Delivery mode and intrapartum antibiotics affect the development gut mycobiome in children

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Introduction

The human gut microbiome consists of bacteria, viruses, fungi, archaea, and protozoa. Bacteria are the most studied part of microbiome but interest has recently grown towards fungi. Various health conditions, such as IBD, IBS, and colorectal cancer have been associated with an altered gut fungal microbiome, i.e. mycobiome. The development of fungal colonization and mycobiome is poorly understood in infants and children. Here we investigate the development of gut mycobiome in a prospective cohort study.

Materials and Methods

We enrolled 140 newborn infants at birth: 56 newborn born vaginally, 24 born vaginally and exposed to intrapartum antibiotics, and 60 born via Caesarean section. Stool samples were collected at birth (first-pass meconium), at 6 months, and at 18 months. All families gave their written informed consent for the study.We performed ITS gene sequencing for the samples using IonTorrent PGM platform. ITS sequences were analyzed using QIIME2. Taxonomic analysis was performed using UNITE database.

Results

We found a detectable mycobiome in all fecal samples. Meconium samples were dominated by *Candida*. At 6 months, the gut mycobiome consisted of mostly *Malassezia* and *Cystofilobasidium*, and at 18 months, the mycobiome had shifted towards *Trichosporon* and unidentified fungi.

Figure 1. Taxonomic figures for each time point, with the taxa drawn from phylum level to genus level

When comparing the gut mycobiome of infants born vaginally vs. infants born via C-section, we found statistically significant differences in alpha and beta diversity as well as relative abundances of fungi.

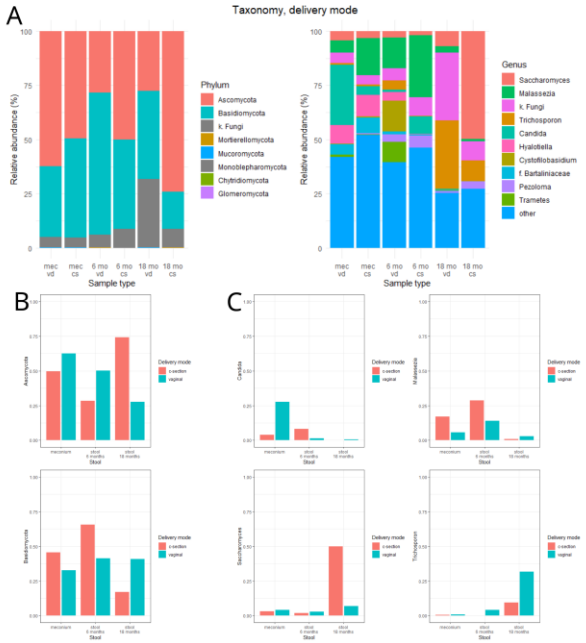

Figure 2. Taxonomic figures for each sample type based on the mode of delivery. A: Relative abundances of the taxa at the phylum (left) and genus (right) level. The top 10 most abundant taxa are colored in, and the rest are collapsed into the “other” group. B. Changes in the abundance of Ascomycota (top) and Basidiomycota (bottom) over time in the vaginal delivery and C-section delivery groups. C: Changes in the abundance of *Candida* (top left), *Malassezia* (top right), *Saccharomyces* (bottom left) and *Trichosporon* (bottom right) over time in the vaginal delivery and C-section delivery groups.

When comparing the gut mycobiome of infants exposed to intrapartum antibiotics vs. infants not exposed, we found statistically significant differences again in alpha ánd beta diversity, and relative abundances of fungi.

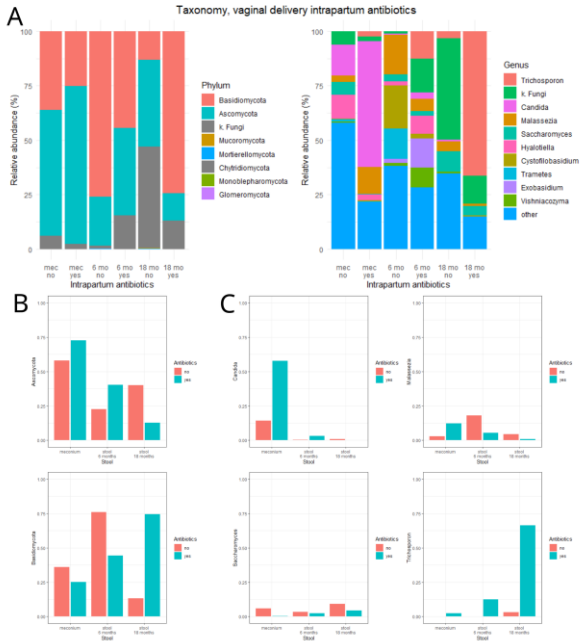

Figure 3. The taxonomic figures for each time point showing the effect of intrapartum antibiotic exposure. A: Relative abundances of the taxa at the phylum (left) and genus (right) level. The top 10 most abundant taxa are colored in, and the rest make up the “other” group. B. Changes in the abundance of Ascomycota (top) and Basidiomycota (bottom) over time in the groups with and without intrapartum antibiotics. C: Changes in the abundance of *Candida* (top left), *Malassezia* (top right), *Saccharomyces* (bottom left) and *Trichosporon* (bottom right) over time in the groups with and without intrapartum antibiotic exposure.

Conclusions

In this prospective cohort study, the development of human gut mycobiome was evident already at birth and continued to develop and change until 18 months of age.

Gut mycobiome was affected by the delivery mode and the usage of intrapartum antibiotics. These changes were detected still at the 18 months of age.

Gut mycobiome needs to be studied as a part of gut microbiome, because it may have significant health effects on infants at later life.

References

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Acknowledgements

Funders:
- Academy of Finland
- Finnish Pediatric Research Foundation

Science with Arctic Attitude