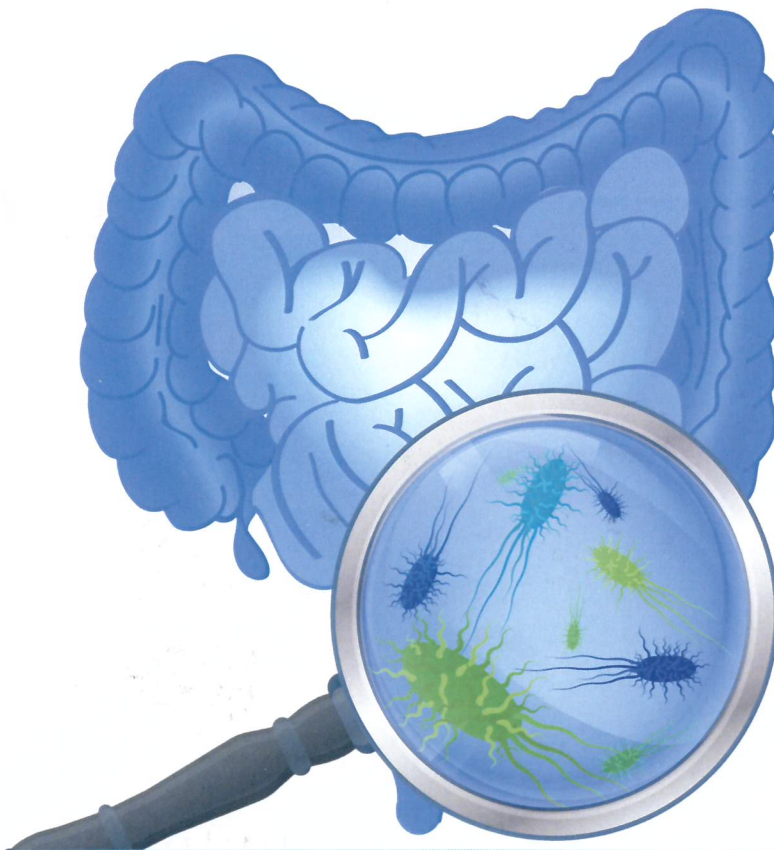


# ILSI Europe's Session on 'Gut Barrier Function and Microbial Metabolism'

21 June 2016,  
Marriott Hotel Budapest, Hungary  
11.00-12.30



Organised by ILSI Europe's  
Prebiotics and Probiotics Task Forces

## Toward Microbial Fermentation Metabolites as Markers for Health Benefits of Prebiotics (and Probiotics)

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The intestinal gut microbial ecosystem produces a wide range of metabolites that interact with the host's cells and in this way influence the physiological processes in the colon.

The aim of the study was to evaluate the available evidence on the bioactive, nutritional and putative detrimental properties of gut microbial metabolites to support a more integrated view of how prebiotics might affect host health throughout life. To proceed, a literature inventory was performed that targeted evidence for the physiological and nutritional effects of metabolites, e.g. short chain fatty acids (SCFA), the potential toxicity of other metabolites and attempted to determine normal concentration ranges. Furthermore, the biological relevance of more holistic approaches like faecal water toxicity assays and metabolomics and the limitations of faecal measurements were addressed. We found that existing literature indicates that protein fermentation metabolites (phenol, p-cresol, indole, ammonia), typically considered as potentially harmful, occur at concentration ranges in the colon such that no toxic effects are expected, either locally or following systemic absorption. The end products of saccharolytic fermentation, SCFA, may have effects on colonic health, host physiology, immunity, lipid and protein metabolism and appetite control. However, measuring SCFA concentrations in faeces is insufficient to assess the dynamic processes of their nutrikinetics. Existing literature on the usefulness of faecal water toxicity measures as indicators of cancer risk seems limited. At present, there is insufficient evidence to use changes in individual faecal bacterial metabolite concentrations as markers of prebiotic effectiveness. Integration of results from metabolomics and metagenomics holds promise for understanding the health implications of prebiotic microbiome modulation but adequate tools for data integration and interpretation are currently lacking. Similarly, studies measuring metabolite fluxes in different body compartments to provide a more accurate picture of their nutrikinetics are needed.

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### Biography

**Prof. Kieran Tuohy** received his PhD from the University of Surrey, UK, in 2000. Between 2000 and 2006, he worked as a post-doctoral researcher in the Food Microbial Sciences Unit of Prof. Glenn Gibson at the University of Reading, UK, and in 2006, he was appointed lecturer in the Department of Food Science and Nutrition at the University of Reading. He now leads the Nutrition and Nutrigenomics Group at Fondazione Edmund Mach, Trento, IT. His research focuses on the health effects of diet and microbe interactions in the gut, and his group has expertise in microbial ecology, dairy microbiology, yeast, nutrition, functional food design and testing, metabolomics and metagenomics. He has about 90 international, peer-reviewed publications in the area of food and gut microbiology, a h-index of 37 (Google Scholar), and is Co-Editor of the book *Diet-Microbe Interactions in the Gut* by Elsevier Press.



Prof. Tuohy is Co-Chair of the Functional Foods Task Force and a member of ILSI Europe's joint Functional Foods and Prebiotics Task Forces' 'Exploring the Role of the Major Gut Microbiota Clusters on Nutritional and Functional Benefits of Nutrients and Non-nutrients' Expert Group. In addition, Prof. Tuohy was member of the previous Prebiotics Task Force 'Microbial Fermentation and Metabolism' Expert Group, whose work is summarised in this talk.