Association Between Intestinal Changes and Systemic Cytokines in Mouse Dysbiosis Models

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Background/Objective:
Gut dysbiosis has been linked with the development of low-grade inflammation in part due to an increase in pro-inflammatory cytokines and a decrease in short chain fatty acid production. This project aims to study the effects of antibiotics-driven dysbiosis on host gene expression in murine ilea. Additionally, we will examine the ilea for morphological differences among treatment groups.

Methods:
Wild-type C57Bl/6J mice were given either an antibiotic (ampicillin, neomycin, vancomycin, or metronidazole) in water or water alone from 5 to 16 weeks of age. Mice were euthanized at 16 weeks, and the ilea were collected. RNA isolation and quantification were performed using the QIAgen RNeasy Lipid Tissue Mini Kit and BioTek Cytation 5 with Take3 plate, respectively. Histology of the ilea will be performed using hematoxylin and eosin (H&E) staining.

Results:
The average RNA yield was 3.91 ± 1.14 µg/mg of tissue, and the average RNA purity, reported as the 260/280 nm ratio, was 2.06 ± 0.02. A Kruskal-Wallis test revealed there was no statistically significant difference in the average RNA yield between experimental groups (p-value = 0.15). Transcriptomes of isolated samples will be sequenced, and results will be analyzed in association with 16S sequencing (Zymo) of bacterial communities of the gut. Based on prior murine studies, we expect upregulation of pro-inflammatory cytokines and downregulation of tight junction proteins, which contribute to inflammation and increased gut permeability.

Conclusion and Scientific Impact:
At this time, conclusions on the effects of antibiotics-driven dysbiosis on murine ileal gene expression and H&E staining cannot be made as further results and analysis are pending. However, the RNA sequencing and H&E results will be important to examine the impact of changes to the gut microbiome resulting from the administration of various antibiotics and further understand the relationship between antibiotics-driven dysbiosis and the microbe-host relationship.