Inference of phenotypes for amino acid metabolism in human gut microbiome using subsystems approach

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Background: The human gut microbiome is a complex and diverse microbial community, where amino acid metabolic pathways (microbial phenotypes) play crucial role for the mammal, specifically for human, host.

Amino acids are building blocks of proteins and peptides, and also serve as precursors of many essential metabolites including nucleotides, cofactors, etc. Many members of microbial communities are not capable to synthesize some amino acids (auxotrophs), while other members possess complete biosynthetic pathways for these nutrients (prototrophs). Therefore, amino acid exchange between auxotrophs and prototrophs can be an important factor shaping microbial community structure.

Results: We use a comparative genomics-based approach to assess in silico the metabolic potential for biosynthesis of essential amino acids of the 2310 bacterial members of the human gut microbiome. For each consortia member we determined their reference phylogenetic neighborhoods constituting groups of closely-related strains/species with sequenced genomes available in public databases (PATRIC). Intragenomic distances were calculated using the Mash technique (Ondov et al., 2016), and the threshold was chosen to include all strains of the same species. We further applied the subsystems-based approach as implemented in the SEED genomic database/tool to identify components of the selected metabolic pathways and uptake transporters for nutrients in 2310 analyzed genomes. We focused on reconstruction of biosynthesis and salvage pathways for amino acids, to deduce their predicted auxotrophies/prototrophies. We also analyzed genomic distributions of known uptake transporters for amino acids. The predicted pathways allowed us to classify the studied organisms with respect to their biosynthetic and transport capabilities.

Conclusions: The studied bacteria showed high level of conservation of amino acid biosynthesis phenotypes on the taxonomic level of species. Incomplete biosynthesis pathways for some amino acids suggest certain amino acid deficiencies can be alternatively supplemented by their metabolic precursors. Overall, amino acid auxotrophic phenotypes are rare in the human gut microbiota, whereas the larger number of studied bacteria is capable of de novo synthesis of all 20 amino acids.

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