

Altered fecal microbiome in patients with irritable bowel syndrome with diarrhea is related to bile acid synthesis, not to rapid colonic transit

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INTRODUCTION

Bile acid (BA) diarrhea (BAD) affects up to 30% of patients with irritable bowel syndrome with diarrhea (IBS-D).

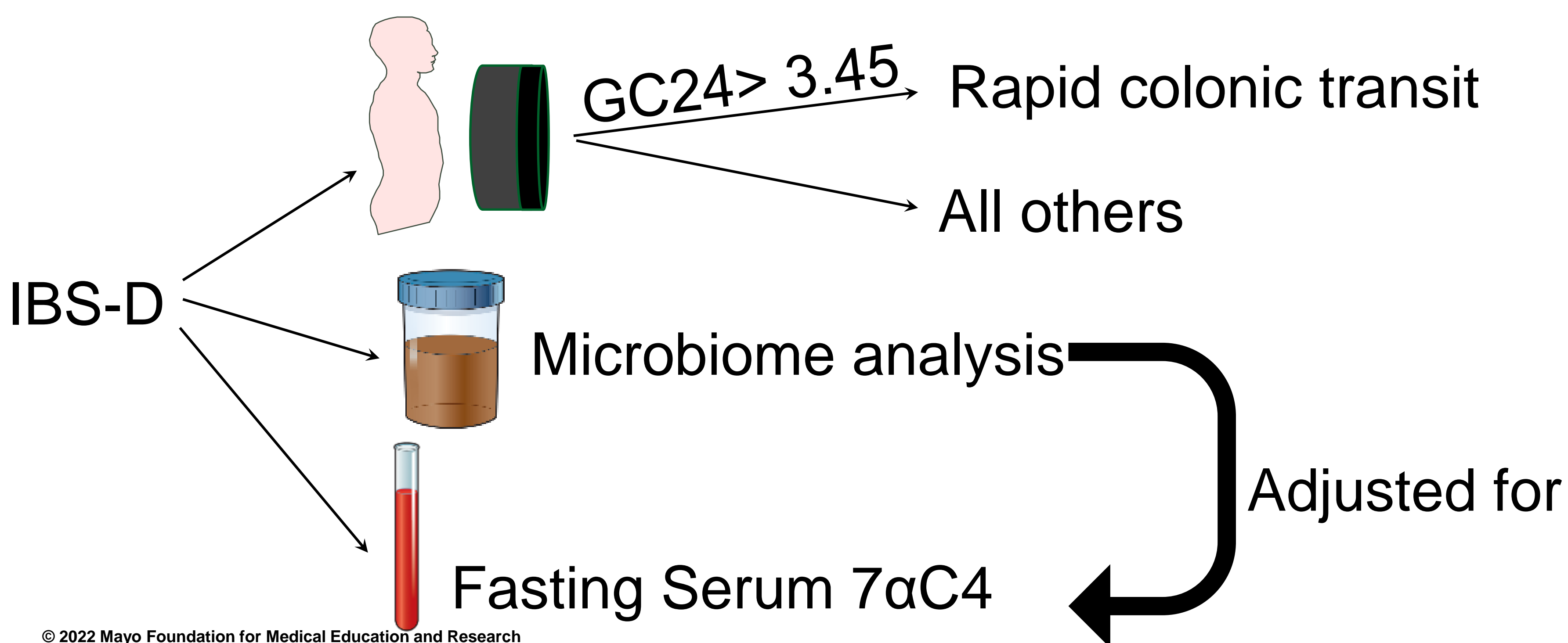
In a cohort of 194 patients with IBS-D, 43 had BAD (serum 7αC4 > 52 ng/mL). Patients with BAD had a faster colonic transit, lower microbial α diversity, and a different microbial compositional profile based on β diversity compared to IBS-D without altered BA metabolism (ABAM) (PMID 35580964).

However, the effect of colonic transit on the relationship between BAs and the microbiome was not evaluated.

AIM

Our aim was to compare the microbiome composition in the same cohort of patients with IBS-D (total 183), with and without rapid colonic transit as measured by the geometric center at 24 hours (GC24) before and after adjusting for ABAM (elevated serum 7αC4).

METHODS



RESULTS

Figure: Firmicutes/Bacteroidetes ratio, and microbial α and β diversity in patients with IBS-D with or without rapid colonic transit, before (Pre) and after (Post) adjustment for age, sex, BMI and 7αC4

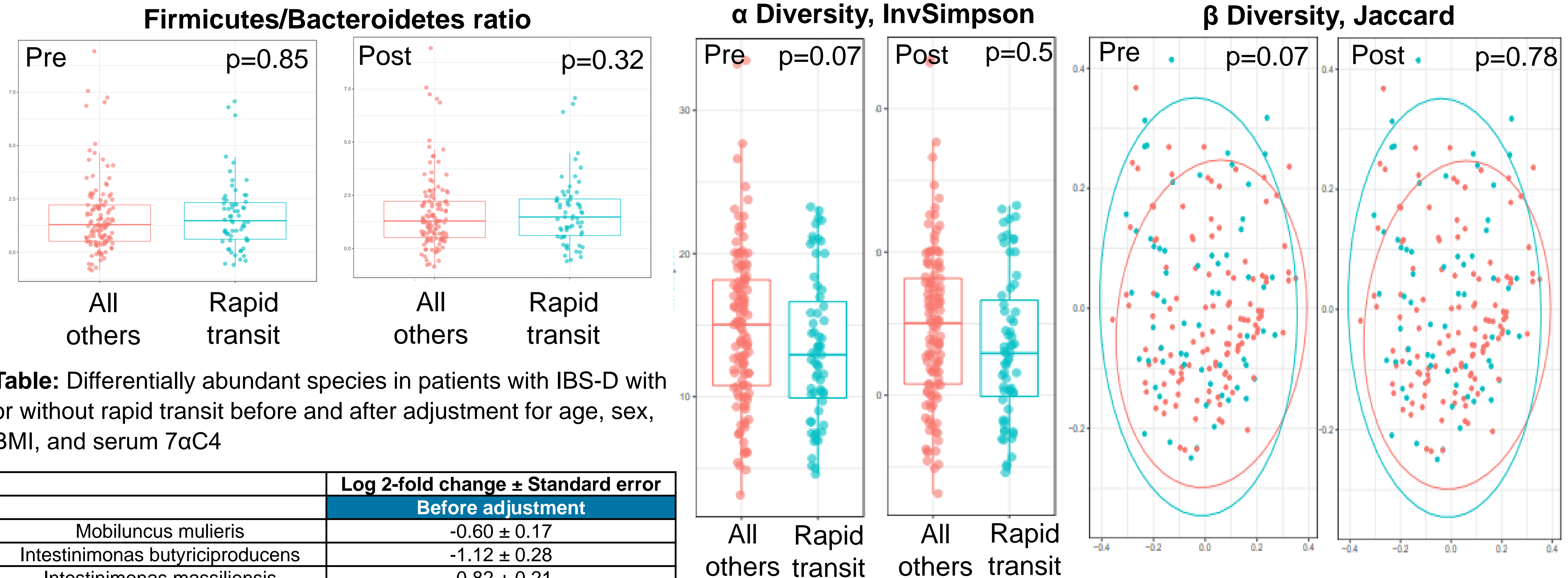


Table: Differentially abundant species in patients with IBS-D with or without rapid transit before and after adjustment for age, sex, BMI, and serum 7αC4

	Log 2-fold change ± Standard error
	Before adjustment
Mobiluncus mulieris	-0.60 ± 0.17
Intestinimonas butyriciproducens	-1.12 ± 0.28
Intestinimonas massiliensis	-0.82 ± 0.21
Pseudoflavonifractor capillosus	-0.75 ± 0.20
Anaerosalibacter massiliensis	-0.92 ± 0.27
Anaerofustis stercorihominis	-1.79 ± 0.48
Lachnospiraceae bacterium MC2017	-0.99 ± 0.28
Oscillibacter sp. KLE 1745	-1.13 ± 0.35
Anaerotruncus colihominis	-0.75 ± 0.20
Megasphaera genomosp. Type 1	-1.32 ± 0.38
Clostridium polynesiense	-1.62 ± 0.32
Clostridium cellulosi	-0.94 ± 0.29
Ruminococcaceae bacterium AE2021	-0.61 ± 0.17
Caloramator australicus	-0.35 ± 0.11
	After adjustment
Clostridium polynesiense	-1.34 ± 0.33

CONCLUSION

Altered fecal microbiome composition in patients with IBS-D and rapid colonic transit is significantly impacted by a biomarker of bile acid synthesis, serum 7αC4, rather than resulting from the rapid transit.