



DIFFERENCES IN THE MICROBIAL COMPOSITION IN CORD BLOOD AND PLACENTA BY MATERNAL IBD STATUS

- results from the MECONIUM study -

J. Hu¹, J. Torres^{1,2}, Q. Mao^{1,3}, C. Eisele¹, L. Tarassishin¹, A. Barré¹, N. Nair¹, JF. Colombel⁴, I. Peter¹

1- Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai, New York, NY, United States; 2- Gastroenterology Division, Hospital Beatriz Ângelo, Lares, Portugal; 3- Thoracic Surgery, Nanjing Medical University Affiliated Cancer Hospital, Nanjing, Jiangsu, China; 4- Gastroenterology, Icahn School of Medicine at Mount Sinai, New York, NY, United States

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).

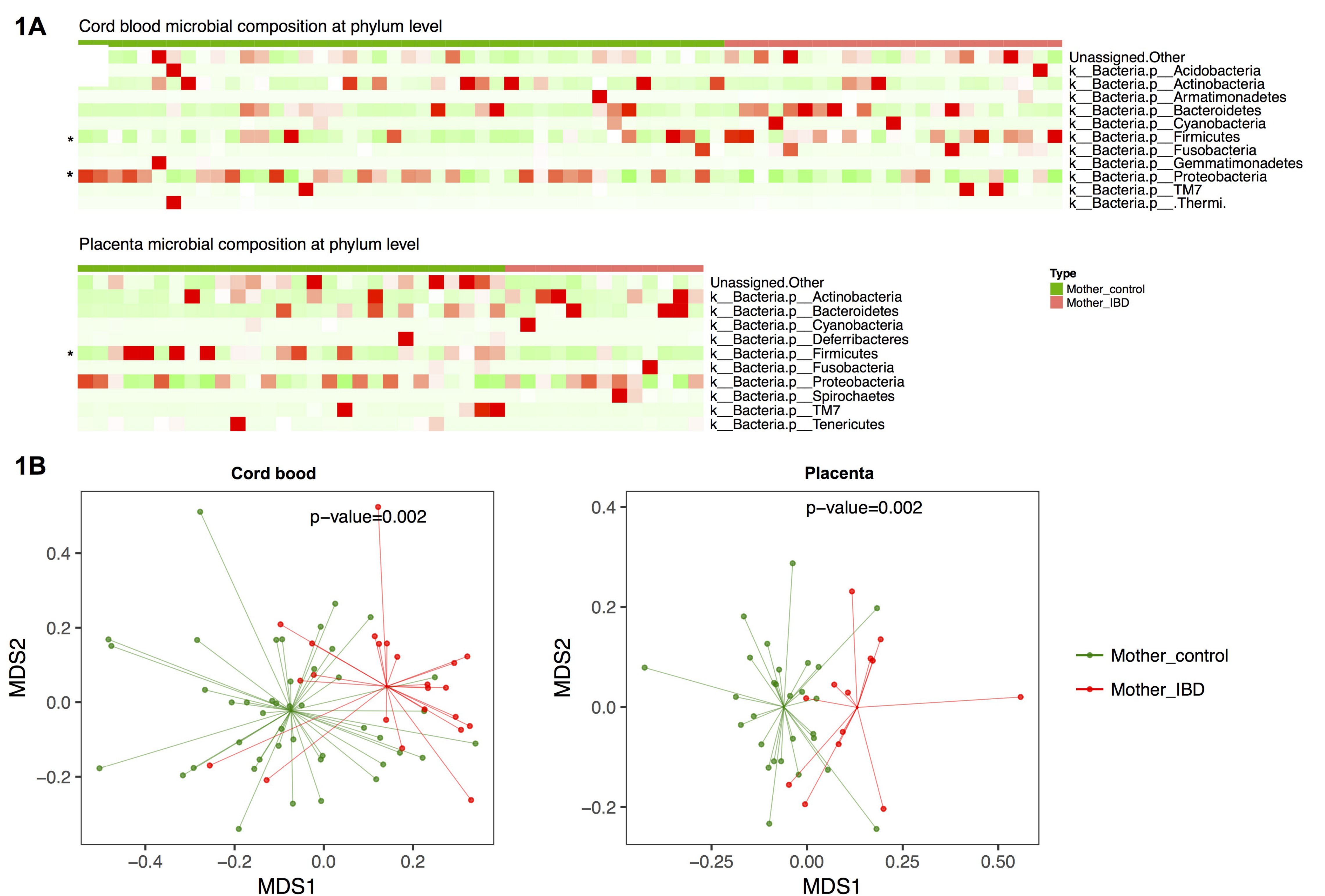


Figure 1. Microbial composition and diversity in umbilical cord blood and placenta. A. Heatmap plots presenting the microbial composition at the phylum level. Top bar color-coding indicates IBD status (* denote significant differential taxa by IBD status, p -value <0.05 by *Kruskal-Wallis* test with *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 findings warrant further studies to explore bacterial transmission from the mother to the baby in the setting of IBD.