DIFFERENCES IN THE MICROBIAL COMPOSITION IN CORD BLOOD AND PLACENTA BY MATERNAL IBD STATUS
- results from the MECONIUM study -

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BACKGROUND AND GOALS
Emerging evidence suggests the existence of diversified microbiota in low microbial biomass samples, including placenta and umbilical cord blood. Yet, the microbiome survey of those samples is challenging due to a high level of experimental and environmental contamination. Our data in pregnant women participating in the MECONIUM (Exploring MEChanisms Of disease tranSMission In Utero through the Microbiome) study showed significant differences in the gut microbiota by IBD status. Herein, we investigated whether microbial composition in cord blood or placenta is associated with maternal IBD status.

METHODS
Total DNA was extracted from 67 umbilical cord blood (23 IBD) and 41 placenta samples (13 IBD) using bead-beating methods. Bacterial 16S hypervariable V3-V4 region was amplified and sequenced on 2x250 paired-end Illumina HiSeq2500. Sequencing reads were further filtered by length and quality and assigned with taxonomy information by sequence similarity. Several negative controls were used to detect and filter out background contamination. We then compared the microbial diversity and composition at the phylum level between IBD cases and controls.

RESULTS

Diversified microbial communities were found in all umbilical cord blood and placenta samples. IBD mothers presented with significantly different relative abundance of Proteobacteria and Firmicutes in umbilical cord blood (Bonferroni-adjusted p=0.038 and 0.013, respectively) and Firmicutes in placenta (Bonferroni-adjusted p=0.05) as compared to the healthy controls (Figure 1A). The overall microbiome composition significantly differed by maternal IBD status (p-value=0.002) in both umbilical cord blood and placenta, by PERMANOVA test (Figure 1B).

![Figure 1A](image-url) Cord blood microbial composition at phylum level
![Figure 1B](image-url) Cord blood and placenta microbial composition at phylum level

**Figure 1.** Microbiome composition and diversity in umbilical cord blood and placenta. A. Heatmap plots presenting the microbial composition at the phylum level. Top bar color-coding indicates IBD status (* denote significant differential taxa by IBD status, p-value<0.05 by Kruskal-Wallis test with Bonferroni correction). B. Nonmetric multidimensional scaling (NMDS) plots presenting microbial diversity in umbilical cord blood and placenta by IBD status (p-value=0.002 by PERMANOVA test).

CONCLUSIONS
The 16S survey suggests that microbial composition and diversity in the umbilical cord blood and placenta samples from pregnant women are significantly altered by maternal IBD status. These finding warrant further studies to explore bacterial transmission from the mother to the baby in the setting of IBD.