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Food Bioactives – interactions with gut microbiota structure and function

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Recent metagenomic studies have highlighted significant associations between dysregulation of the intestinal microbiome and chronic disease risk in humans. Indeed, many diet and life-style associated diseases, obesity, type 2 diabetes, autoimmune diseases and certain cancers, all appear to possess characteristic profiles of gut bacteria and dysbiosis at the genetic level, with differences both in microbial diversity and relative abundance of important groups of gut bacteria compared to healthy individuals. However, clear links between aberrant microbiota composition and disease mechanisms in the host remain elusive. This presentation will focus on metabolic links between host and microbiome, metabolic links which appear to be altered in disease states and which in turn appear to be modifiable through dietary intervention. Interactions between specific dietary components, e.g. fermentable fibers/prebiotics, polyphenols and aromatic amino acids, appear to strongly influence both the composition and metabolic output of the gut microbiota and modify metabolites of known importance in physiological pathways regulating host metabolism and immune function. Similarly, high resolution MS based metabolomics is presenting a detailed picture of host:microbiome co-metabolism of many complex dietary components, providing novel biomarkers of intake and new putative therapeutic targets. Using data from model systems and human dietary interventions, the ability of host:microbiota co-metabolism to impact significantly on the risk of metabolic disease will be discussed using examples combining microbiome 16S rRNA sequence based profiling (metataxonomics) and biofluid targeted and untargeted MS based metabolomics. Using this combined "metataxonomic" and metabolomic approach, we have observed clear partitioning of microbiota metabolic output according to community structure at the taxonomic level, providing a useful tool linking microbiota structure with metabolic function.



Kieran Michael 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 Professor Glenn Gibson, University of Reading and in 2006 was appointed lecturer in the Department of Food Science and Nutrition. He now leads the Nutrition and Nutrigenomics Group at Fondazione Edmund Mach, Trento, Italy (<http://www.fmach.it/eng/CRI/general-info/organisation/Chief-scientific-office/Food-Quality-and-Nutrition/Nutrition-and-Nutrigenomics-unit>).

His research focuses on measuring diet:microbe interactions in the gut and how they influence host health and disease risk. He is particularly interested in how prebiotics, fibers, polyphenols and probiotics mediate their purported health effects, especially those linked to metabolic disease risk an dobesity, healthy ageing and immune function. Currently co-chair of the ILSI Europe task force on Functional Foods and associate editor at the European Journal of Nutrition. He currently has about 100 international peer reviewed publications in the area of gut microbiology and functional foods.

