

Abstract

Gut Microbiome Composition Associated with Body Weight in People with Type 1 Diabetes and Related to Dietary Factors [†]

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Abstract: Background and Objectives: The gut microbiome composition has emerged as a potential contributor to metabolic health and it is influenced by several factors, such as dietary factors. Individuals with type 1 diabetes (T1D) experience metabolic dysregulation, including alterations in body weight; as a result, the prevalence of overweight/obesity is increasing in this population. Limited research has addressed the role of the gut microbiota on body weight in people with T1D. Our aim is to evaluate the association between BMI and gut microbiome composition in T1D patients, also exploring the relationship between dietary factors and the microbiota. Methods: A cross-sectional study was conducted involving T1D patients ($n = 101$) of both sexes, aged 18–79 years. Anthropometric parameters were measured, and the European Prospective Investigation into Cancer and Nutrition (EPIC) questionnaire was administered to evaluate dietary habits. Patients collected stool samples that were analyzed by shotgun metagenomics sequencing for the evaluation of the gut microbiota composition. Associations between BMI, gut microbiome composition, and dietary factors were evaluated by Pearson's bivariate correlation. Results: BMI was correlated inversely with the Bacilli ($r = -0.296$, $p = 0.004$) and Gammaproteobacteria ($r = -0.280$, $p = 0.009$) classes and directly with the abundance of the Clostridia class ($r = 0.220$, $p = 0.031$) and one of its species *Faecalibacterium prausnitzii* ($r = 0.264$, $p = 0.010$). The presence of these taxa was associated with dietary factors: Bacilli was inversely correlated with the consumption of animal protein ($r = -0.242$, $p = 0.019$), monounsaturated fatty acids ($r = -0.214$, $p = 0.038$), linolenic acid ($r = -0.236$, $p = 0.022$), oleic acid ($r = -0.205$, $p = 0.048$), and cholesterol ($r = -0.204$, $p = 0.048$); *Faecalibacterium prausnitzii* was directly associated with the intake of cholesterol ($r = 0.218$, $p = 0.034$) and simple sugars ($r = 0.226$, $p = 0.028$). Clostridia was correlated directly ($r = 0.225$, $p = 0.027$) and Gammaproteobacteria inversely ($r = -0.216$, $p = 0.045$) with alcohol intake. Discussion: BMI was associated with the Clostridia, Bacilli, and Gammaproteobacteria classes. These bacteria were related to various dietary factors. Therefore, changes in the gut microbiota could be a possible link between dietary habits and overweight/obesity in people with T1D.

Keywords: gut microbiome; body weight; dietary factors; type 1 diabetes



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