



The 13th European Nutrition Conference, FENS 2019, was held at the Dublin Convention Centre, 15–18 October 2019

Diet quality, anthropometrics, and gut microbiota composition in healthy adults

Anna M. Malinowska¹, Marcin Schmidt² and Agata Chmurzynska¹

¹Poznan University of Life Sciences/Institute of Human Nutrition and Dietetics, Poznań, Poland and

²Poznan University of Life Sciences/Department of Biotechnology and Food Microbiology, Poznań, Poland

Abstract

Human gut microbiota may affect metabolism and health by synthesizing metabolites and processing of food components. Those processes are specific to genus and species (or even strain), and dietary intake and metabolic state (such as obesity) can affect the composition of gut microbiota. The aim of the study was to assess the effect of dietary patterns and intake of several groups of food products and macronutrients, as well as the impact of anthropometric parameters on gut microbiota composition.

The study group consisted of 200 men and women between 31 and 50 years of age. The diet was assessed using three-day dietary records and the dietary pattern was determined with the use of the original score method and two dietary indices, namely the Diet Quality Index – International (DQI-I) and the Healthy Eating Index (HEI). Bacterial DNA was isolated from the feces of the participants and microbiota composition was determined using metagenomic sequencing of the V3–V4 region of the 16S rRNA gene.

Dietary indices and intake of energy from macronutrients did not correlate with the *Firmicutes* to *Bacteroidetes* phylum ratio. However people with greater abundance of the *Firmicutes* phylum compared to *Bacteroidetes* consumed higher amounts of fermented milk beverages, hard cheese, and salt (78%, 48%, 14% higher intake respectively; $p < 0.05$). A higher diet quality as measured by the diet indices was positively correlated with the relative abundance of the *Firmicutes* phylum, *Bacilli*, *Clostridia* class, *Lachnospira*, *Faecalibacterium*, *Coprococcus*, and *Prevotella* genus and negatively correlated with the relative abundance of the *Bacteroidetes* phylum, *Bacteroidia* class, and *Bacteroides* genus. Higher dietary fiber intake positively correlated with the relative abundance of the *Coprococcus*, *Lachnospira*, and *Roseburia* genera, whereas energy intake from simple carbohydrates was positively correlated with the relative abundance of the *Tenericutes* phylum and the *Mollicutes* class. Energy intake from alcohol correlated positively with the relative abundance of *Bacteroidetes* phylum and *Bacteroides* class and correlated negatively with *Firmicutes* phylum and *Clostridia* class. Lower waist-to-hip-ratio, body mass index, and fat mass led to higher abundance of the *Faecalibacterium* genus.

Both diet and anthropometric parameters are associated with gut microbiota composition. Associations between diet and the relative abundance of microbiota are nutrient-specific.

Funding

National Science Centre, Poland (2015/17/D/NZ9/01959)

Conflict of Interest

There is no conflict of interest