

Integrating Dietary Data into Microbiome Studies: A Step Forward for Nutri-Metaomics

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Introduction: Nowadays it is accepted that gut microbiota, plays a key role in human's health and that diet may influence its composition. Commonly, dietary intake is obtained from long dietary assessment methods, what could lead to misreporting and low collaboration. Furthermore, this relationship is typically evaluated using specific populations groups together with concrete or extreme diets. Thus, we decided to (1) design a new semi-quantitative and simplified FFQ (sFFQ); (2) undertake a relative validation analysis; (3) perform a reproducibility analysis; and (4) correlate dietary intake with microbiome data.

Methods: We conducted two consecutive studies (n = 84: a first pilot study (n = 40) to build a web-based, semi-quantitative simplified FFQ (sFFQ) based on three 24-h dietary recalls (24HRs); a second study (n = 44) served to validate the newly developed sFFQ using three 24HR as reference method. Information about microbiota was obtained from 2 fecal samples by each participant. Gut microbiome profiling (16S rRNA gene) was combined with the extracted dietary and lifestyle data.

Results: Relative validation analysis provided acceptable classification and agreement for 13 out of 24 (54%) food groups and 20 out of 29 nutrients (69%) based on intraclass correlation coefficient, cross-classification, Spearman's correlation, Wilcoxon test, and Bland–Altman. Microbiome analysis showed that higher diversity was positively associated with age, vaginal birth, and intake of fruit. In contrast, microbial diversity was negatively associated with BMI, processed meats, ready-to-eat meals, sodium, and saturated fat.

Discussion: Our results suggest that the new sFFQ could be applied for future dietary studies. On the one hand, through the sFFQ, we were able to associate high microbial diversity, which is considered a health-promoting factor, with the intake of fruits and low diversity with less “healthy options” such as total fat, saturated fatty acids, and sodium intake. However, still there is need to test the sFFQ in a larger cohort as well as to improve information from microbiota using –omics data.