The Microbiome Inferred Fiber Degradation Profile and its Relationship With the Host Diet

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Background

The human gut microbiome, plays a key role in breaking down, fermenting, and ultimately converting dietary fibers into a variety of beneficial metabolites, including most notably, short chain fatty acids. Such end products of fibers’ fermentation affect host metabolism and have been implicated in multiple diseases. Importantly, however, the types of fibers that each microbial species can degrade differ substantially between taxa, and consequently, the composition of the gut microbiome governs which dietary fibers can be utilized by the microbiome and how. Moreover, as microbial substrates, dietary fibers consumption can modulate the composition of the gut microbiome, promoting the growth of some taxa while attenuating the growth of others.

There is therefore an immense potential for modulating the gut microbiome and the production of beneficial metabolites via personalized dietary fiber recommendation. This promising route, however, is hindered by our limited understanding of dietary fiber degradation by the microbiome, and specifically, the lack of a systematic approach for predicting the impact of dietary fiber consumption on the microbiome.

Computational framework

A) Annotation of A) enzymes and B) fibers to chemical bonds.
B) Heatmap representation of the resulted fiber enzyme interaction matrix.
C) Construction of fiber degrading enzymes database.

Results

We utilized 4 publicly available datasets with distinct dietary fiber consumption regime to explore the relationship of the microbiome fiber degradation profile using our novel framework and IFDP profile. In all of the datasets, we show that the dietary fiber profile closely matches the host food items consumed.

A) Bar plot describing the ability of inulin degradation potential in mice. B-D) Volcano plots of B) folivore and non-folivore primates C) Hadza tribe population on dry and wet seasons and D) two distant Peruvian tribes.

Furthermore, we show that this profile is extremely informative, allowing better sample classification than taxonomy or functional profile and to detect inner-specie functional difference.

A-D) Bar plots describing the ability of A) cellulose degradation potential in primates B) inulin degradation potential in Hadza tribe among seasons C) pectin degradation potential in Hadza tribe among seasons plots of D) arabinoxylan degradation potential in two Peruvian tribes.

Conclusions and future

• The inferred profile matches the host’s diet more closely than microbiome taxonomic or functional profiles and can be used to successfully predict dietary regimes.
• We additionally provide evidence that different dietary fiber consumption markedly changes the composition of the dietary fiber degradation profile.
• Our framework allows researchers to gain a deeper understanding of the interaction between microbiome and diet, informing efforts towards customized and personalized nutritional recommendation.

A) ROC curves for 5 different random forest classifiers B) Hierarchical clustering of 1100 Prevotella copri genomes fiber degradation profiles. Labels corresponds to the clade the genome is a part of.