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Impacts of habitual and recent alcohol intake on gut microbiome diversity and composition among Black Americans



Introduction: Alcohol intake can alter the gut microbiome, which may play a role in the development of cancer and other chronic diseases. However, there have been limited population-based studies investigating the associations of habitual and recent alcohol intake with the gut microbiome, particularly among Black Americans.

Methods: We investigated the association of alcohol intake with the gut microbiome among 538 Black American participants of the Southern Community Cohort Study (150 men and 388 women). Habitual and recent alcohol intake was assessed at cohort baseline (2002–2009) and stool collection (2018–2021), respectively. DNA was extracted from fecal samples for gut microbiome profiling using shotgun metagenomic sequencing. Generalized linear models were employed to evaluate the associations between alcohol intake and gut microbiome diversity and composition, with adjustments for sociodemographic characteristics, other lifestyle factors, and comorbidities. False discovery rate (FDR) < 0.1 was considered statistically significant.

Results: The mean age at enrollment was 53.2 ± 7.7 years, with a mean interval of 13.8 years (range: 9.0–18.1 years) between baseline and stool collection. Neither habitual nor recent alcohol intake was associated with microbiome diversity indices, and recent alcohol intake was not associated with microbial taxa abundance either. However, habitual alcohol intake, both total amount and subtypes, showed significant associations with microbial taxa abundance primarily in men, including *Actinobacteria*, *Proteobacteria*, *Firmicutes*, and classes *Bacilli* and *Clostridia* within these phyla (all FDR < 0.1). Specifically, total alcohol and red wine intakes were inversely associated with genus *MGYG-HGUT-02719* in class *Clostridia*; beer consumption was inversely associated with genus *Anaerostipes*; white wine intake showed negative associations with order *RF32* and genus *Eubacterium* and a positive association with genus *Paenibacillus*. Most of these associations remained significant after adjusting for BMI and history of cardiometabolic diseases or cancer.

Conclusions: We identified gut microbiome taxa associated with habitual alcohol intake among Black American men, including several with anti- or pro-gastrointestinal-cancer properties. However, the magnitudes of these associations were generally small. Further research is needed to determine if these bacteria play a mediating or modifying role in alcohol-disease relationships.