Effects of prenatal antibiotics on the infant gut microbiome

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INTRODUCTION

The purpose of this project was to study the effects of antibiotics during pregnancy, not delivery, on the neonatal gut microbiome, focusing on Bifidobacteriaceae, Bacteroidaceae, and Enterobacteriaceae.

MATERIALS & METHODS

➢ 80 pregnant women/infant dyads, 40 dyads per group from the University of Colorado Hospital OB clinic.
➢ Third trimester, 18-34 years old, pre-pregnancy BMI 18.5-30, singleton pregnancy, and documented GBS negative.
➢ Exposed: received at least a single dose of any systemic antibiotics (PO/IM/IV) during the second or third trimester.
➢ Control: who were not given antibiotics at any time during the pregnancy.
➢ 16s rRNA sequencing following PCR amplification of DNA.
➢ Negative binomial and generalized linear mixed models for analysis of data.

RESULTS

Figure 1. The relative abundance at birth for the control group (A) and exposed group (B) of the three primary bacterial families

Figure 2. The overall microbial diversity at birth for the control group (C) and exposed group (D).

CONCLUSION

Bifidobacterium – prominent bacterial genus found in healthy infant gut microbiome. Lower relative abundances associated with increased rates of atopy, celiac disease, and obesity.

Bacteroides fragilis (subset of the Bacteroidaceae family) – implicated as an important player in gut health and neurodevelopment.

Enterobacteriaceae – increased abundance of Enterobacter associated with disease, such as necrotizing enterocolitis in pre-term infants. Whereas Escherichia coli plays an important role in healthy microbiome development.

Microbiome composition is very complex with an important interplay between a host’s genetics, nutrients, and environmental factors. Further investigation is needed to establish causality.

Future directions –
➢ Finish recruitment, perform DNA extraction, and analyze the data.
➢ Repeat this pilot study with a larger sample size.
➢ Examine microbiome changes and effects on nervous and immune system development (most research so far in animal models).
➢ Assess longer term outcomes (incidence of NCDs) using larger prospective cohort studies with longer period of follow-up time (years).

Limitations –
➢ Generalizability considering younger and healthier cohort.
➢ Tremendous effects of confounders on microbiome research.

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REFERENCES

DISCLOSURES

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