

Individual and group-based differences in gut microbiota responses to *in vitro* fiber interventions

Can mixtures of prebiotics contribute to harmonized beneficial effects?

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Abstract

Fibers are increasingly recognized as a way to influence gut microbiota composition and function, but selecting the right fiber in a background of enormous individual variation in microbiome composition is challenging. To deal with this high inter-individual variation in gut microbiome composition and the diversity of individual responses to gut microbiome-targeted interventions, it is important to develop models that can replicate this diversity and that can be successfully applied for pre-clinical studies and assessments of efficacy.

Fecal samples collected from healthy donors and donors affected by Irritable bowel Disease (IBD) were investigated in an advanced *in vitro* model of the human gut microbiota for individual and group-based differences in their response to fiber treatments.

Differences in microbiota composition and metabolite (short-chain fatty acids and branched-chain fatty acids) profiles between different individuals after incubation with single fibers were found. The combination of multiple fibers, tested on fecal material from IBD subjects, resulted in more similar effects across individual microbiota. Furthermore, differences in microbiota composition between healthy and IBD subjects after incubation with fiber were found. However, these did not translate into differences in functional metabolic response towards fibers.

Here we show that advanced *in vitro* models of the human gut microbiota can be successfully applied to study personalized compositional and metabolic response to fiber treatment. Different individuals may benefit from interventions with different dietary fibers depending on their personal baseline microbiota and on the desired compositional and functional microbiota effect. We propose that mixtures of fibers are better adapted to overcome individual variations in microbiome composition than single prebiotic fibers and thereby may achieve broader beneficial effects in humans.