

Lifecourse Epidemiology of Adiposity & Diabetes (LEAD) Center

colorado school of public health



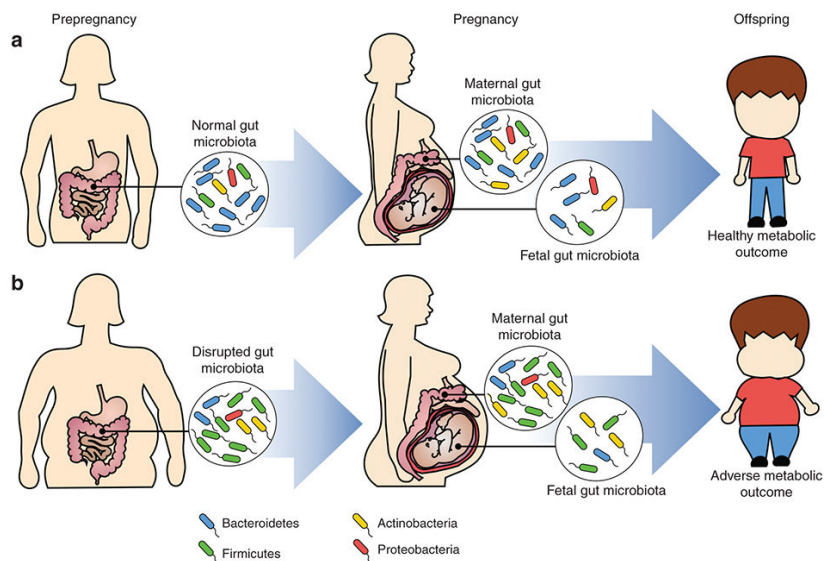
Trainee Profile: Maggie Stanislawski, PhD, (2017)

Dr. Stanislawski received her PhD in Epidemiology from the Colorado School of Public Health in May 2017. She previously received an MSc in statistics from Colorado State University. For her PhD she studied the microbiome in two Norwegian birth cohorts and in the EPOCH study to determine if differences in the mother's microbiome (gut bacteria) predicted obesity in offspring in adolescents as well as predicting early liver disease.

The association between infant gut microbiota, childhood BMI, and the role of mother's pre-pregnancy weight: a prospective longitudinal study

Background: Childhood obesity is a growing problem around the globe with serious consequences for health. Recent research suggests that the gut microbiota may play an important and potentially causal role in the development of obesity, and that it may be one mechanism to explain the transgenerational transmission of obesity risk.

Objective: To investigate the association between infant gut microbiota and later childhood BMI, and to examine the role of maternal weight in shaping the infant gut microbiota.



Methods: We performed 16s rRNA sequencing on fecal samples from 165 infants at six time points during the first two years of life. We calculated sex-specific BMI-for-age z-scores throughout the first two years of life, as well as later in childhood (median age: 11.7 years, IQR: 11.4-12.3), and categorized

the infants according to maternal pre-pregnancy body mass index [overweight/obese (OW/OB), BMI>25, N=69] or non-overweight/obese, BMI<25, N=96). We examined whether: 1) the infant gut microbiota over the first two years of life was predictive of BMI at age 12 using random forests; 2) whether infant gut microbiota characteristics predictive of later BMI were also associated with maternal OW/OB using permutational ANOVA and regression methods; and 3) the longitudinal trends of BMI z-scores over the course of childhood were related to gut microbiota using regression models.

Results: Infant gut microbiota samples from days 4, 10, 30 and 120 post-birth explained approximately 15% (range across sampling times: 14.6-15.9%) of the variation in BMI z-scores at age 12; samples from 1 year explained 35.5% (95% CI: 34.5-36.5%) of the variation and samples from 2 years explained 53.0% (95% CI: 51.5-54.3%). The gut microbiota features at 1 month post-birth that were highly predictive of BMI were also significantly associated overall with exposure to maternal OW/OB (p=0.03), and some of the individual taxa selected at each sampling time as predictive of BMI also showed consistent associations with maternal OW/OB. Children who were OW/OB at age 12 showed no difference in BMI z-scores at age 2 years relative to non-OW/OB children.

Conclusions: Infant gut microbiota was predictive of BMI at age 12. Maternal overweight/obesity showed associations with gut microbiota features predictive of BMI. Infant gut microbiota may offer potential as a biomarker for childhood obesity.

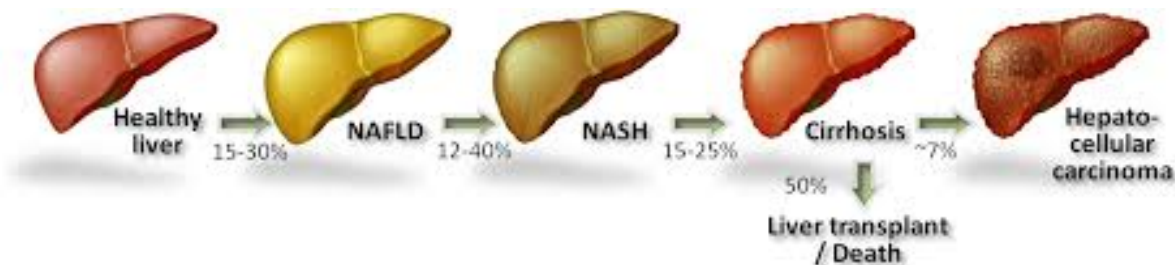
How are 16S sequence data analyzed?

- Usually interested in **taxa**, not **genotypes**
- Sequences can be grouped into taxa by:
 - Traditional taxonomic classification (phylotypes)
 - Phylogenetic tree
 - Operational taxonomic units (OTU)
- **Operational taxonomic units (OTUs)** are used to represent groups of related organisms
- OTUs at 3% sequence difference are used as a **proxy** for species-level diversity



Gut Microbiota in Adolescents as a Biomarker for NAFLD: the EPOCH Study

Context: Recent evidence supports a biological basis for the role of the gut microbiota in the pathophysiology of non-alcoholic fatty liver disease (NAFLD). Since many diagnostic techniques for NAFLD are expensive or highly invasive, the gut microbiota may offer potential as an early biomarker for NAFLD. Objective: We investigated the association between gut microbiota and hepatic fat fraction (HFF) in 107 adolescents in the EPOCH study.



Methods: Magnetic Resonance Imaging (MRI) was used to assess HFF. Fecal samples were collected and 16S rRNA sequencing was performed. Dietary intake was assessed using Food Frequency Questionnaires. BMI z-scores were calculated. We examined the association between gut microbiota

alpha diversity and HFF, and assessed the predictive accuracy for HFF of 1) taxonomic composition, 2) dietary intake, 3) demographic and comorbid conditions, and 4) the combination of all of these. We used linear regressions, controlling for important clinical factors, and random forests.

Results: Lower alpha diversity was associated with higher HFF in adjusted regression models ($\beta=-0.19$, 95% CI -0.36, -0.02). Seven taxa were selected as associated with HFF and explained 17.7% (95% CI: 16.0-19.4%) of the variation. The combination of 2 of these taxa, Bilophila and Paraprevotella, with dietary intake of monounsaturated fatty acids and BMI z-scores explained 32.0% (95% CI: 30.3-33.6%) of the variation in HFF.

Conclusions: Our results suggest that gut microbiota is associated with hepatic fat accumulation in adolescents and may offer potential as a non-invasive early biomarker for NAFLD, particularly in combination with dietary information and BMI.

Stanislawski MA, Lozupone CA, Wagner BD, Eggesbo M, Sontag MK, Nusbacher N, Martinez M, Dabelea D: Gut microbiota in adolescents and the association with fatty liver: The EPOCH study. *Pediatr Res* 2018; DOI: 10.1038/pr.2018.32

Stanislawski MA, Dabelea D, Wagner BD, Iszatt N, Dahl C, Sontag MK, Knight R, Lozupone CA, Eggesbø M. 2018. Gut microbiota in the first 2 years of life and the association with body mass index at age 12 in a Norwegian birth cohort. *mBio* 9:e01751-18. <https://doi.org/10.1128/mBio.01751-18>.

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