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ORIGINAL ARTICLE

Abundance and Composition of the Meconium Microbiota in Preterm Infants with Infections, Feeding Intolerance, or Necrotizing Enterocolitis

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SUMMARY

Background: **The role of the microbial flora of the gut of a newborn is of scientific and practical interest. The aim of this study was to assess the abundance and composition of the meconium microbiota in preterm infants with infections, feeding intolerance, or necrotizing enterocolitis (NEC).**

Methods: **Eighty-four preterm infants born by cesarean section were prospectively enrolled in this study. Out of the 28 diseased infants, 23 developed infections, including 8 cases of sepsis, 10 cases of pneumonia, 1 case of enterocolitis, and 4 cases of NEC. Fifty-six (66.67%) preterm infants without these characteristics served as control group. General clinical information (gender, gestational age, birth weight, presence of preterm rupture of membranes, Apgar 1-minute score, and duration of hospitalization) was collected. First-pass meconium samples were collected for 16S rRNA microbiological analysis.**

Results: **Compared with the control group, the diseased infants had a lower gestational age ($p < 0.001$) and lower body weight ($p = 0.014$). In addition, the hospitalization time of the diseased infants was longer than that of the control group ($p < 0.001$). On the α-diversity measure, there was no difference in species abundance and diversity between the two groups; on the β-diversity measure, the differences in the microbial composition of the two groups were subjected to PCoA analyses, which showed that there was a difference between the disease group and the control group. At the phylum level, the dominant phylum in both groups was *p_*Proteobacteria, with higher abundance of *p_*Firmicutes in the disease group. At the genus level, the dominant genus in both groups was *g_Novosphingobium*. Microbiome phenotype prediction by BugBase revealed that microbial phenotypes 'Gram-positive' and 'Anaerobic' were abundantly increased in the disease group; microbial function prediction did not differ between the two groups in terms of significant function.**

Conclusions: **The impact of infections, feeding intolerance, and NEC on a host is complex. Preterm infants delivered by cesarean section have *p_*Proteobacteria as the dominant phylum, with a higher abundance of *p_*Firmicutes in the disease group, a difference contributed by g_*Peptoniphilus*.**

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Supplementary Data

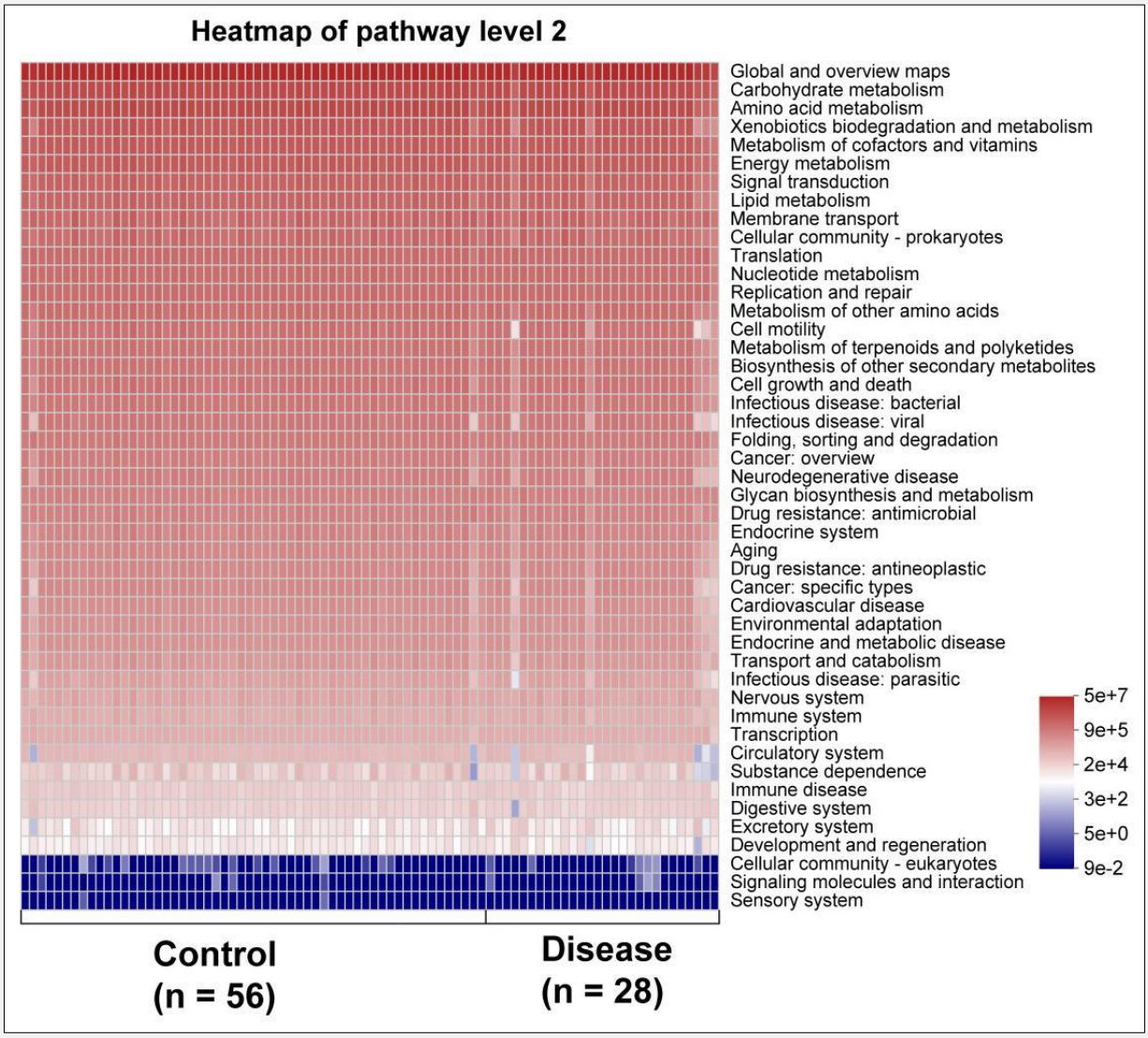


Figure S1. KEGG pathway analysis.