Gut Microbial Composition and Stunted Length Growth of the Preterm Baby

Katie Chang[1], Diana H. Taft[2], Alexander W. Thorman[3], Ardythe L. Morrow[3]

[1]University of Cincinnati College of Medicine; [2]Department of Food Science and Technology, University of California-Davis; [3] University of Cincinnati College of Medicine, Department of Environmental Health

Introduction: Growth faltering in preterm infants is common and associated with adverse health and developmental outcomes, especially in regard to growth in length. The gut microbiome has been implicated in growth faltering in other populations but is understudied in preterm infant growth.

Hypothesis: We hypothesized that poor length growth during hospitalization is associated with the early gut microbiota in preterm infants.

Methods: 134 stool samples collected from weeks 1 and 3 of life were analyzed from 76 preterm infants born <30 weeks gestational age (GA). Infants included for study survived free of early onset sepsis and necrotizing enterocolitis and had data on length at birth and at hospital discharge (36 weeks corrected GA). The gut microbiome was sequenced by Illumina MiSeq. Z-scores for length were calculated using the 2013 Fenton growth chart. Sequence data was analyzed in relation to growth using QIIME2 and R. Stunting was defined as a Z-score length below -1.5. Microbial community composition was analyzed in terms of alpha diversity (Shannon index), beta diversity (weighted and unweighted UniFrac distances), and microbial markers for growth - identified using the selection balance (Selbal) method.

Results: At hospital discharge, 47 (62%) infants were below -1.5 Z-score for length. In fecal samples from week 1 of life, the microbiota differed between infants who were stunted, compared to those appropriately growing at hospital discharge; identified differences were in beta-diversity (unweighted UniFrac distance, $p=0.004$) and abundance of Staphylococcaceae and Clostridiaceae families ($p<0.05$). In fecal samples from week 3 of life, the microbiota again differed between infants who were stunted compared to the appropriately growing at hospital discharge; identified differences were in alpha diversity ($p=0.016$), and in the comparative abundance of Moraxellaceae, Tannerellaceae, and Clostridiales Family XI ($p<0.05$).

Conclusion: Our findings indicate that length growth in preterm infants is associated with microbial community composition. Improving growth may require managing the early gut microbiota. Greater attention to the microbiota and growth in preterm infants is warranted.

Acknowledgements: This study was supported in part by NIH grant T35DK060444. I would like to thank my co-authors, Dr. Nick Ollberding, Dr. David Haslam, and the MSSRP for mentorship and guidance.