

No consistent faecal microbiota or SCFA signature of symptom severity in Irritable Bowel Syndrome: a longitudinal study

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INTRODUCTION

- Alterations in fecal microbiota and short chain fatty acids (SCFA) have been observed in Irritable Bowel Syndrome (IBS) patients, but consensus is lacking.
- This can be due to the large individual variation and cross-sectional study designs.
- Recently, a microbial signature associated with IBS severity was identified cross-sectionally.

AIM

We assessed the longitudinal dynamics of fecal microbiota and SCFAs in different IBS severity groups compared to controls and how these are associated with stool pattern, diet, depression, anxiety and quality of life.

METHODS

We performed an observational study with two timepoints including 91 IBS patients and 30 controls (Figure 1). Data was stratified for IBS severity (no, mild, moderate and severe symptoms).

Microbiota composition in fecal samples was determined by sequencing the V4 region of the 16S ribosomal RNA gene, whereas SCFAs were analyzed by High-Performance Liquid Chromatography.

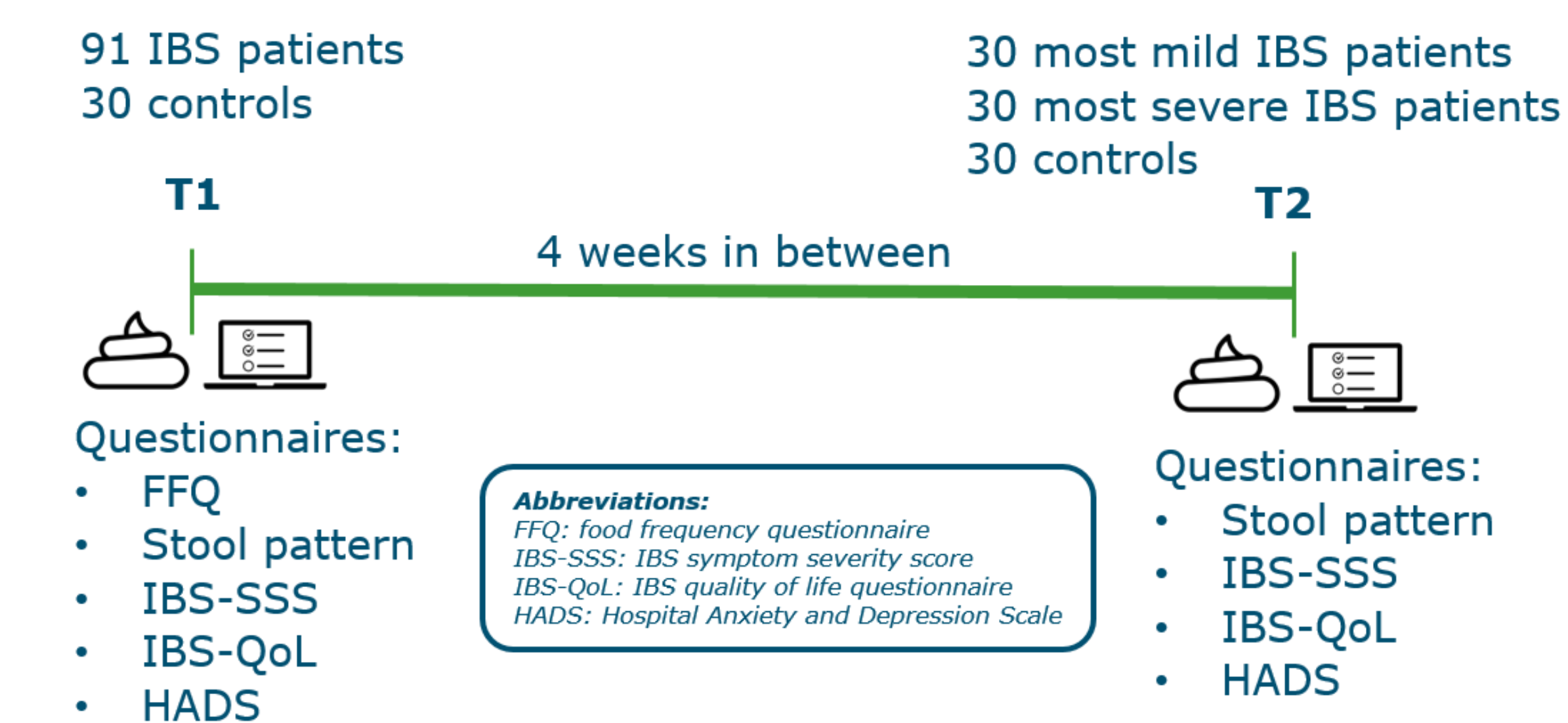


Figure 1 Study design

RESULTS

- Large within person variation was seen: 36% of IBS patients changed in severity group, and 53% changed in predominant stool pattern between T1 and T2.
- No difference in alpha or beta microbiota diversity, or SCFA levels between IBS and controls or severity groups.
- No consistent association between psychological factors and microbiota composition or with diet
- Bifidobacterium*, *Terrisporobacter* and *Turicibacter* were consistently different between IBS and controls, but not between IBS severity groups**

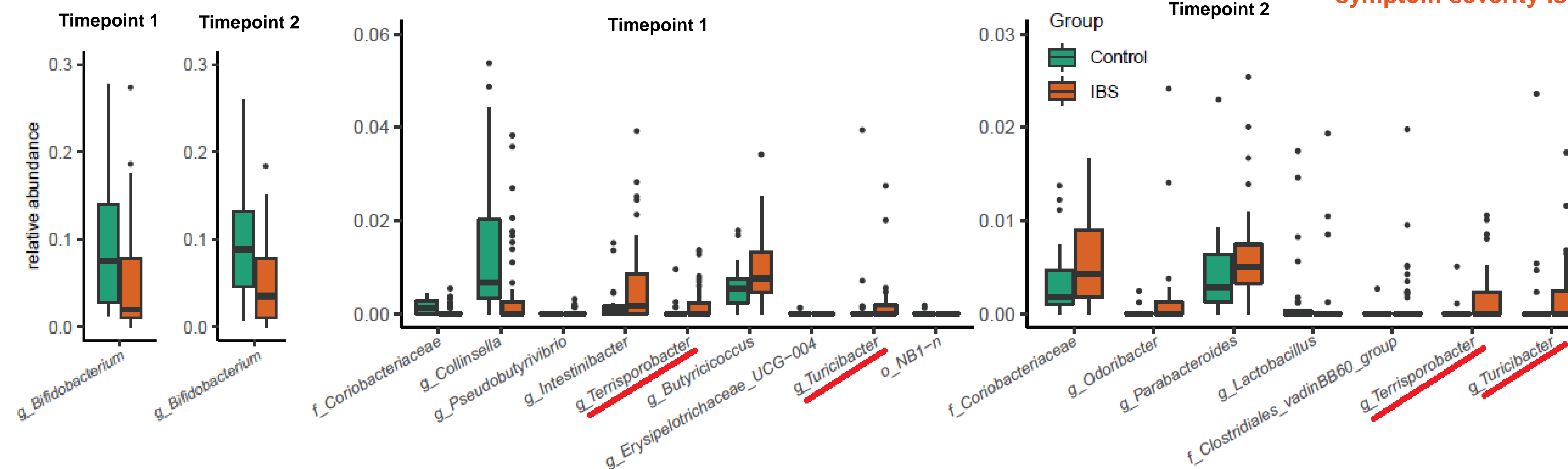


Figure 3 Alterations in genus taxa across the different timepoints

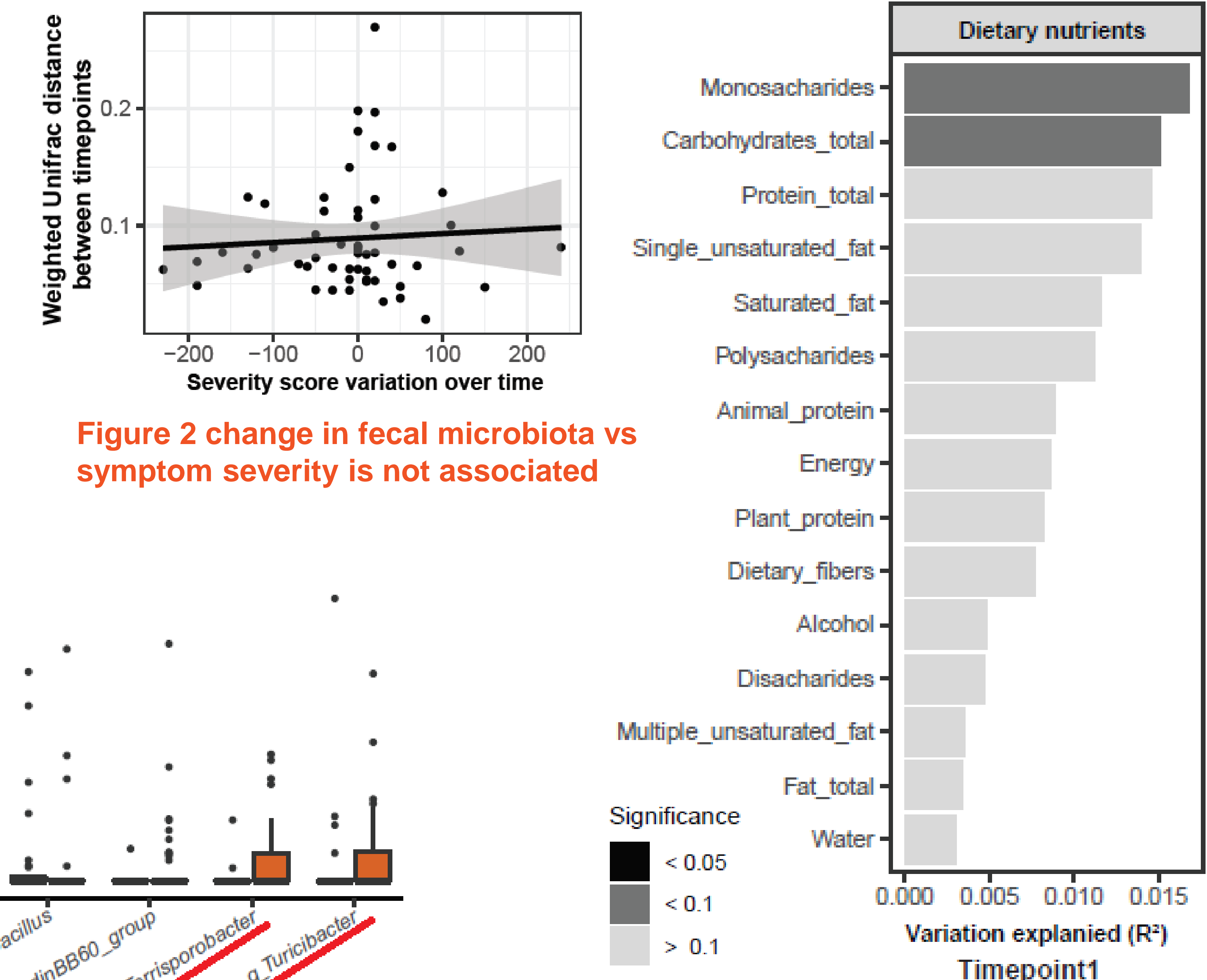


Figure 2 change in fecal microbiota vs symptom severity is not associated

Figure 4 No associations between dietary intake and fecal microbiota variation

CONCLUSIONS

- No consistent fecal microbiota and SCFA signature associated with IBS severity was found.
- The genera *Bifidobacterium*, *Terrisporobacter*, and *Turicibacter* were consistently different between IBS and controls over time.
- The importance of inclusion of multiple timepoints was demonstrated by the large within and between person variation of observed IBS symptom severity, stool pattern and their association with fecal microbiota composition over time. Hence, conclusion of single-timepoint studies in the past should be reconsidered, and future studies are highly recommended to take time-dynamics into account.

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