The human ileo-mucosal microbiota: a first actor in dietary fiber degradation as evidenced by a functional metagenomic screening

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The Human Gut Microbiota

The human gut microbiota is a complex anaerobic ecosystem which is involved in a profusion of functions maintaining homeostasis in the gastrointestinal tract such as the metabolism of dietary fibers. Microbial fermentation of plant cell wall polysaccharides is now recognized as providing human health benefits but the fibrolytic community is still misunderstood, especially in the small intestine, because of its poor accessibility and sampling.

We focused here on the ileo-mucosal microorganisms, to examine their capabilities to degrade plant cell wall polysaccharides from dietary fibers using a functional metagenomic screening on a large insert metagenomic library. Glycoside hydrolase (GH) activities were detected using several polysaccharides as substrates.

CAZymes: Carbohydrate Active Enzymes

GlycosylHydrolases (GH)
Polysaccharide Lyases (PL)
Carbohydrate Esterases (CE)
GlycosylTransferases (GT)

Plant cell-wall polysaccharides
Fibrolytic bacteria

Glycoside Hydrolase (GH) activities from dietary fibers using a functional metagenomic screening on a large insert metagenomic library. Glycoside hydrolase (GH) activities were detected using several polysaccharides as substrates.

Metagenomic library construction

The large fragment DNA insert of bioactive clones was sequenced and the encoded enzymes deduced

Bioinformatic Analyses

The screening of the 20,000 metagenomic clones of the ileo-mucosal library evidenced genes encoding proteins involved in the degradation and fermentation of plant cell wall polysaccharides, mainly GH families in the small intestine.

Functional microorganisms in the upper part of the gastrointestinal tract are not only included in sugar metabolism but also in dietary fiber (polysaccharides) degradation.

Functional metagenomic screening is a powerful tool to decipher major functions of the human gut microbiota

Conclusion

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GH genes evidenced in the microbiota might be used as good predictive markers of individual health status using quantitative metagenomics. (Le Chatelier et al., Nature 2013)