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O0445 Characterization of vaginal microbiome in women with preterm labor with intact membranes

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Background: One of the main clinical challenges in the management of women with preterm labor with intact membranes (PTL) is the detection of those who will actually deliver within a few days and whose newborns will have a worse neonatal outcome. Microbial invasion of the amniotic cavity (MIAC) and intraamniotic inflammation (IAI) are associated with worse outcome. Most of the microorganisms that cause MIAC have an endogenous origin. The purpose of this study was to characterize the vaginal microbiome in patients with PTL.

Materials/methods: Sixty-nine patients with PTL were included and categorized into 3 groups according to amniotic fluid (AF) analysis: MIAC (positive amniotic fluid culture and/or detection of microbial 16S ribosomal RNA); IAI (Interleukin-6 (IL-6) ≥13.4 ng/mL without MIAC); and control (no MIAC no IAI). Vaginal swabs from these patients were collected. DNA was extracted (PureLink™ Microbiome, Invitrogen) and a 16S rRNA sequencing library was constructed (Nextera XT, Illumina) targeting the V3 and V4 hypervariable regions. Sequencing was performed on a MiSeq platform. Taxonomic affiliations were assigned using the *rdp_classifier*. Statistical analyses were performed using R version 3.4.2**.**

Results: Seven women presented IAI; 18 MIAC; and 44 were controls. Alpha diversity (Shannon index) was higher in IAI and MIAC group than in controls. At *phylum* level, *Firmicutes* and *Synergistetes* were significantly associated with better clinical and biological phenotype, whereas *Fusobacteria* was significantly associated with a worse one. At the family level, the percentage of *Lactobacillaceae* was higher in the control group than in both MIAC and IAI. Presence of *Lactobacillaceae* was inversely correlated with clinical phenotype ($r=-0.31$, $p<0.05$), IL-6 concentration in AF ($r=-0.28$, $p<0.05$) and glucose in AF ($r=-0.32$, $p<0.05$). In the MIAC group, the family corresponding to the microorganisms identified in the AF was found (>1% reads) in 12/18 samples (min 3.4%, max 81.0%).

Conclusions: Changes in the vaginal microbiome correlate with clinical and biological phenotypes and may provide new insights into the pathophysiology of PTL. Further studies will be required to establish the potential role of the vaginal microbiome to predict the risk of MIAC and IAI in patients with PTL in addition to IL-6 levels.