Differential composition of vaginal microbiome is associated with successful intrauterine insemination (IUI) in couples with idiopathic infertility: a prospective observational study.

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Background. Vaginal and seminal microbiome have gained increasing interest for their involvement in reproductive health and fertility. However, their role in reproductive outcome is not fully ascertained yet. In this study, we aimed to characterize vaginal and seminal microbiome in 23 couples with idiopathic infertility undergoing intrauterine insemination (IUI) treatment, correlating it to the clinical pregnancy rate after IUI.

Methods. Vaginal swabs and seminal fluids were collected on the day of IUI procedure and analyzed through PCR amplification of variable regions 3 and 4 (V3–V4) of 16S rRNA genes and Illumina MiSeq sequencing. The taxonomic data were then correlated to IUI success, together with a panel of clinical and laboratory variables.

Results. We observed a differential composition of vaginal microbiome in our cohort of women with different IUI outcome. In particular, women experiencing IUI success showed a clear domination by *L. crispatus*, marker of a healthy vaginal ecosystem, while women experiencing IUI failure featured a more diverse pattern, even with non-*Lactobacillus* species. Importantly, considering all investigated variables, vaginal *L. crispatus* domination was the only factor strongly correlated to IUI success (p-value = 0.0002).

Discussion. Our results strengthen the potential role of *L. crispatus* in promoting a favorable environment for pregnancy and suggest that microbiome characterization could be useful, together with standard clinical and laboratory assessments, in the pre-IUI evaluation of infertile couples.