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&

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Progress and challenges: What's happened to keystone taxa and their metagenomic footprints in human gut microbial cometabolism ?

Microbiome metabolic impacts and essential functions in the human host have co-evolved with *Homo sapiens*. The growing appreciation of the role of microbiomes in host essential life functions raises the question of whether keystone species and ancient human microbiomes can yield metabolic footprints that can demystify broader issues in human evolution and to what extent microbiota has been shaped by western diet, drug metabolism and lifestyle. This talk will in part, review keystone *Actinomyces* and keystone organism and gene impacts on carbohydrate metabolism that influence the overall glycomiome of the gut microbiome and host interactions. Despite the gaps and challenges, metabolic footprints of targeted host-microbiome interactions indicative of health and toxicity will likely become important components of our overall understanding of food, drug and toxicant metabolism. The conceptual view of keystone taxa and groups is intriguing, and the search for missing genomic links to essential functionalities through integrated omics and imaging technologies opens up exciting possibilities for devising prediction and control strategies for microbial communities in the future. Focusing research efforts on understanding the importance of the co-evolution of keystone species and community ecology, inter-kingdom conserved metabolic genes and microbial-host interactions for ecosystem functions has promising potential for development of biologically-based interventions aimed at enhancing immune system development, energy metabolism, and human performance.

Biography

Linda C Duffy has served for many years as Professor of Pediatrics and Infectious Disease Epidemiology at the State University of New York-Buffalo and has served in the U S Federal Government since 2004. Currently, she is a Health Scientist Administrator at the National Institutes of Health, Department of Health and Human Services [NIH/DHHS]. She leads trans-NIH and inter-agency innovation in areas of multi-omics validation technologies in understanding the role of keystone groups and genes in their related probiotic and microbiota essential interactions with the human host. She has received prestigious awards in recognition of her contributions and has published extensively in journals and co-authored numerous agency technical reports and bookchapters.

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