

TITLE: ASSOCIATION BETWEEN THE NEWBORNS' MICROBIOTA AND THE GESTATIONAL AGE

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ABSTRACT:

The first newborn's fecal matter is called meconium. The meconium's microbiota is acquired from the mother and represents the baby's gut microbial community. Possible microbial sources came from the umbilical cord, the mother's intestinal and vaginal microbiota and from the swallowed amniotic fluid. These microorganisms start the formation and regulation of nutritional and immunological functions, being determinant for susceptibility to future diseases. The aim of this work was to evaluate the microbial community in meconium of newborns and verify the influence of gestational age at meconium's bacterial diversity. A total of 102 meconium samples from babies born after 28 to 41 gestational weeks were collected at Hospital de Clínicas de Porto Alegre (HCPA), south region of Brazil. Microbial DNA was isolated using the QIAamp Fast DNA Stool Mini Kit (Qiagen, Valencia, CA). The V4 region of the 16S rRNA gene was amplified and sequenced using the Ion Torrent PGM platform. The sequences generated were processed following recommendations from the pipeline of the Brazilian Microbiome Project and grouped into operational taxonomic units (OTUs) with 97% similarity. A total of 2,206,608 high-quality sequences were obtained. They were grouped into 32,899 OTUs. Diversity analysis showed that the microbial diversity did not change from 28th to 41st weeks of gestational age, but the structure of the microbial community from the seventh to the ninth month of gestation was significantly different ($p < 0.05$). The meconium was almost entirely composed of *Proteobacteria* (with a total frequency of 47.9%), *Bacteroidetes* (22.6%) and *Firmicutes* (17.1%). OTUs identified as belonging to the *Pseudomonas* and *Prevotella* genera were the most abundant, with a total average per sample of 17.6% and 12.6% respectively. These genera together with *Escherichia/Shigella* and *Streptococcus* increase their relative abundance throughout the months. On the other hand, *Staphylococcus*, *Burkholderia*, *Bradyrhizobium*, and *Phenylobacterium*, usually associated with preterm delivery, decrease in the ninth month. To conclude, our data indicated the microbial diversity from the newborn's meconium did not change, but the microbial composition changed from the 28th to the 41st week of gestation.

Keywords: 16S rRNA, gestational age, meconium, microbial diversity

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