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Effects of prenatal antibiotics on the infant gut microbiome

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INTRODUCTION

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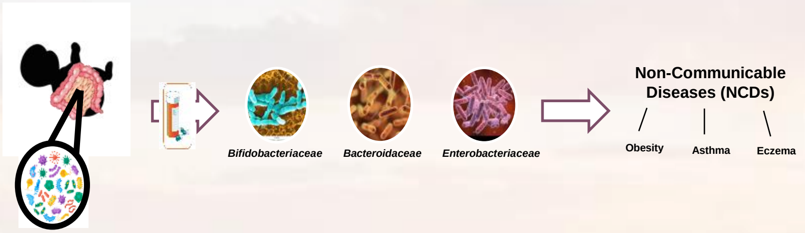

OBJECTIVE

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

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- 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 antibiotic (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.

HYPOTHESES

	Control	Exposed
Relative abundance of Bifidobacteriaceae	↑	↓
Relative abundance of Bacteroidaceae	↑	↓
Relative abundance of Enterobacteriaceae	↓	↑
Overall bacterial diversity	↑	↓

RESULTS

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****We are currently recruiting participants and as such do not have any results to report. Below is example data of the planned results section****

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

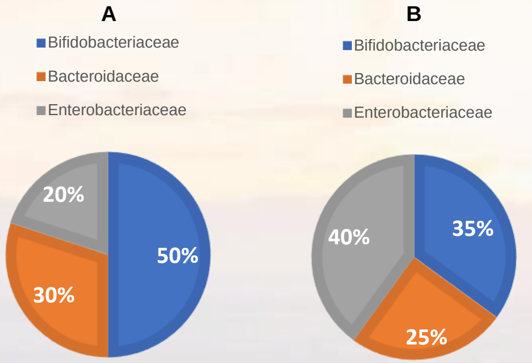
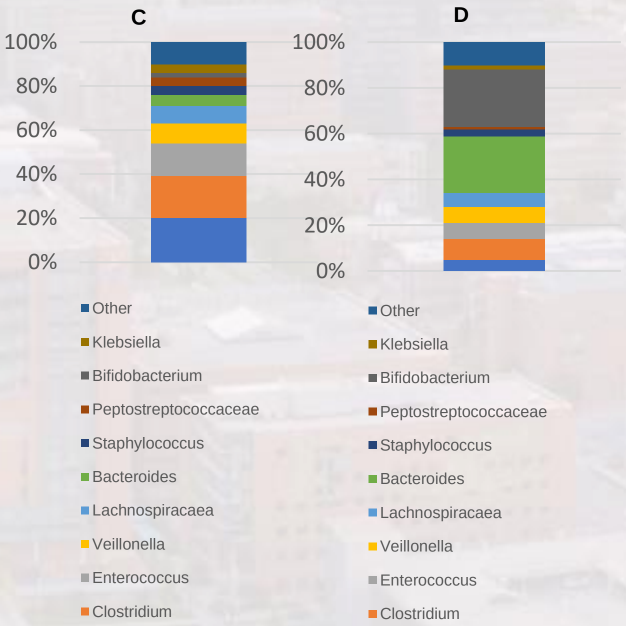


Figure 2 – The overall microbial diversity at birth for the control group (C) and exposed group (D).



CONCLUSION

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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 healthy gut microbiome, infant development, and the risk for disease later in life.

Important to understand how antibiotics used during pregnancy perturb the infant gut microbiome and in turn have downstream effects.

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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DISCLOSURES

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