



Swapping white for high-fibre bread exceeds fibre target and improves microbiome diversity

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A majority of Australians consume a limited range of different dietary fibres and insufficient total dietary fibre⁽¹⁾. This contributes to low intestinal microbial diversity and impaired microbial function, such as capability in producing beneficial metabolites like short-chain fatty acids (SCFA). This diet-induced dysbiosis is associated with poor gastrointestinal health and a broad range of non-communicable diseases⁽²⁾. Our study aimed to determine whether one dietary change, substitution of white bread with a high fibre bread improves faecal microbial diversity and butyrate-producing capability. Twenty-six healthy adults completed a randomised, cross-over, single-blinded intervention. Over the two intervention phases separated with a 4-wk washout, participants consumed either 3 slices of a high fibre bread (Prebiotic Cape Seed Loaf with BARLEYmax®) or control white bread as part of the usual diet, each for 2 weeks. At the beginning and end of each intervention period, participants completed a 24-h diet recall, a gut symptoms rating questionnaire and provided a faecal sample for microbiome analysis. The composition of faecal microbiome was characterised using 16S rRNA amplicon sequencing (V3-V4) and a marker of butyrate synthesis capability, the faecal content of butyryl-CoA:acetate CoA-transferase (BCoAT) gene was assessed using Real-time PCR. The high fibre bread intervention increased the servings of whole grain from 1.5 to 4 per day and increased total dietary fibre intake to 40 g/d which was double the amount of fibre consumed by participants at baseline or during the white bread intervention. Compared to white bread, the high fibre bread increased richness and evenness (Shannon, $p = 0.014$) of the gut microbiota and increased the relative abundance of SCFA producing taxa Lachnospiraceae ND3007 group ($p < 0.001$, FDR = 0.019). In addition, the high-fibre bread tended to increase relative abundance of butyrate-producing genus *Roseburia*, and microbial BCoAT gene content compared to white bread. In conclusion, the substitution of white bread with high-fibre bread improved the diversity of gut microbiota, specific microbes involved in SCFA production and may enhance the butyrate production capability of gut microbiota in healthy adults.

Keywords: dietary fibre; gut microbiome; microbiome diversity; butyrate

Ethics Declaration

Yes

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References

1. Fayet-Moore F, Cassettari T, Tuck K *et al.* (2018) *Nutrients* **10**(5):599.
2. Cronin P, Joyce SA, O'Toole PW *et al.* (2021) *Nutrients* **13**(5):1655.