INTRODUCTION:
The gut microbiota is extensively studied given its role in health and disease, with special attention to dietary modulation. Dietary fibre is considered a key component in modulating the gut microbial community composition and functionality to sustain gut health. Research so far has mainly focused on the benefits derived from fermentation of soluble dietary fibre. However, insoluble, partly non-fermentable fibres might form an interesting additional niche for gut microbes to adhere, grow or metabolically interact on. Our study focused on wheat bran, consisting of a unique combination of fermentable and non-fermentable fibres, as it is the most concentrated source of insoluble dietary fibre in the European diet.

METHODS:
In a first stage, 48 hours in vitro batch incubations were conducted combining wheat bran with the microbial community derived from fecal samples of ten subjects. Three subjects were selected for a long-term study using the Simulator of the Human Intestinal Microbial Ecosystem (SHIME). During one week of stabilization and five weeks of wheat bran treatment the short chain fatty acid (SCFA) and ammonium production were analyzed. The microbial population density was followed up using flow cytometry and 16S rRNA gene qPCR. At several time points the microbial community in the luminal phase, as well as attached to the washed non-fermentable bran residue and metabolic profile were determined through Illumina 16S rRNA gene amplicon sequencing and metabolomics.

RESULTS:
The response of the luminal microbial community after 48 hours in vitro batch incubation with wheat bran was largely donor-dependent, both functionally, and with respect to the microbiome composition. Depending on the donor, wheat bran fermentation yielded proportionally more propionate or butyrate. On the wheat bran residue Clostridium cluster XIVa and, depending on the donor, Prevotella, Roseburia, Megamonas, Bifidobacterium and Bacteroides species were enriched. These genera include species with the documented ability to serve as primary degraders of wheat bran components and other species depending on cross-feeding to obtain their energy. Both functional groups were present in all donors despite the large inter-individual differences, suggesting that primary degraders and cross-feeders are united in a trophic network on the bran. From the follow-up experiment in the SHIME system, where wash-out presents an important selective pressure, it becomes apparent that the established network on bran is highly dynamic and mainly consisting of Prevotella, Lactobacillus, Dialister and Bifidobacterium for the selected donors. Prevotella and Dialister were also found to dominate the luminal communities, along with Bacteroides and Clostridium cluster XIVa. The microbial population density and SCFA production remained stable in spite of the large community shifts over time, confirming the large functional redundancy of the gut microbiota.

DISCUSSION:
To conclude, further characterization of the microbiota associated with dietary particles in the gut will contribute to a better understanding of the colonization process of the human gut by micro-organisms, leading to a more comprehensive view of the complex microbiota-host symbiosis, eventually offering new possibilities for steering the gut microbial community. Wheat bran is a promising candidate in this regard.

KEYWORDS: Probiotics, Insoluble dietary fibre, In vitro simulation of the GIT, Inter-individual variability, Dietary particle attached microbiota, Illumina 16S rRNA gene amplicon sequencing
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