Department of Food and Nutritional Sciences

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In vitro fermentation of NUTRIOSE®, a wheat dextrin soluble fibre, in a continuous culture human colonic model system

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Background

The composition and metabolic activity of the human gut microbiota is influenced by many factors, including adiposity. Accordingly, there is growing interest in nutritional modulation of the gut microbiota and its implications for obesity and metabolic diseases, such as type 2 diabetes(1). NUTRIOSE®, a wheat dextrin soluble fibre, has been shown to have beneficial effects on markers of insulin resistance(2), appetite regulation(3) and weight management(4), possibly acting via mechanisms governed by the selective modulation of the gut microbiota.

Aims

We sought to investigate the effects of NUTRIOSE® fermentation on the microbial composition and metabolic end products using an *in vitro* three-stage continuous culture human colonic model (gut model) system.

Methods

Three gut models, each comprising of vessels designed to simulate the human digestive tract, were run (see Fig. 1).

To mimic human ingestion, 7 g NUTRIOSE® was administered to the gut models twice daily at 10.00 and 15.00, for a total of 18 days.

Samples were collected at the start and end of the treatment period and analysed for total bacterial populations and bacterial groups, *Atopobium*, *Bacteroides, Bifidobacterium* genus, *Clostridium coccoides-Eubacterium rectale* and *Clostridium histolyticum* group, *Escherichia coli, Lactobacillus* genus and *Roseburia/E. rectale* group, by 16S rRNA-based fluorescence *in situ* hybridisation.

Concentrations of principle short-chain fatty acids (SCFA), acetate, propionate and butyrate, were determined by gas chromatography.

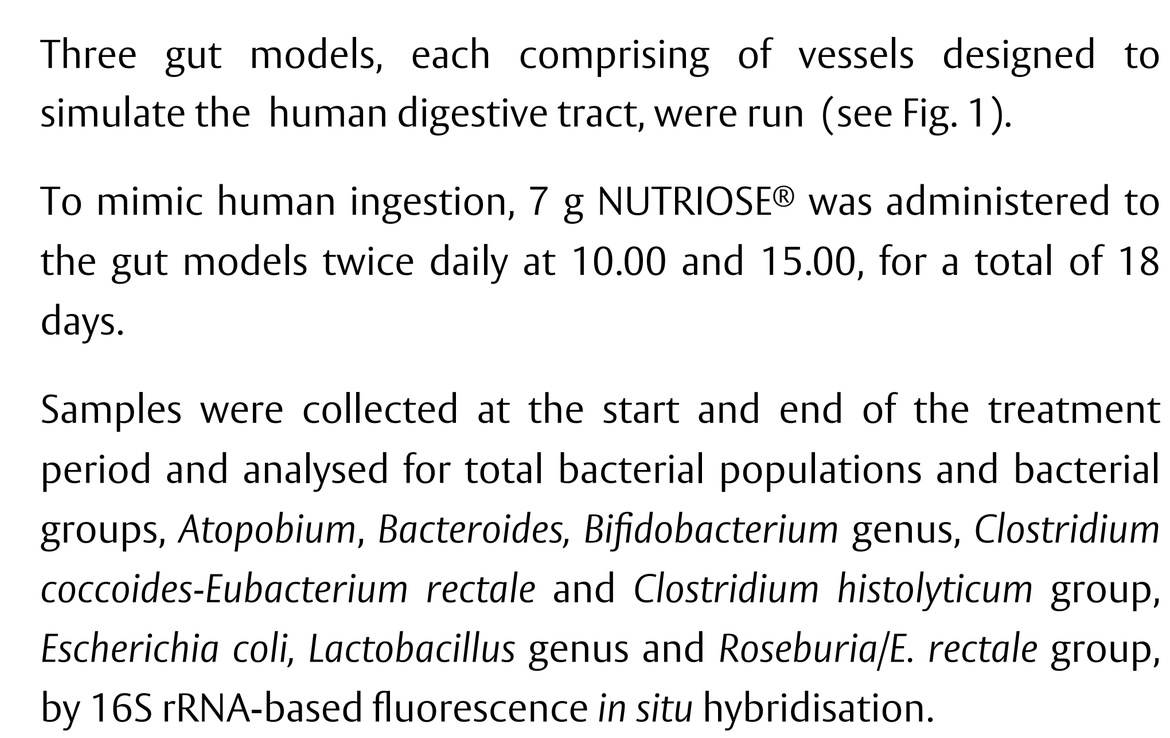

Fig. 1. Three-stage continuous culture human colonic model system(5)

Results

NUTRIOSE® administration increased counts of total bacteria (V2 and V3) and key butyrate-producing bacteria, *Clostridium* cluster XIVa and *Roseburia* genus (V1,V2 and V3). No significant differences were found for the other bacterial groups.

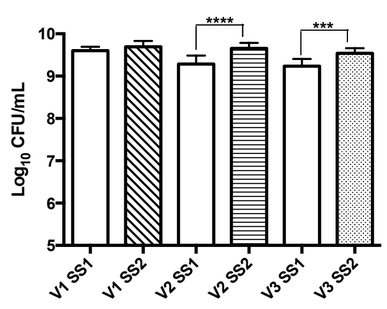

Fig. 2. Total bacteria

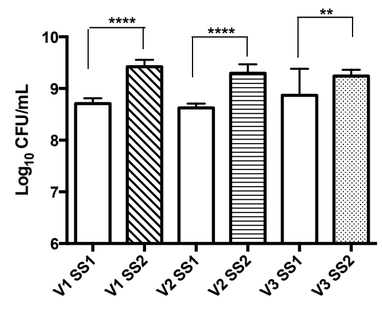

Fig. 3. Most members of *Clostridium* cluster XIVa

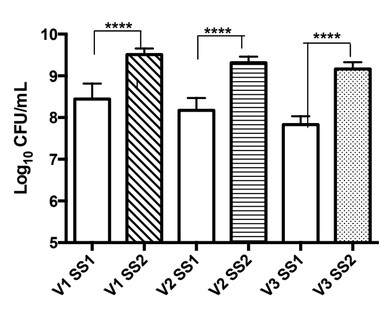

Fig. 4. *Roseburia* genus

Concentrations of butyrate concomitantly increased in all three vessels of the gut model systems. Furthermore, acetate and propionate concentrations increased in V2 / V3, and V3, respectively.

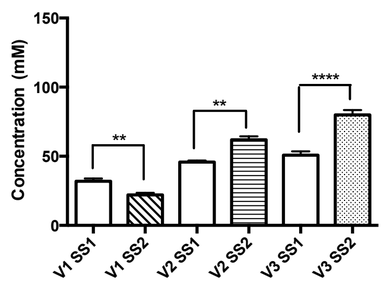

Fig. 5. Acetate

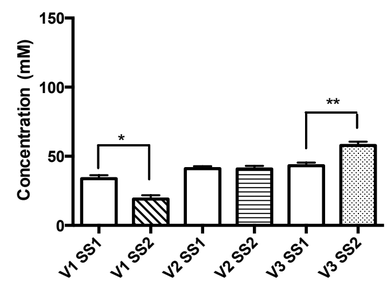

Fig. 6. Propionate

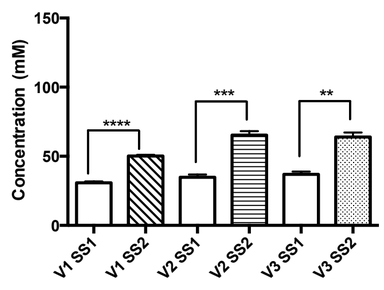

Fig. 7. Butyrate

Summary and conclusions

NUTRIOSE® was selectively fermented by *Clostridium* Cluster XIVa and *Roseburia* genus in all vessels of the gut model.

NUTRIOSE® favourably altered the metabolic profile of the gut ecosystem, with elevated concentrations of butyrate and propionate, which have both been purported to have energy metabolism and appetite-regulatory properties(5).

Future work: A human intervention study is now underway to determine the effects of NUTRIOSE® in an *in vivo* setting.

References

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