P735 Exploring mechanisms of inflammatory bowel disease transmission in utero through the microbiome: the MECONIUM Study Pilot

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Background

New evidence suggests that the GI tract of newborns starts to become colonised in utero. The source of these microbiota is of continued interest as the initial colonisation of bacteria is believed to play a crucial role in the development of the immune system. Yet, no data exist on the effect of IBD on gut microbiota of pregnant women and the bacteria they pass to their newborns.

Methods

The MECONIUM Study is a prospective study aimed to investigate the role of IBD on pregnancy and baby's microbiome. Clinical data, stool, and saliva samples were collected from women with and without IBD during pregnancy. After delivery, serial stool samples were collected from the infants. The gut microbiota composition was evaluated using the 16s rRNA gene V3-V4 region.

Results

In this pilot, 10 pregnant women (5 with IBD) and their 10 infants provided a total of 67 samples (mother 14 stool and 14 saliva, and infant 9 meconium and 30 stool samples collected at days 7, 14, 30, 60, and 90). All IBD cases were in remission throughout pregnancy. No mother was being treated with antibiotics or probiotics at the time of stool collection. Mean gestational age was 39.2 weeks. Five infants were born via C-section (3 from IBD mothers), and none had complications at delivery. Maternal saliva microbiome clustered independently from the microbiome of maternal stool samples, which clustered separately from the infant´s stool (Figure 1A and 1B). The microbiome composition of pregnant women with IBD was significantly different from that of controls (p = 0.03) and was enriched in Enterobacteriaceae previously reported in non-pregnant IBD patients (Figure 1C). A trend towards a difference in the oral microbiome was observed between pregnant women with and without IBD (p = 0.07). Importantly, at the taxa level the LEfSe analysis identified differential features in the meconium and follow-up infant stool samples by IBD status, including the enrichment of Enterobacteriaceae (Figure 1C) in the meconium samples. No differences were observed in the microbiome of infants by delivery mode, likely because of a small sample size.

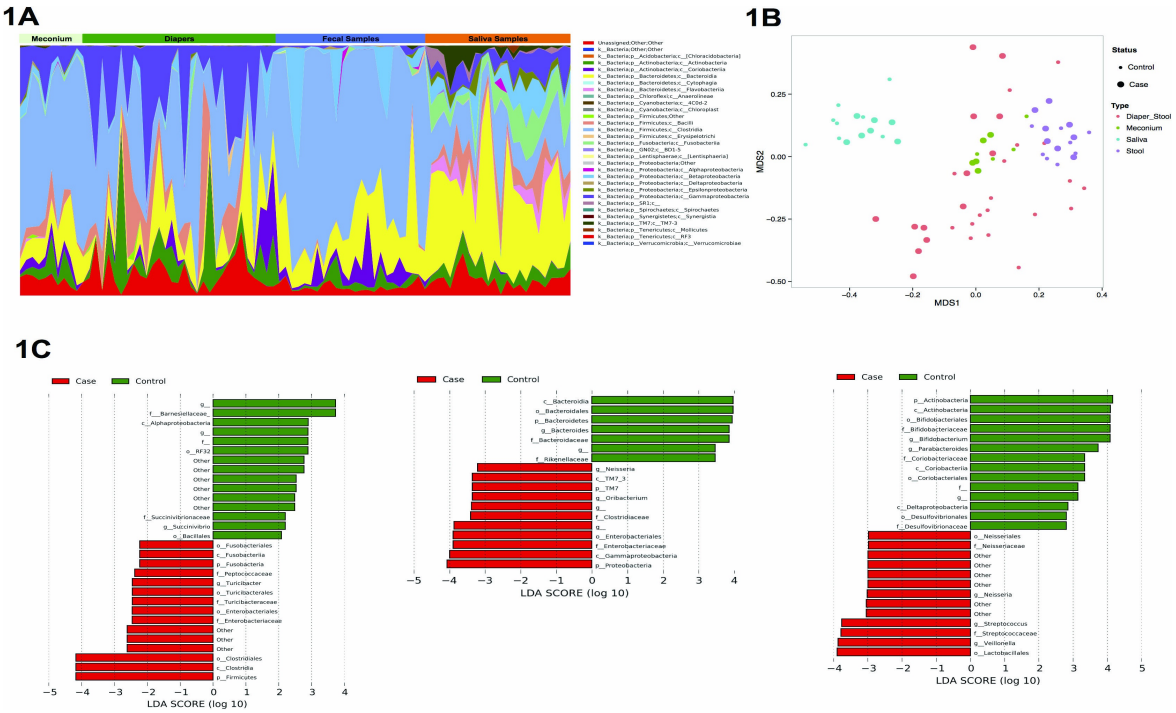

Figure 1. The microbiota composition of study samples. **1A.** The diversified microbiota at the class level for maternal stool, saliva, baby meconium, and baby diapers. **1B.** The overall microbiota dissimilarity measured by Bray-Curtis distance matrices at the genus level. Results show the distinct clusters of the microbiome in meconium and baby stool from maternal fecal and saliva samples. **1C.** LEfSe analysis of microbiota composition for cases (IBD mother or infants of IBD mothers) and controls.

Conclusion

Our findings suggest that pregnant women with IBD have a distinct faecal and oral microbiota composition compared with controls. The gut microbiome of mothers with IBD and their infants' meconium was enriched in IBD-associated Enterobacteriaceae. Ongoing recruitment will allow to validate these results and help identify particular bacterial strains transmitted from the mother to her baby in the context of IBD.

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