**Genetic Effects of High Fat Diet on Mouse Fecal Metabolomics**

Metabolomics Analysis: RTI RCMRC

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**Abstract:**

We will study expression of a large series of metabolites in fecal samples from a genetically diverse set of mouse strains (BXD type). Separate cohorts of animals are maintained either on a 6% low fat diet or on a 60% high fat diet and at several points during normal life span. We predict that these dietary differences will have profound effects on the gastrointestinal (GI) tract and fecal metabolites, and that the differences will be influenced strongly by genetic factors. We also expect that fecal metabolite data will be a useful predictor of major outcome measures, such as fat mass, longevity, and mitochondrial state. All metabolite data will be entered into the GeneNetwork web service for genetic analysis of the effects of metabolites and diet on GI tract metabolism.

This study includes 72 female mice with 4 mice from each of the 18 mice strains. Two mice from each strain were fed a high fat diet (Harlan Teklad 06414) and two mice were fed a normal fat diet (Harlan Teklad 2018). The 36 mice fed a normal fat diet will serve as the controls. All mice are age 27.6 weeks or older at the time of sacrifice.

This metabolomics study was conducted to characterize the effects of a low versus a high fat diet on the fecal metabolome of aging female mice. This information will serve to address Specific Aim 1 of this study: to determine the effects of genetics and diet on fecal metabolomics. Additionally, a small number of strains was selected to study age-related changes in fecal metabolomics as a function of age. The information gathered for Specific Aim 1 will additionally be used for Specific Aim 2: multiscale modeling of GXE effects on health, metabolic biomarkers, and molecular networks.

The data required for the metabolomics analysis can be found in the accompanying files:

Procedures: 1. WILLIAMS Metabolomics Procedure.docx

Study Design Table: 2. WILLIAMS Design Table And\_Subject\_ID.xlsx

Metadata: 3. WILLIAMS MetaData and Analytical Metadata.xlsm

Processed Data: 4a. Williams-Feces-RP-POS-Phenotypic and Normalized Data.xlsx

4b. Williams-Feces-RP-NEG-Phenotypic and Normalized Data.xlsx

Raw Data: 5a. Williams\_Feces\_RP-POS-Zipped LC-MS Data.zip

5b. Williams\_Feces\_RP-NEG-Zipped LC-MS Data.zip

**Notes:**

Sample FAC256, FAC253, FAC255 were excluded from the alignment of Reversed-Phase Positive ion mode data. Because of high interference, these samples could not be aligned.

**Reference:**