CHRD 2024: Abstract Submission Form

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Presenter Status
Post-Doctoral Fellows

Role in the project
Analyze Data
Write Abstract

Research Category
Basic Science

Title
Human milk microbiota: associations with human milk bioactive protein, minerals, and B vitamin profiles in the CHILD cohort

Background
Human milk (HM) is rich in bioactive components, including bacteria, which are often studied in isolation.

Objective
While previous research has shown that HM microbiota shapes infant gut colonization and health outcomes, the complex interactions between these bioactive components and HM's microbial composition remain poorly understood.

Methods
We studied a subset of 268 participants from the CHILD Cohort Study with available data for HM bacterial composition (16S rRNA gene sequencing) at 3-4 months, alongside biochemical analysis of 11 minerals (inductively coupled plasma-mass spectrometry), 22 vitamers of B-vitamins (ultra performance liquid chromatography - tandem mass spectrometry) and 7 bioactive proteins (Mesoscale Discovery System). The association of each component with microbiota diversity and composition were identified using Pearson and Spearman correlations, network visualization, and correction for multiple comparisons. Maternal and environmental factors were also considered.

Results
We found associations between several HM bioactive components and microbiota composition. Notably, fibroblast growth factor-21 (FGF-21), calprotectin, leptin, potassium, iron, and several vitamers of B-vitamins correlated significantly with microbiota diversity indices, bacterial network structures and relative abundances of specific taxa, such as Staphylococcus, Gemella, Streptococcus, Rothia, and Bifidobacterium. For example, calprotectin was negatively correlated with alpha diversity (r=-0.142, p=0.02), while flavin adenine dinucleotide (FAD) was positively correlated with Streptococcus (r=0.125, p=0.04) and negatively with Staphylococcus abundance (r=-0.135, p=0.02). Maternal BMI was positively correlated with milk leptin (r=0.403, p<0.001) and Staphylococcus (r=0.139, p=0.02). Additionally, household size, current infant age, infant gestational age at birth, and maternal height showed correlations with bacterial diversity and abundance.

Conclusion
These findings underscore the interplay between HM microbiota and other HM components, along with maternal and environmental factors, with possible implications for the infant gut microbiota and health. Understanding these interactions is important for optimizing breastfeeding practices to support infant health.

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