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To cite this version:
Clémence Frioux, Arnaud Belcour, Méziane Aite, Anthony Bretaudeau, Falk Hildebrand, et al.. Assessment of metabolic complementarity in large-scale microbiotas for the identification of key species. IHMC 2021 - 8th International Human Microbiome Consortium Congress, Jun 2021, Barcelone, Spain. pp.1. hal-03438983

HAL Id: hal-03438983
https://hal.archives-ouvertes.fr/hal-03438983
Submitted on 22 Nov 2021

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Assessment of metabolic complementarity in large-scale microbiotas for the identification of key species

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Context

• Microbiota analyses through metagenomic sequencing lead to huge resources of data in order to determine the organisation of microbial communities.
• Understanding the interactions within communities entails the identification of functions carried out by microbes as well as the redundancy of and complementarity between these functions.
• Genome-scale metabolic network (GSMN) reconstruction is validated method to model and simulate organisms’ functions

How to efficiently screen the metabolic functions and metabolic complementarity in hundreds or thousands of species?

How to identify key species and minimal communities associated to functions of interest?

Application to 1,520 reference genomes of the gut microbiota

• 1,520 reference genomes from culturable bacteria of the human gut microbiota [3]
• 1,520 GSMNs to be compared and analysed
• Identification of key species (KS) within the 1,520 GSMNs for groups of metabolic end-products (lipids, carbohydrates…)
• Enumeration of minimal communities associated to these metabolites
• Analysis of associations between KS within reduced communities: identifications of bacterial groups with equivalent roles in the community with respect to the metabolic end-products.

Fig 4: Analysis of the association between species in minimal communities associated to groups of metabolites. Power graphs depict the association of KS within all enumerated minimal communities. Nodes (species) are coloured based on their phylum. (a) illustrates how to read the composition of any community among the 58,520 equivalent minimal communities suitable for lipids productivity (see Table 1).

Table 1: Community reduction analysis of the metabolite categories in the gut. All minimal communities were enumerated, starting from the set of 1,520 GSMNs with respect to sets of target metabolites. KS: key species, ES: essential symbionts, A: alternative symbionts, Fms: Firmicutes, Bct: Bacteroidetes, Act: Actinobacteria, Prot: Proteobacteria, Fuso: Fusobacteria.

Suitability of metabolic modelling to MAGs

• 913 Metagenome Assembled Genomes (MAGs) of the cow rumen microbiota [2] were randomly degraded: removal of 2% of genes, 5% of genes in 80% or 100% of MAGs, removal of 10% of genes in 70% of genomes.
• MAGS characteristics are comparable to those of GSMNs obtained with reference sequences.
• M2M analyses on metabolic potential of associated GSMNs, cooperation potential, community reduction and key species show a stability of the predictions to moderate degradations of genomes.

Fig 3: Comparison of the outputs of M2M for various degradations of MAGs in a set of 913 rumen MAGs from [2].

References