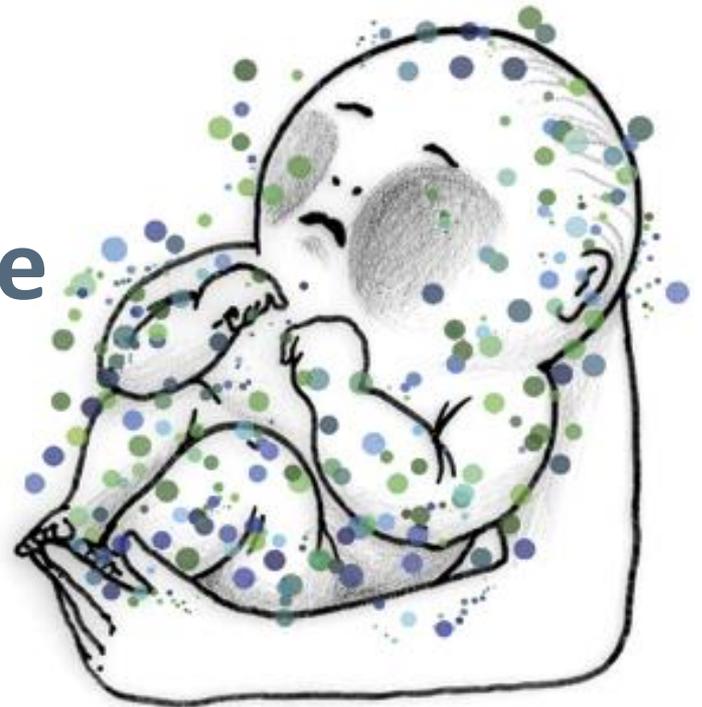


Effects of formula supplementation on the composition of the infant microbiome

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University of Utah
<http://learn.genetics.utah.edu>

The human microbiome

- The “forgotten organ”
- **Co-evolved with humans**
- 100 trillion organisms in the intestine
- 1000 species Qin J et al. 2010
- 10 microbes for every human cell
- 100 microbial gene for every human gene
- Innate and adaptive immunity evolved to *require* microbial interactions during development Lee YK et al. 2010, Chow et al. 2010

Consequences for health

- Out-competing pathogens
- Conferring resistance to infection (Gill et. al. 2012, Britton and Young 2012, Olszak et. al. 2012)
- Reducing susceptibility to inflammatory and metabolic disorders (Frank et. al. 2011, Nieuwdorp et. al. 2014)
 - Microbial diversity in the *first weeks of life* related to allergy at school age (Wang et al. 2008; Bisgaard et al. 2011)

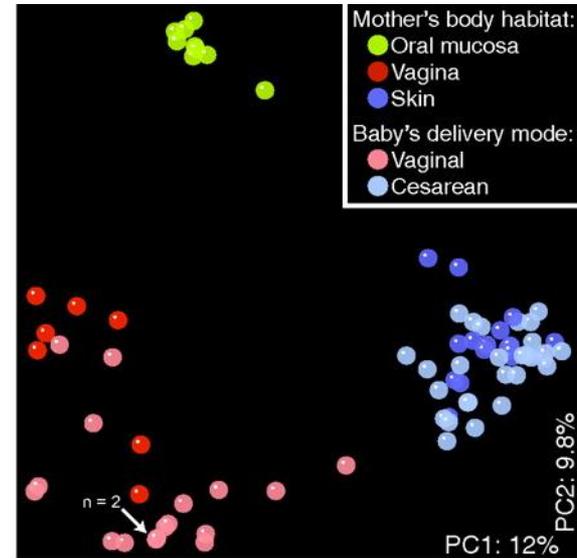
The microbiome at birth

- Recent evidence points to some exposure of fetus to microbes through placenta, umbilical cord and/or amniotic fluid (Jiménez et. al. 2007, Aagaard et. al. 2014)
- Major colonization event at birth
 - Vaginal microbiome shifts during pregnancy to become dominated by *Lactobacillus* (Aagaard et. al. 2012)
 - Human milk oligosaccharides promote the proliferation of *Bifidobacterium infantis* in infant intestinal tract (Coppa et. al. 2004)

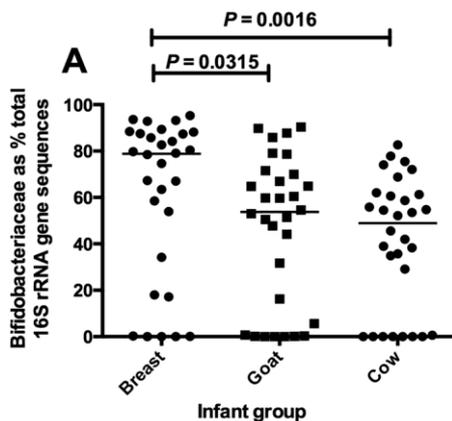


Delivery mode and feeding

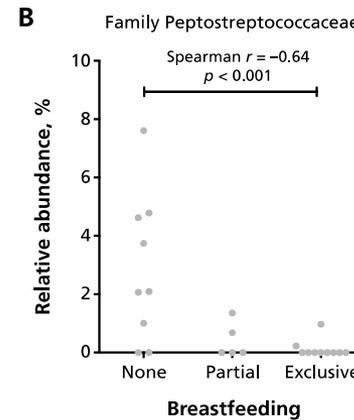
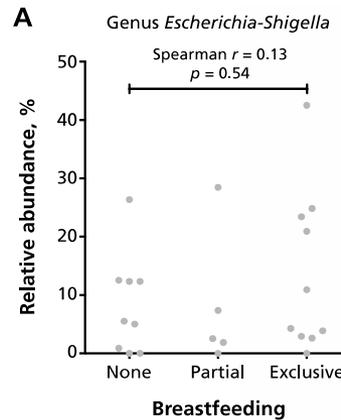
Feeding method (breast milk vs formula) and delivery mode (vaginal vs. C-section) are the most commonly found correlates of microbiome composition in young infants



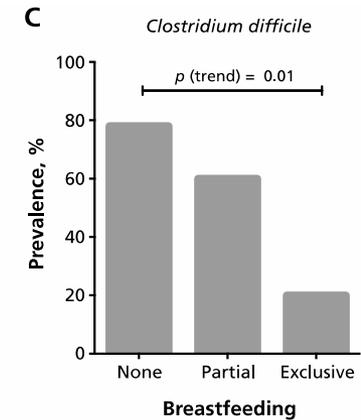
Maria G. Dominguez-Bello et al. 2010



Tannock et. al. 2013

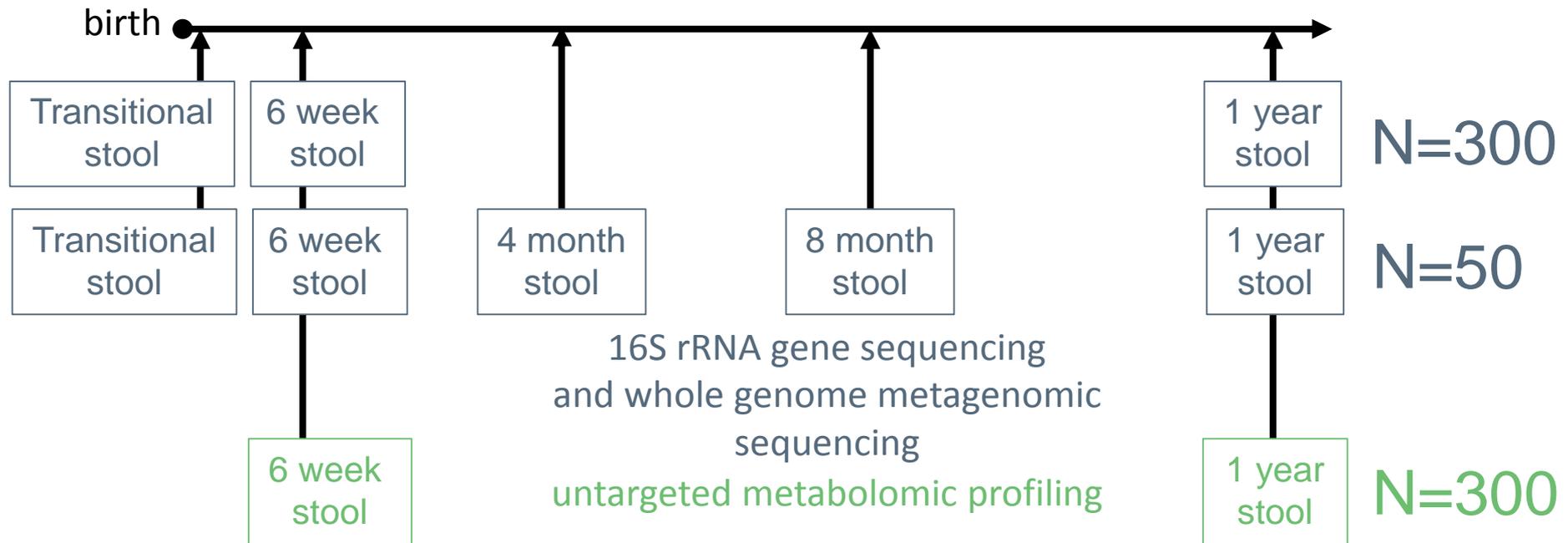


Azad et. al. 2013



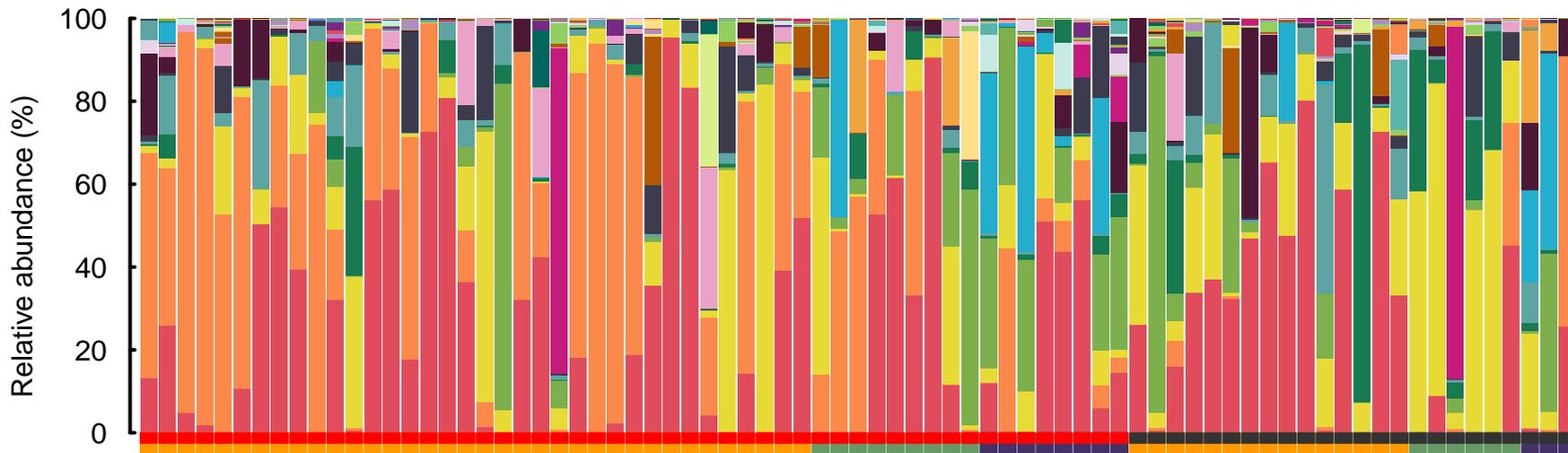
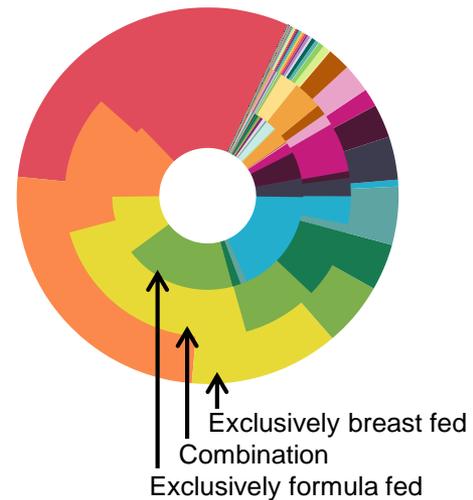
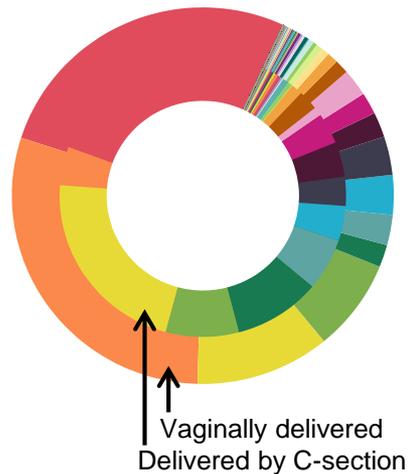
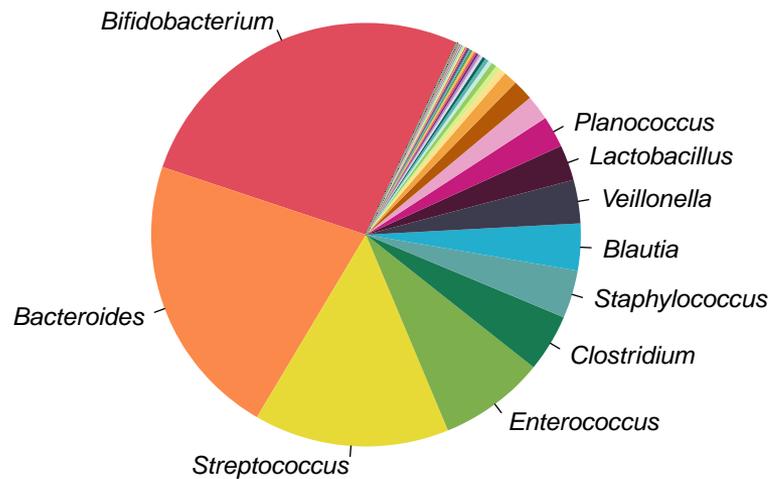
New Hampshire Birth Cohort Study

- 1500 mothers who used a private well enlisted during 2nd trimester of pregnancy
- Infant stool collection:



Exposure data

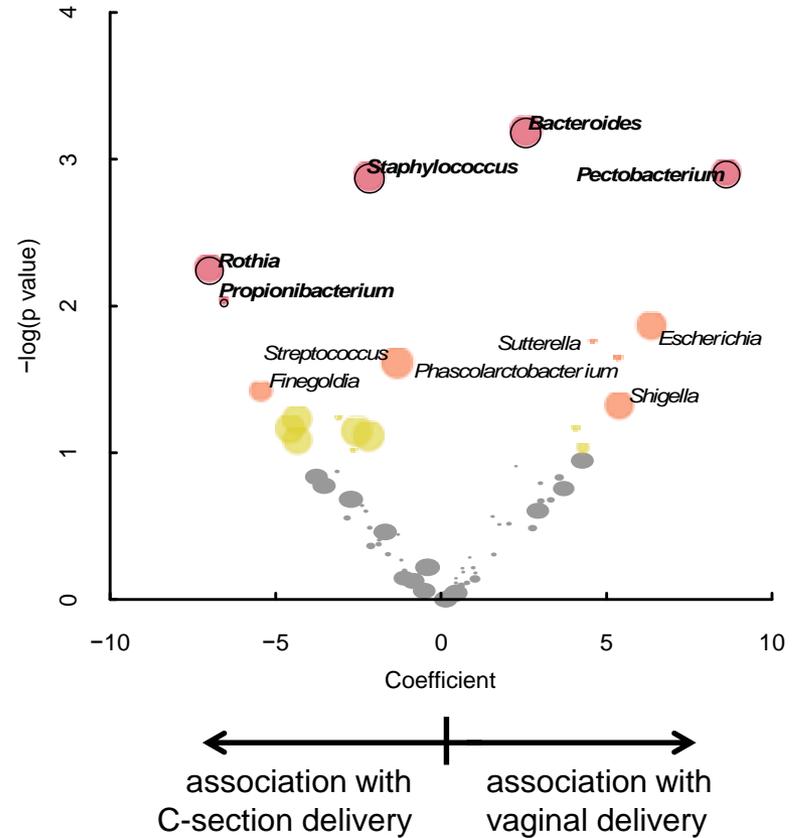
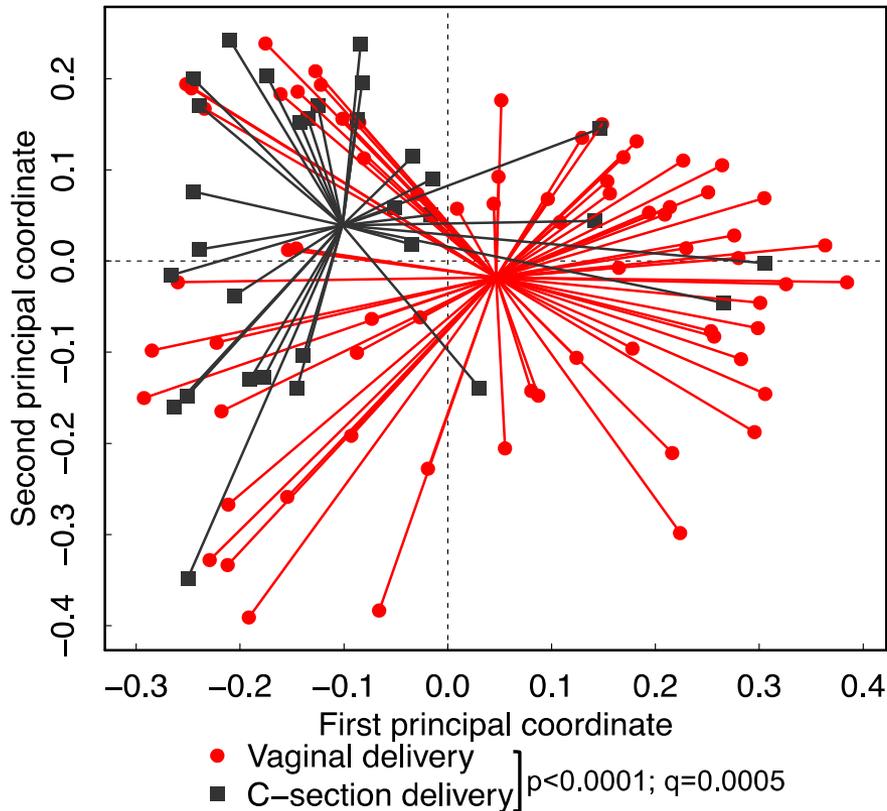
- Delivery mode abstracted from delivery medical record
- Infant feeding over first 6 weeks of life ascertained by follow-up questionnaire
 - Exclusive breast feeding
 - Partial breast feeding ('combination feeding')
 - Exclusive formula feeding
- Infant urinary arsenic concentration measured at time of 6 week stool collection



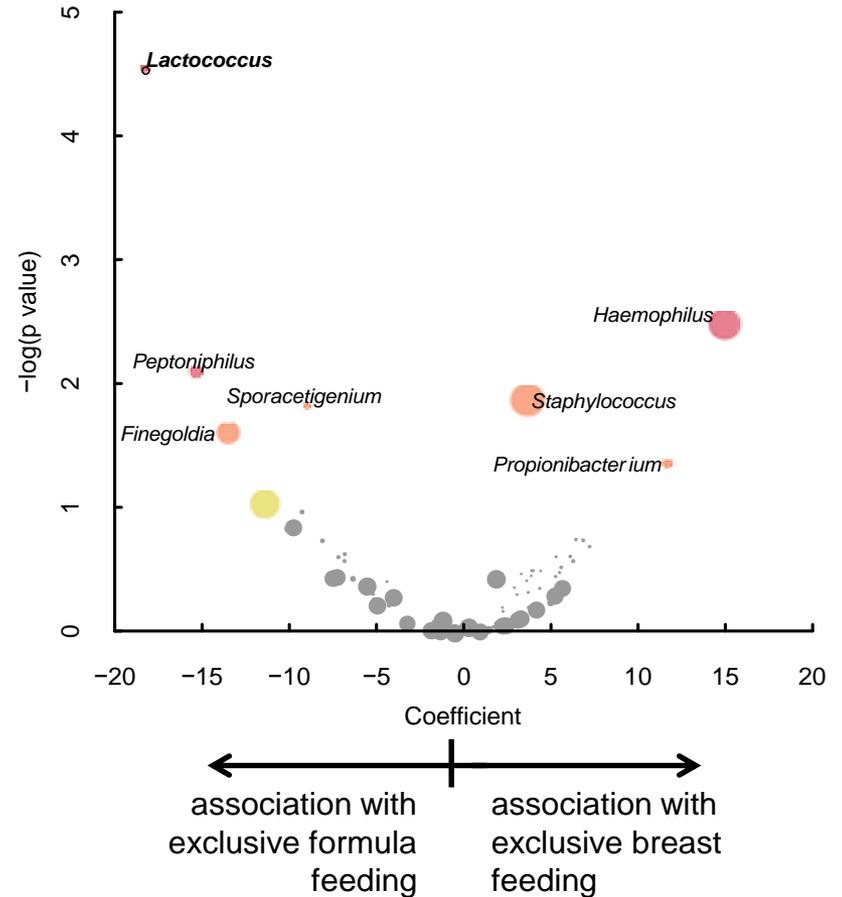
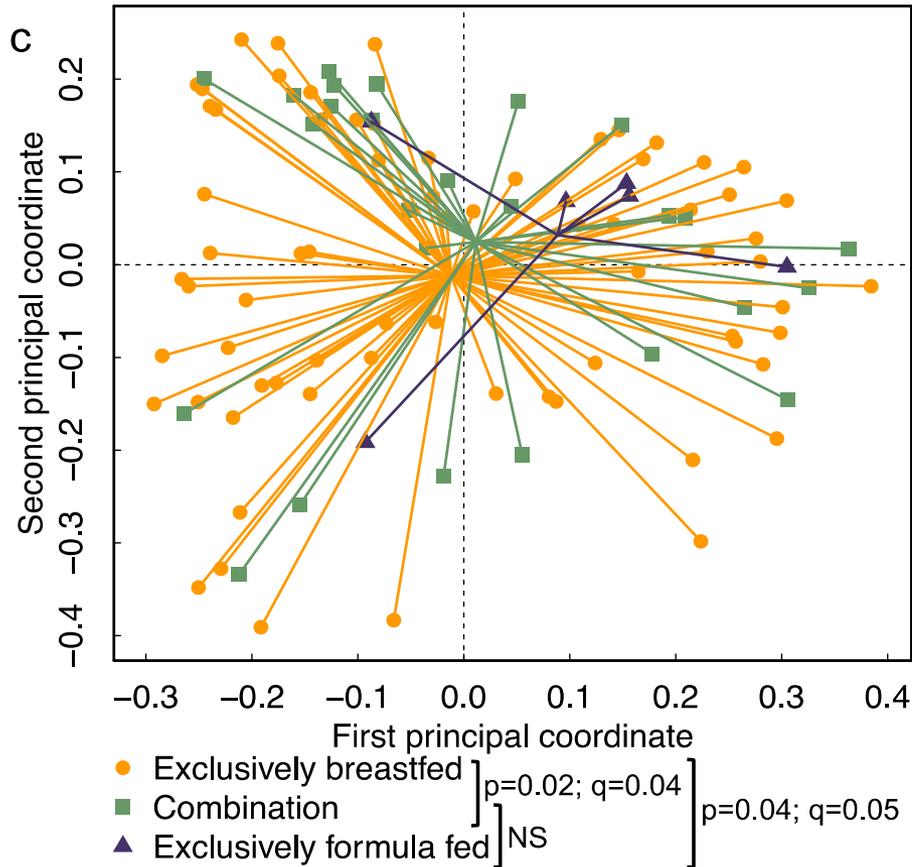
6 week stool samples (n=77)

- Exclusively breastfed (n=51)
- Vaginal delivery (n=53)
- Combination (n=15)
- C-section delivery (n=24)
- Exclusively formula fed (n=11)

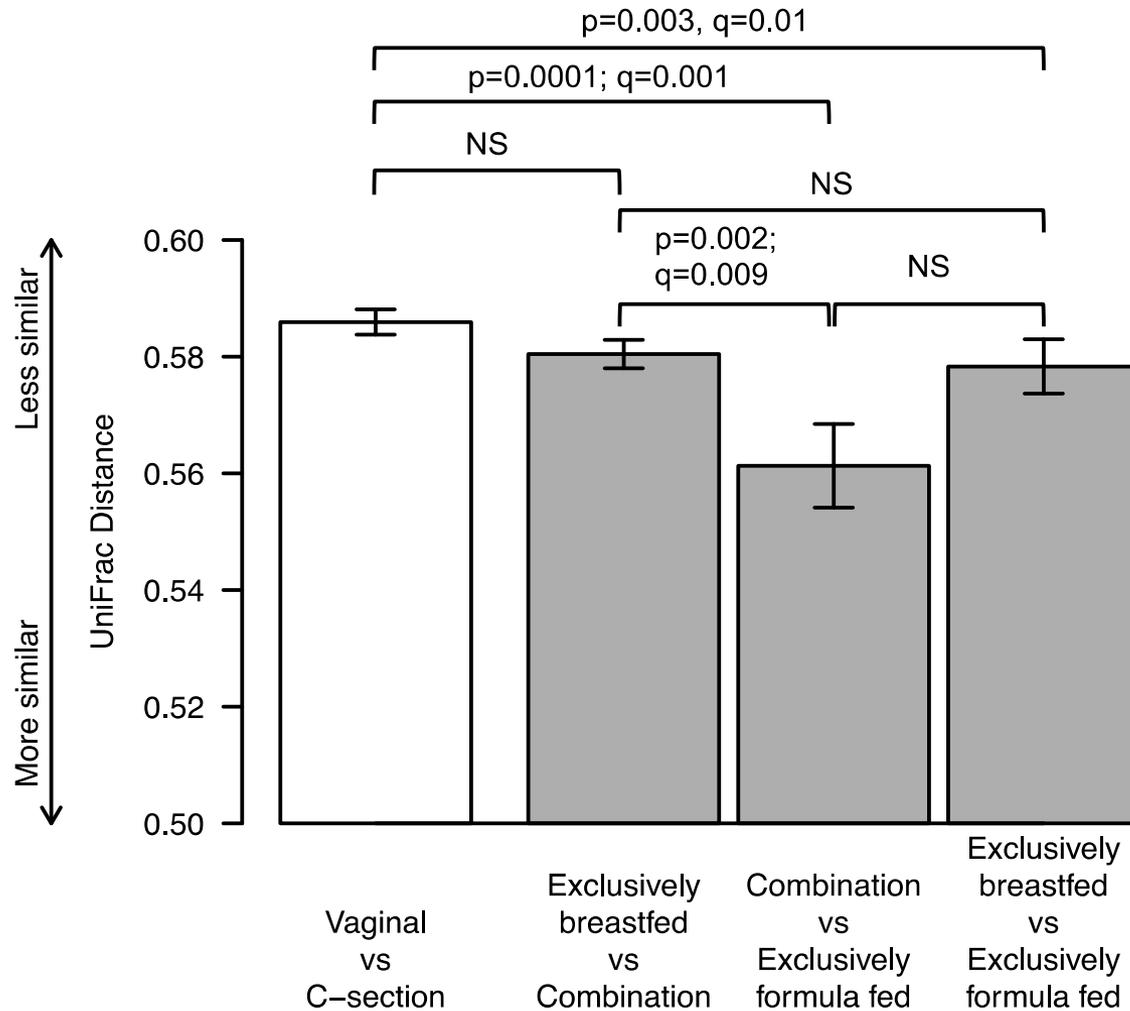
Delivery mode



Feeding

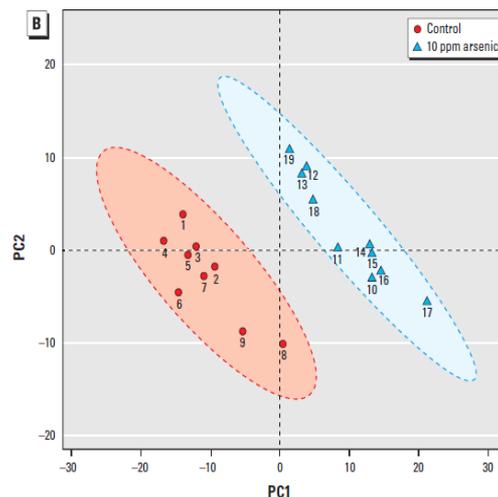
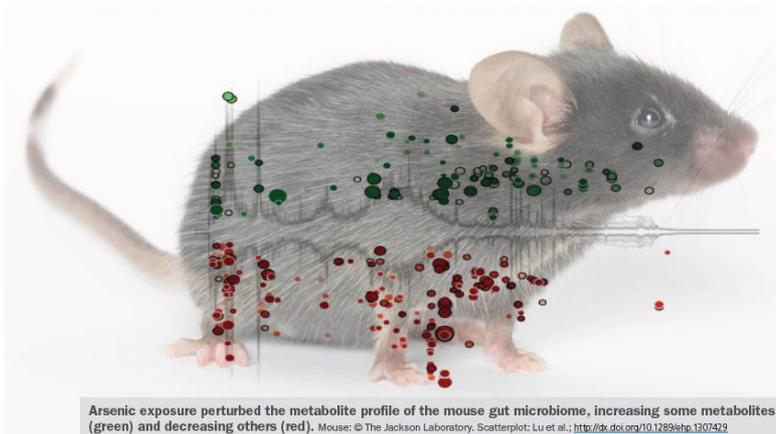


Between-group comparisons

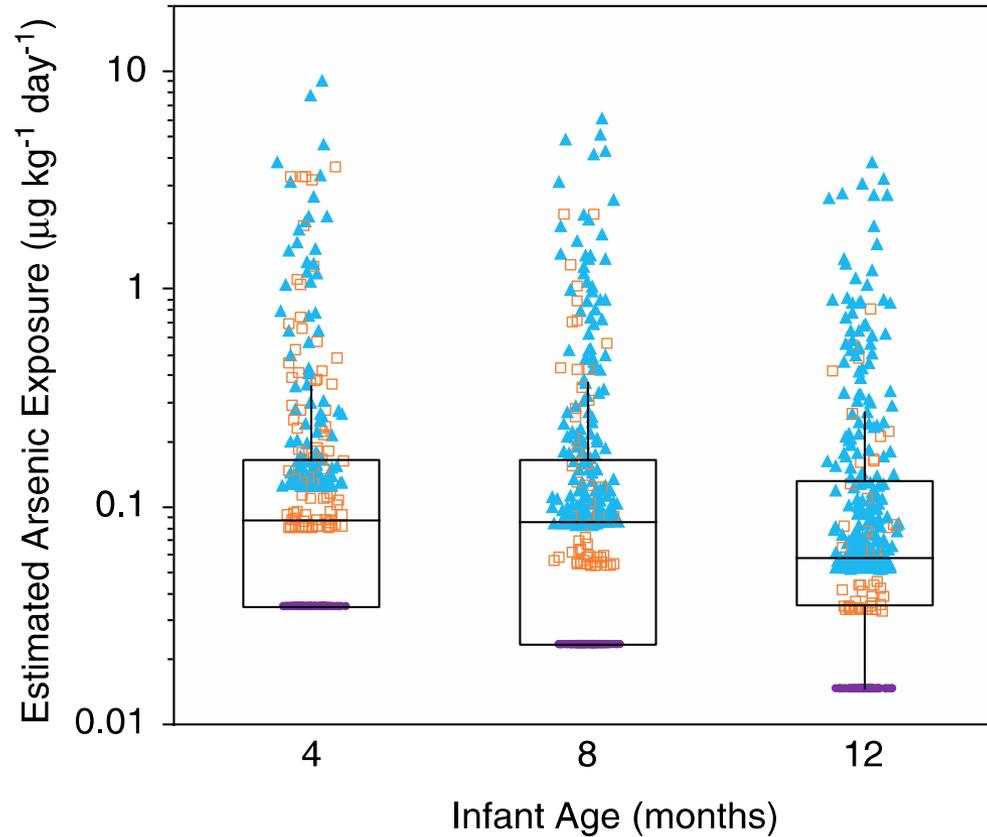


Arsenic and the microbiota

- Mouse model: 10 ppm As for 4 weeks in drinking water Lu et al. 2014
- As significantly perturbs the gut microbiome composition
- Metabolomics revealed metabolites perturbed



NHBCS arsenic exposure model



▲ Fed exclusively formula

◻ Fed both breast milk and formula

● Fed exclusively breast milk

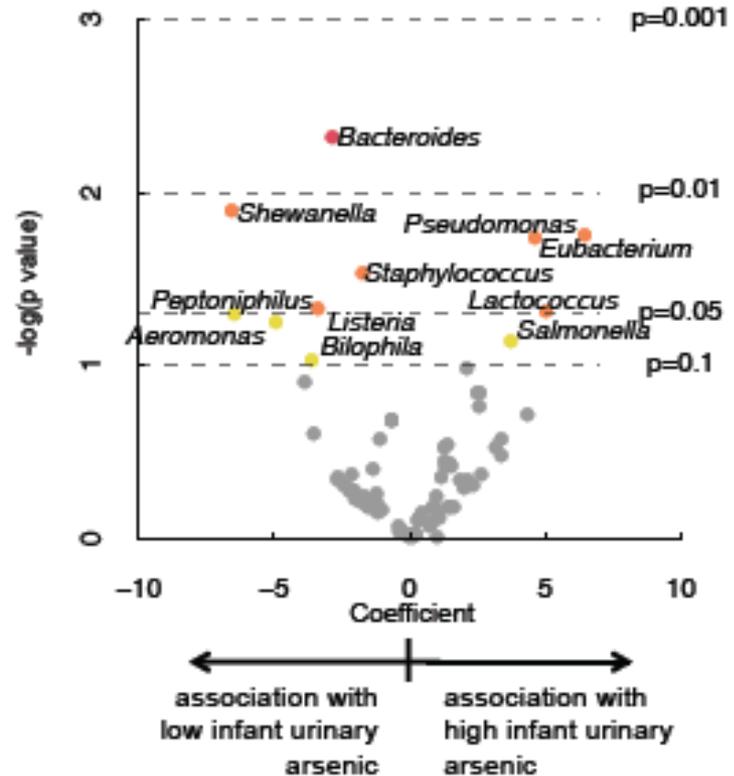
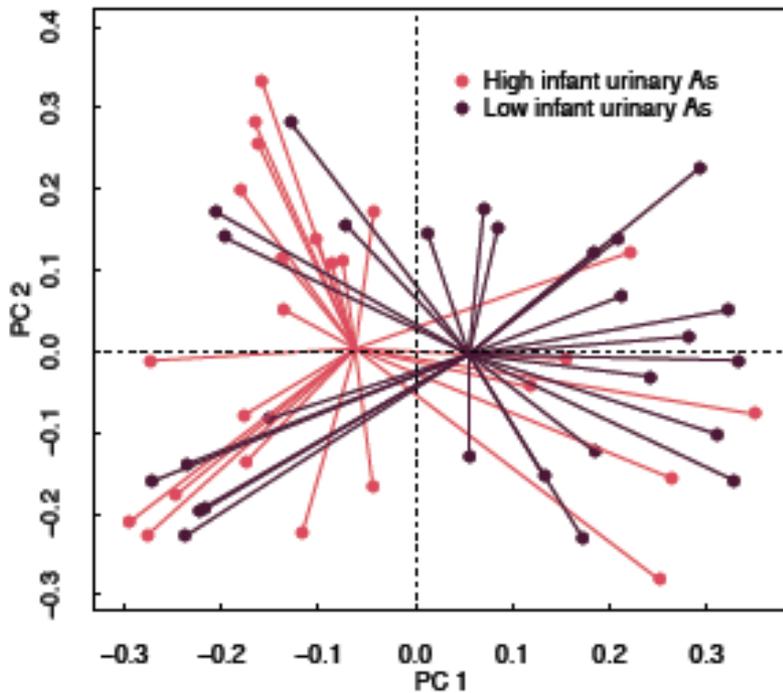
Infant Urinary Arsenic

Significant association between microbiome composition
and

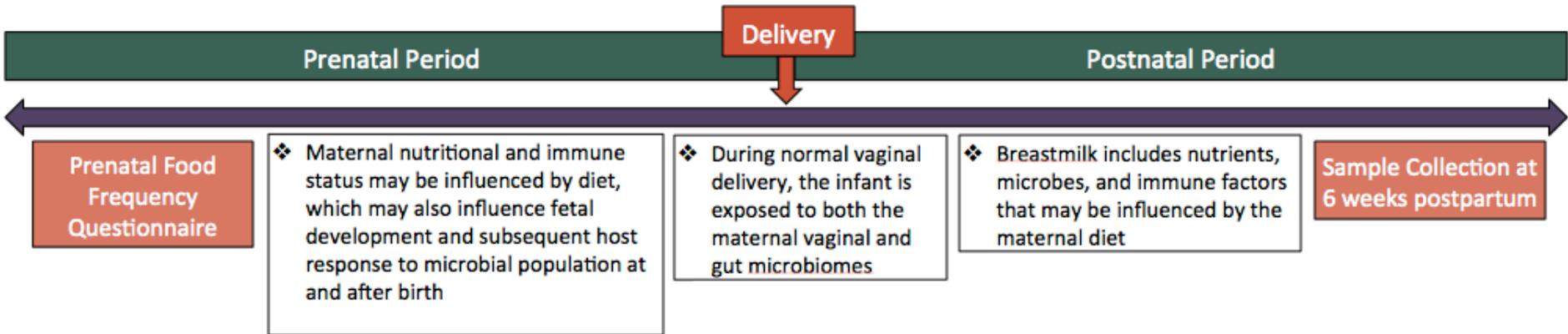
$\ln(\text{infant urinary arsenic concentration})$ $p=0.006$

Among exclusively breast fed infants $p=0.38$

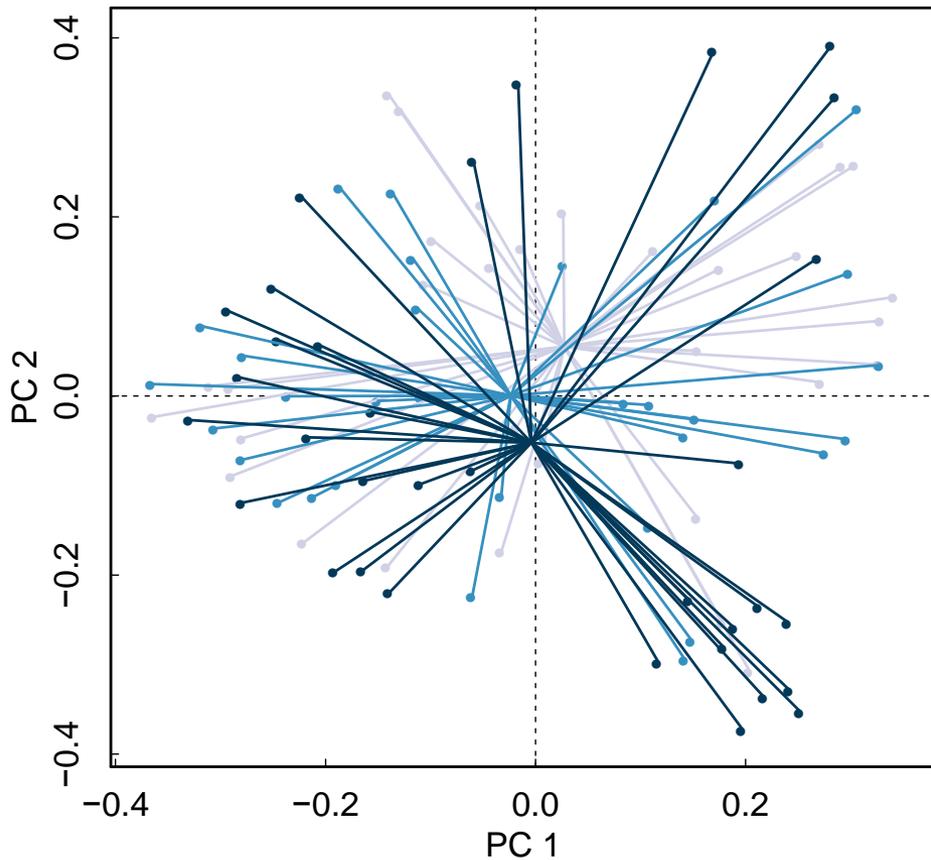
Among formula fed infants $p=0.009$



Maternal diet

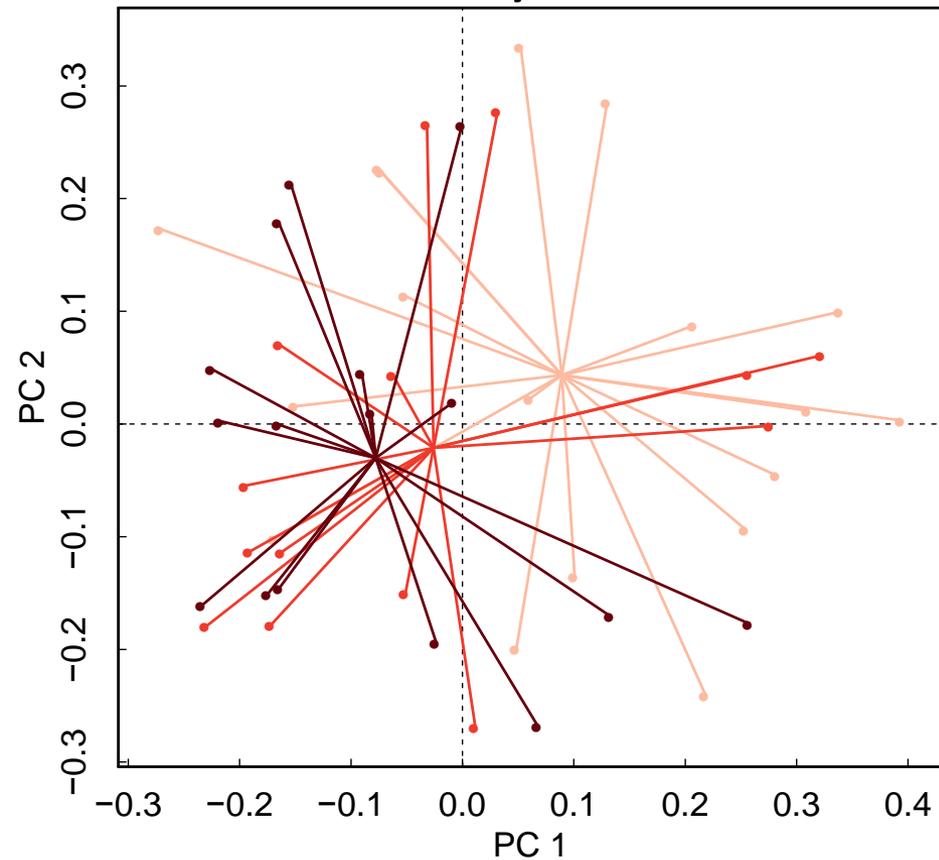


**PCoA of Generalized UniFrac Distances
Colored by Fruit Consumption Tertiles
in Infants Born Vaginally**



- 1st Tertile
- 2nd Tertile
- 3rd Tertile
- ▲ Continuous crude p-value = .04 *
- ▲ Continuous adjusted p-value = .03 *
- Tertile crude p-value = .10
- Tertile adjusted p-value = .14

**PCoA of Generalized UniFrac Distances
Colored by Dairy Consumption Tertiles
in Infants Born by Cesarean Section**



- 1st Tertile
- 2nd Tertile
- 3rd Tertile
- ▲ Continuous crude p-value = .04 *
- ▲ Continuous adjusted p-value = .04
- Tertile crude p-value = .007 **
- Tertile adjusted p-value = .001 ***

Future plans

- High between-subject variation—need for longitudinal sampling
- Identify other factors important in shaping stool microbiome—likely a wide range
- Metabolomics to understand **functional** associations
- Exposure → **microbiota** → health outcomes
- Microbe-microbe interactions



THE CHILDREN'S ENVIRONMENTAL
HEALTH & DISEASE PREVENTION
RESEARCH CENTER AT DARTMOUTH

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