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Personalized gut microbial models to host phenotype

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Abstract

Microbial metabolism has been used as the main approach to assess function and elucidate environmental and host-microbiome interactions but limited to culturable and characterized bacteria. Genome scale metabolic models (GEMs) could present a comprehensive computational platform for filling the gaps in metabolic networks and investigates the metabolic capacity of whole microbiome; uncharacterised and characterized metagenome species and culturable and unculturable bacteria. Additionally, GEMs models could be utilized for population stratification based on microbiome composition, the underlying metabolic potential and community level metabolic models. To address this, using the updated gut microbiome integrated catalog and the MSP (metagenomic species pan-genome) profiles, we generated MSP-associated genome scale metabolic models. The personalized gut microbiome reaction abundance profiles, reactobiome and the bacterial community models for the subjects were constructed based on the models and MSP abundance. We revisited the concepts of enterotype and microbiome richness introducing the reactobiome as a stratification method to unravel the metabolic features of the human gut microbiome. We described five reactotypes in healthy populations from 16 countries, with specific amino acid, carbohydrate, and xenobiotic metabolic features. It helped us to improve the understanding of gut microbiome capacity and examined the gut microbiome reaction composition of the human population. The reactobiome were used to analyse the association of the gut microbiome over 1-year with matched plasma biochemistry and metabolome sampling, at four-time points, to give a detailed picture encapsulating the complexity of the host microbiome interactions.