Alcoholic beverage intake and gut microbiome composition

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Background and motivation

The gut microbiota are a complex community of microbes, which are crucial for in human health. Its composition evolves throughout life and variations have been linked to many metabolic and inflammation-related diseases. Diet is a key modifiable factor that can impact intestinal microbiota composition and diversity.

Whether intake of alcoholic beverages is beneficial or harmful for our gut microbiota is controversial. Most evidence comes from animal studies or studies in alcoholics. These studies suggest that high alcohol intake disrupt the gut microbiota, but that moderate intake of certain alcoholic beverages, i.e. red wine (polyphenols) or beer (yeast), may be beneficial.

Indeed, the first and so far only population-level analysis of determinants of gut microbiome among humans pointed towards beer as an important determinant of the gut microbiome. Among all dietary factors examined, they identified intake of fiber, beer, and chocolate to be linked to microbiome diversity among >1,000 Flemish subjects (Falony et al., Science 2016).

However, this study did not examine gut microbiota communities in more detail, did not study different alcoholic beverages and did not examine potential non-linear associations.

Objective

To examine whether moderate alcohol intake and intake of different alcoholic beverages is associated with microbial diversity and with microbial communities at taxonomic levels of genus, family, order, class, and phylum among ~1,500 Dutch adults participating in a population-based cohort in the Netherlands.

Methodology

Design: the Rotterdam Study, a large ongoing population-based cohort.

Participants: Approximately 1,500 participants, living in Ommoord, Rotterdam, ≥45 years.

Exposure: Detailed information on dietary intake, including many alcoholic and non- alcoholic beverages, was measured using a 389-item food-frequency questionnaire (FFQ).

Outcome: An automated stool DNA isolation kit (Diasorin, Saluggia, Italy) was used to isolate bacterial DNA and microbiome profiling was based on sequencing the V3 and V4 variable regions of the bacterial 16S rRNA gene. We assessed relative abundance data (weighted analysis) in all taxonomic levels including: Domain, Phylum, Class, Order, Family, and Genus. We used Operational Taxonomic Unit (OUT) to express the abundance data.

Covariates: In all analyses we will take into account age, sex, smoking status, educational level, antibiotics use, physical activity, fiber intake, overall diet quality and technical covariates (run batch, time in mail of stool sample).

Analyses: We will analyze associations between alcoholic beverage intake with gut microbiome diversity

and with composition at many different levels (from class to genus). We will investigate associations of total alcohol intake, and specific beverages separately. We will examine whether associations differ for men and women and by different levels of alcohol intake. Analyses will be performed in R version 3.3.2 using the MaAslin package, which was recently developed for these types of analyses by the Huttenhower Research Group (dept. of Biostatics, Harvard School of Public Health).