

A picture of the vaginal microbiome during pregnancy and puerperium

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Background:

The composition of the vaginal microbiome can vary throughout a woman's life and, it undergoes marked changes during pregnancy. The aim of this study was to analyze the vaginal environment and identify the presence of antibiotic resistance genes in a cohort of women throughout different gestational ages and puerperium.

Methods and Results:

For each subject (n=63) and time point (n=4), both the vaginal bacterial composition (16S rRNA sequencing) and the vaginal metabolic profiles (¹H-NMR) were analyzed.

During the pregnancy evolution, we found a significant increase of *Lactobacillus* and related metabolites (lactate and amino acids) and a decrease of bacterial vaginosis (BV)-related bacteria, whereas, during the puerperium, we observed the opposite behavior. BV and the presence of *Megasphaera* were correlated to the positivity to antibiotic resistance genes (*ermB*, *ermF*, *tet(W)*). Finally, *Gardnerella vaginalis* clade 2, or the presence of multiple clades, was related to major shifts in the vaginal microbial composition.

Conclusions and Significance:

A deep comprehension of the vaginal ecosystem may unravel pregnancy's pathophysiology and provide markers to identify women at risk of complications. Considering that microbial communities can be transferred from the mother to the newborn, this study can open new perspectives for infant's microbiome development and future health.

Keywords:

Vaginal microbiota, pregnancy, *Gardnerella vaginalis*, resistance genes, metabolome

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Thematic Area:

- Frontiers in Microbiome Research

Infrastructures:

N.A.