endometrial physiopathological conditions is not yet clear. However, it is known that the microbiome is closely linked to women's health and pregnancies.

Methods and Results:

The study was conducted on endometrial tissue of 19 pregnant women after elective caesarean delivery (ECD). Biopsies were taken after delivery of newborns and placenta release. Bacterial composition analysis was performed by a deep metabarcoding NGS procedure addressing the V5-V6 hypervariable region of the 16S rRNA gene. 2.4 million paired-end reads were obtained in 57 distinct datasets (corresponding to analysis in triplicate) and analysed through ASV inference and taxonomic classification with BioMaS. Taxonomic analysis showed six bacterial genera (*Propionibacterium*, *Escherichia*, *Staphylococcus*, *Acinetobacter*, *Streptococcus* and *Corynebacterium*) present in most samples that may be part of the core endometrial microbiota.

Conclusions and Significance:

We succeeded in performing DNA metabarcoding analysis of the difficult endometrial tissue in women subjected to ECD. Results showed the presence of an endometrial core microbiome, including six bacterial genera. This analysis paves the way for further studies investigating the correlation between the endometrial microbiome composition and successful pregnancies.

Keywords:

Endometrium; microbiota; metabarcoding; metagenomics.

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References:

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Thematic Area:

- Microbiome: from Research to Clinics

Infrastructures:

This project took advantage of the omics and computational facilities provided by the Italian Node of ELIXIR (ELIXIR-IT), the European Research Infrastructure for Life Science, including the advanced equipment acquired by the CNR BiOmics infrastructural project (PIR01_00017) for carrying sequencing and subsequent bioinformatics analysis.