

Cross-over randomized trial. Patients with quiescent CD were randomised to 21 days of typical Australian diet or low FODMAP diet with over 21 days washout in between.

Primary endpoints: The primary end point was the difference in fecal microbiota on the low FODMAP vs typical Australian diets as measured by total and specific bacterial abundance.

Results: N=9

- SCFA, pH and total bacterial abundance remained unaltered, but relative abundance was higher for butyrate-producing Clostridium cluster XIVa (P=0.008) and mucus-associated Akkermansia muciniphila (P=0.016), and lower for Ruminococcus torques (P=0.034) during the Australian compared with low FODMAP diet.
- The diets had no effects on calprotectin, but symptoms doubled in severity with the Australian diet (n=9; P=0.001)

Conclusion:

In clinically quiescent Crohn's disease, altering dietary FODMAP intake is associated with marked changes in fecal microbiota, most consistent with a prebiotic effect of increasing FODMAPs as shown in an irritable bowel/healthy cohort.

Measure	Bacteria	Australian diet	Low FODMAP diet	P-value	Habitual diet
Absolute abundance (Log <sub>10</sub> copies of 16S rRNA gene/g)	Total bacteria	9.48 (9.17–9.79)	9.53 (9.20–9.86)	0.641	9.60 (9.19–10.0)
	<i>Clostridium</i> cluster IV	7.58 (6.65–8.50)	7.59 (6.49–8.68)	0.773	7.56 (6.34–8.78)
	<i>F. prausnitzii</i>	6.79 (5.77–7.80)	6.81 (5.64–7.98)	1.00	6.96 (5.73–8.20)
	<i>Clostridium</i> cluster XIVa	<b>8.73<sup>a</sup> (8.42–9.03)</b>	<b>7.94 (7.55–8.34)</b>	<b>0.008</b>	<b>8.01 (7.57–8.46)</b>
	<i>Roseburia</i>	7.02 (6.03–8.00)	6.95 (5.80–8.09)	0.313	7.16 (6.32–8.00)
	<i>Lactobacilli</i>	6.11 (5.70–6.52)	6.48 (6.01–6.96)	0.078	6.29 (5.84–6.73)
	<i>Bifidobacteria</i>	7.33 (6.87–7.80)	7.12 (6.54–7.70)	0.078	7.33 (6.60–8.07)
	<i>A. muciniphila<sup>b</sup></i>	<b>5.08<sup>a</sup> (3.19–6.97)</b>	<b>3.75 (1.97–5.54)</b>	<b>0.016</b>	<b>4.11 (2.44–5.78)</b>
	<i>R. gnavus</i>	7.11 (6.79–7.44)	7.20 (6.90–7.50)	0.547	7.26 (6.81–7.71)
	<i>R. torques</i>	5.65 (4.65–6.65)	6.13 (5.28–6.99)	0.195	6.14 (5.41–6.86)
Relative abundance (percentage of total bacteria)	<i>Clostridium</i> cluster IV	2.70 (0.63–4.78)	2.69 (0.93–4.46)	0.383	3.02 (0.77–5.26)
	<i>F. prausnitzii</i>	0.47 (0.21–0.72)	0.66 (0.14–1.19)	0.250	0.81 (0.09–1.54)
	<i>Clostridium</i> cluster XIVa	<b>19.2<sup>a</sup> (11.2–27.3)</b>	<b>2.81 (1.88–3.74)</b>	<b>0.008</b>	<b>2.90 (1.80–4.01)</b>
	<i>Roseburia</i>	0.94 (0.21–1.68)	0.81 (0.18–1.44)	1.00	0.68 (0.23–1.13)
	<i>Lactobacilli</i>	0.06 (0.01–0.10)	<b>0.17<sup>a</sup> (–0.01 to 0.35)</b>	0.195	<b>0.06 (0.03–0.08)</b>
	<i>Bifidobacteria</i>	1.27 (0.11 to 2.43)	1.11 (–0.55 to 2.76)	0.383	2.09 (–0.54 to 4.71)
	<i>A. muciniphila<sup>b</sup></i>	<b>0.15<sup>a</sup> (–0.05 to 0.35)</b>	<b>0.01 (–0.02 to 0.04)</b>	<b>0.016</b>	<b>0.01 (–0.01 to 0.03)</b>
	<i>R. gnavus</i>	1.17 (–0.25 to 2.59)	1.39 (–0.38 to 3.17)	0.461	2.26 (–1.51 to 6.03)
	<i>R. torques</i>	<b>0.10 (–0.04 to 0.24)</b>	<b>0.16 (–0.03 to 0.34)</b>	<b>0.039</b>	0.15 (–0.05 to 0.35)

