

POSTER ABSTRACT ISAPP 2022 STRUCTURE AND FUNCTION OF NON-DIGESTIBLE CARBOHYDRATES IN THE GUT MICROBIOME

R. A. Rastall¹, M. Diez-Municio², S. Forssten³, B. Hamacker⁴, A. Meynier⁵, F. J. Moreno⁶, F. Respondek⁷, B. Stahl^{8,9}, K. Venema¹⁰, M. Wiese¹¹

¹The University of Reading, Food Biosciences; ²Instituto de Investigación en Ciencias de la Alimentación; ³IFF Health & Biosciences; ⁴Purdue University; ⁵Mondelez European Biscuit Research and Development Saclay, Nutrition Research; ⁶Instituto de Investigación en Ciencias de la Alimentación; ⁷CP Kelco; ⁸Nutricia Research BV, HMR-AS; ⁹Utrecht University Utrecht Institute for Pharmaceutical Sciences, Department of Chemical Biology & Drug Discovery; ¹⁰Maastricht University - campus Venlo, Centre for Healthy Eating & Food Innovation (HEFI); Maastricht University; ¹¹TNO, Department of Microbiology and Systems Biology

Presenting person: F. Respondek

Carbohydrates entering the complex microbial ecosystem resident in the human gut can be fermented to different degrees by the bacterial species present. Whilst insoluble carbohydrates may be fermented to a low degree, they may still be classed dietary fibres. More extensively fermented carbohydrates frequently display a selectivity towards particular microbial groups; if the end result of this process is an improvement in host health, then we would consider those carbohydrates to be prebiotics.

It is a complex task to identify the structural basis of the fermentation selectivity underlying a prebiotic effect. Individuals vary in terms of the diversity of their gut microbiome and in the response of this microbiome to any given carbohydrate. The task is further complicated by the use of varying microbiology techniques across studies.

Some generic understanding can be identified: It is clear that low molecular weight carbohydrates of a wide range of structure are very readily metabolised by bifidobacteria and are frequently seen to select for this genus in in vitro studies.. This selectivity is explained by the widespread presence of exo-glycosidase and sugar transport system genes in bifidobacterial genomes. Metabolism of higher molecular weight carbohydrates is dependant of organisms possessing the relevant polysaccharide utilisation genes like the bacteroides, rendering them highly adept at polysaccharide metabolism.

To understand the fate of any given carbohydrate in the gut microbiome, however, the presence of cross-feeding networks must be taken into account. We know of some such cross feeding networks likely to operate in the gut but there is much to learn.

ILSI Europe has commissioned an expert group to produce an authoritative view of the state of the art in terms of our understanding of structure function relationships in fermented carbohydrates. This presentation will highlight our current understanding of structure function relationships and point to the gaps in knowledge and the questions that arise in this area.