

## Topic Area: Clinical Research (Including Outcomes of Intervention)

### Abstract Title

Examining the day to day effect of varying FODMAP content on the microbiota: a case study of an IBS patient and a healthy control

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### Abstract

**Introduction:** A low FODMAP diet reduces the intake of prebiotic fructooligosaccharides (FOS) and galactooligosaccharides (GOS) which are substrates used by host microorganisms to confer a health benefit.

**Objective:** to investigate the day to day effect of increasing dietary oligosaccharides on clinical symptoms and the microbiota in an IBS patient and a healthy control.

**Methods:** Two participants one with IBS and one without IBS consumed a diet low in FOS, GOS, sorbitol and fructose for ten days they then switched to a diet high in FOS and GOS for ten days. Weighed food records were collected and analysed on ESHA and the online FODMAP calculator. Daily stool samples were collected. DNA was extracted using the DNAeasy kit. The V4 region of the 16S rRNA was amplified. DNA was sequenced on Illumina MiSeq. Sequence variants were annotated using the Silva database version 128. Data was treated compositionally. Dendrograms of relatedness were generated by unsupervised clustering of Aitchinson distances.

**Results:** 62% of the variation in the microbiome was explained by the difference between the two individuals. At the genus level the IBS patient had more Prevotella and the control more Alistipes. Dendrograms showed that in the IBS patient but not the control there was clustering of samples by diet with one branch only containing samples taken during the low FODMAP diet.

**Conclusions:** Altering the oligosaccharide control of the diet significantly changed the total microbiota of the participant with IBS, however there was less effect on the microbiota of the individual without IBS.

**Significance to the field of dietetics:** Conducting longitudinal studies on a smaller number of individuals may reveal additional and complementary insights into the effect of dietary intervention of the microbiota especially as it reduces the effect of contaminated or unusual microbiota samples.