

The effects of commonly consumed dietary fibres on the gut microbiome and its fibre fermentative capacity in adults with inflammatory bowel disease in remission

Konstantinos Gerasimidis¹, Ben Nichols¹, Mhairi McGowan¹, Vaios Svolos¹, Rodanthi Papadopoulou¹, Margarita Kokkorou¹, Martina Rebull¹, Teresita Bello Gonzalez¹, Richard Hansen², Richard K Russell³, Daniel R Gaya⁴

¹ Human Nutrition, School of Medicine, College of Medical, Veterinary and Life Sciences, University of Glasgow; ² Department of Paediatric Gastroenterology, Hepatology and Nutrition, Royal Hospital for Children, Glasgow; ³ Department of Paediatric Gastroenterology, Hepatology and Nutrition, Royal Hospital for Children, Edinburgh; ⁴ Gastroenterology Unit, Glasgow Royal Infirmary

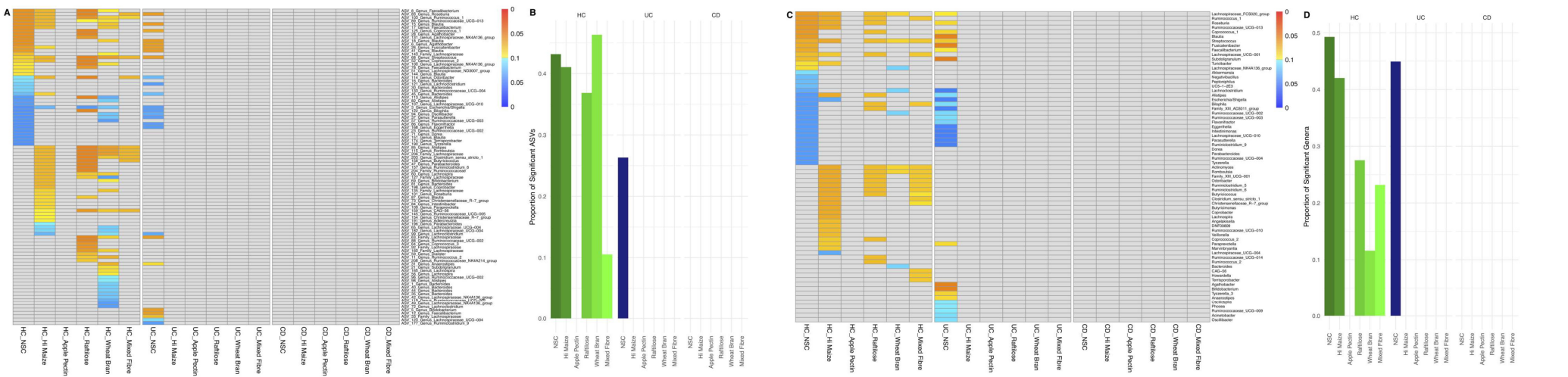
Background & Aim: It has been suggested that the gut microbiome of patients with inflammatory bowel disease (IBD) is unable to ferment dietary fibre. This project explored the in vitro effect of fibre fermentation on production of short chain fatty acids (SCFA) and on microbiome composition.

Methods:

- Faecal samples were collected from 40 adults (>16 y) with IBD (n=20 with Crohn's disease and n=20 with Ulcerative colitis) in clinical remission and 20 healthy controls (HC)
- In vitro batch culture fermentations were carried out using as substrates maize starch, apple pectin, raphilose, wheat bran, α -cellulose and a mixture of the 5 fibres.
- SCFA concentration (umol/g) was quantified with gas chromatography and microbiome was profiled with 16S rRNA sequencing.

Results:

- Fibre fermentation did not correct the baseline microbial dysbiosis or lower diversity seen in either CD or UC.
- For all fibres, up to 51% of baseline ASVs or genera changed in abundance in HC.
- In patients with IBD, fermentation of fibre substrates had no effect on species or genera abundance.
- Production of SCFA varied among the different fibre substrates but this was not different between the two IBD groups and compared to HC after either 5 or 24 hours of fermentation.



Conclusion: Despite extensive microbial dysbiosis, patients with IBD have a similar capacity to ferment fibre and release SCFA as HC. Fibre supplementation alone may be unlikely to restore to a healthy status the compositional shifts characteristic of the IBD microbiome.

