

Personalized Nutrition by Prediction of Glycemic Responses

Abstract:

The past decades have witnessed a surge in the prevalence of obesity, diabetes and metabolic syndrome. Many of these disorders are associated with high post-meal blood glucose responses, but common dietary methods for controlling these responses have limited efficacy, mainly due to high interpersonal variability in the response to even the same meal. One of the factors underlying this variability is the gut microbiome: a huge ecosystem of bacteria, archaea, viruses and eukaryotes with vast potential metabolic capacity. In our work, we developed new tools for the analysis of the gut microbiome and used these tools, along with blood parameters, dietary habits, anthropometrics and physical activity to accurately predict post-meal blood glucose responses to real-life meals. These predictions were then used to design personalized diets which successfully reduced hyperglycemia. Our results suggest that personalized diets can successfully lower post-meal blood glucose and its grave metabolic consequences.

In a recent study, we show that differences in the presence of even a few genes between otherwise identical bacterial strains are associated with critical phenotypic differences in the host. In this study, we uncover several possible mechanistic links between the microbiome and its host, including a region in *Anaerostipes hadrus* that encodes a composite inositol catabolism-butyrate biosynthesis pathway, the presence of which is associated with lower host metabolic disease risk. Overall, our results uncover a nascent layer of variability in the microbiome associated with microbial adaptation and host health.

Suez J et al. Artificial sweeteners induce glucose tolerance by altering the gut microbiota. *Nature*. 2014; 514, 181-186, doi: 10.1038/nature13793

Thaiss CA et al. Transkingdom control of microbiota diurnal oscillations promotes metabolic homeostasis. *Cell*. 2014; 159(3), 514-529. doi: 10.1016/j.cell.2014.09.048

Korem T et al. Growth dynamics of gut microbiota in health and diseases inferred from single metagenomic samples. *Science*. 2015; 349(6252), 1101-1106, doi: 10.1126/science.aac4812

Zeevi D et al. Personalized Nutrition by Prediction of Glycemic Responses. *Cell*. 2015; 163(5), 1079-1094, doi: 10.1016/j.cell.2015.11.001

Biography:

Dr. David Zeevi is a James S. McDonnell Foundation Researcher at The Rockefeller University, United States. He develops computational methods for studying the gut microbiome, and its contribution to health and disease. His research focuses on designing tools for the analysis of gut microbiome and applying these tools for the understanding of relationship between nutrition, health, and gut microbes in human individuals, with the aim of achieving personalized nutrition as personalized preventive medicine. In a recent work, Dr. Zeevi, along with his researchers have shown that small differences in the genome of gut microbes are associated with significant differences in the metabolism and weight of the human host. He also coauthored several key publications in the field of microbiome research including linking the microbiome to the effects of artificial sweeteners and host circadian rhythm, modeling bacterial growth dynamics and taking the first step towards personalized nutrition by predicting the glycemic responses of individuals to complex meals.