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Grant Title: Studies on association between mucin *O*-glycome and gut microbiome

Abstract

Mucins, the principal components of intestinal mucus, play essential roles in host–microbe symbiosis by providing a physical barrier, microbial habitat, and nutritional glycans for the gut microbiota. Since microbial utilization of mucin glycans requires carbohydrate-active enzymes (CAZymes), regional variation in mucin glycosylation is expected to influence microbial community structure. However, direct evidence linking mucin glycan profiles with gut microbiota remains limited. In this study, we investigated the relationship between intestinal mucin glycosylation and microbial communities using mice as a model system.

Female Slc:ICR mice were maintained under conventional conditions, and mucosal samples were collected from different intestinal regions, including the small intestine, cecum, and colon. Mucin *O*-glycan profiling was performed by MALDI-TOF/MS following reductive ß-elimination and permethylation, while microbial communities were characterized by 16S rRNA amplicon sequencing. Functional prediction of glycan-related pathways and CAZyme genes was conducted using PICRUSt2 and run_dbCAN. Glycan localization was further examined by lectin staining.

Analysis of mucin *O*-glycans revealed marked regional variation along the intestinal tract. Glycan profiles formed two major clusters corresponding to the small intestine/cecum and colon, with fecal samples showing intermediate characteristics. Notably, fucosylated glycans were enriched in the colon, whereas unmodified glycans decreased. Lectin staining supported these findings by demonstrating preferential localization of fucosylated mucins in the colon. Microbial analyses revealed significant regional differences in microbial diversity, predicted metabolic pathways, and CAZyme profiles. Correlation analyses further demonstrated significant associations between certain mucin glycans and several bacterial taxa. These findings suggest that fucosylated mucin glycans may influence microbial community structure and support potential microbial cross-feeding interactions.