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.

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, but not between IBS severity groups.
• 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.