Proceedings of the Nutrition Society (2023), 82 (OCE2), E202



CrossMark

46th Annual Scientific Meeting of the Nutrition Society of Australia, 29 November – 2 December 2022, Sustainable nutrition for a healthy life

Advancing dietary assessment in human gut microbiome research: review and gap analysis

K. Duncanson^{1,2}, G. Williams² and E. Hoedt²

¹Food and Nutrition Research Program, Hunter Medical Research Institute, New Lambton Heights, NSW, Australia

and

²Centre of Research Excellence in Digestive Health, University of Newcastle, New Lambton Heights, NSW, Australia

The gut microbiota is increasingly implicated in maintaining health and managing gastrointestinal disorders and diseases. Advancements in gene sequencing indicate that gut-derived metabolites are intermediaries between diet, the gut microbiota and metabolism.⁽¹⁾ Dietary intake influences the abundance, diversity and metabolic influences of gastrointestinal microbiota. Methods used to assess and analyse human dietary intake focus on nutrients that are specific to human digestion rather than gastrointestinal microbial metabolism, so the extent and nature of these influences are poorly understood.⁽²⁾ Nutrients and food compounds with low bioavailability could nourish colonic microbiota, while dietary bioactives and additives that are generally recognised as safe for human health may detrimentally transform microbiota.⁽³⁾ To progress the personalisation of diets towards microbial manipulation for health gains, dietary assessment and analysis methods used in diet-microbiome research need to capture microbiota-relevant data. The aims of this narrative review were (i) to synthesise data about nutrients and compounds from human dietary intake that are microbiota-relevant and (ii) describe methods to assess and analysis these food components. A three-step literature search and data extraction process involved a literature search for systematic reviews and primary studies, extraction and narrative synthesis of findings, consolidated with existing dietary assessment and analysis methods. Systematic reviews and primary studies were included if they assessed associations between at least one dietary factor and the human gut microbiome or microbiota. Fifty-four systematic reviews and ninety-four primary studies were included in the analysis. Dietary factors associated with microbiota were digestible and non-digestible carbohydrates (n = 49), additives (n = 24), proteins, including gluten and amino acids (n = 23), dietary profiles (n = 15), fats (n = 10) and food bioactives (n = 9). Human data were available for all dietary variables except food additives, which were predominantly from animal studies. Less than half (43%) of systematic reviews and primary studies (35%) assessed dietary factors that can be analysed using the Australian composition database. The highest numbers of reported diet-microbiota associations related to dietary variables that required study-specific dietary assessment methods, including food additives (n = 93), wholegrains (n = 60), FODMAPs (n = 50), gluten (n = 43) and amino acids (n = 30). Dietary assessment methods were reported in 36 of the 94 primary studies, and included daily recalls, records or diaries (n = 22), food frequency questionnaires (n = 8) or dietary protocol compliance checklists (n = 6). This review identified the need for increased availability of microbiota-relevant data for dietary variables represented in food composition databases so that use of dietary intake data can be maximised. Improving the sensitivity and specificity of dietmicrobiome analysis methods would enhance the use of dietary manipulation for gut microbiota-mediated health improvement.

References

- Singh RK, Chang H-W, Yan D, et al. (2017) J Transl Med 15, 73. Shanahan E, McMaster J & Staudacher M (2021) J Hum Nutr Diet 34 (4), 631–644.
- 3. Frame L, Costa E & Jackson S (2020) Nutr Rev 78 (10), 798-812.