

The effects of IMMPs on human microbiota in vitro

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Introduction

- Prebiotics are widely used in human and animal nutrition
- The exact effects on microbiota composition and metabolism are not clear
- Meta-Omics allow us to investigate such effects

Here we investigate the effects of Isomalto/Malto-Polysaccharides (IMMPs) - a novel group or prebiotic fibers derived from starch - on microbial composition and function, especially the carbohydrate metabolism, during in vitro fermentation using human fecal microbiota as inoculum.

Conclusions

Our study shows that :

- Prebiotics have a distinct effect on the fecal microbiota in vitro
- They promote growth of lactobacilli and bifidobacteria
- Metabolic interaction between bacterial populations in the carbohydrate breakdown

Materials and Methods

IMMPs prebiotic properties may vary depending on content of the a-1,6- glycosidic linkages and the a-1,4- glycosidic linkages present. Here we investigated the effects of IMMP with different percentages of a-1,6- glycosidic linkages, with 27% of a-1,6glycosidic linkages (IMMP27), 95% (IMMP95), 97% (IMMP97) and IMMP27 treated with a-amylase (IMMP27 pretreated).









Figure 1. Study workflow. Taxonomic classification was performed with BLAST and the LCA algorithm, metabolic mapping with KEGG and Pathway tools.

Results – data flow and result metrics

Figure 4. Temporal patterns of the selected carbohydrate degradation reactions. The majority of the degradation is performed by *Bacteroides*, but a clear increase of *Lactobacillus* and *Bifidobacterium* is visible after 24h.



Figure 5. Overview of how prebiotics influence the metabolism of certain bacterial groups. Coloured reactions indicate differential expression under the influence of prebiotics. Grey were either not detected or not influenced. *Eubacterium hallii* grew only on prebotic IMMP27.

GLC: Glucose. LAC: Lactate. BUT: Butyrate. PYR: Pyruvate. PROP: Propionate.

760 Million reads 630 Million reads 143.000 contigs 202.000 genes 128.000 genes



Figure 2. Data processing flow and the selection criteria

The results of the data processing can be seen in figure 2. Assembly was performed with the data from the control samples, IMMP27 and IMMP97. On average 80% of the reads from all samples could be mapped back to the assembly. Differential expression analysis was performed separately on genus level.

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FUM: Fumarate. SUC: Succinate. SUC-CoA: Succinyl-CoA. PROP-COA: Propanoyl-CoA.

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