

Faecal microbiota composition affects the *in vitro* fermentation of rye, oat and wheat bread

Introduction

- Fermentation of dietary fibre by gut microbes produces short chain fatty acids (SCFA), most importantly acetate, propionate and butyrate.
- Recent *in vitro* studies [1,2] have shown differences in fermentation between microbiota community compositions, with respect to time, SCFA production, and preference to substrate.
- The aim of this study was to investigate how faecal microbiota composition influences the fermentation of oat, rye and wheat breads with differing dietary fibre amount and composition.

Materials and Methods

- Two faecal donors with different microbial community compositions were recruited.
- Whole grain rye bread, whole grain oat bread and refined wheat bread samples were digested chemically and enzymatically and chemical composition of bread and derived fermentation substrate were analysed.
- *In vitro* fermentation model was used to study SCFA and gas production, degradation of dietary fibre, pH, and changes in microbiota composition at 8h and after 24-hour fermentation experiments.

Results

- Higher acetate ($p=0.003$) and butyrate ($p<0.0001$) levels at 24h were seen in donor II with high relative abundance of *Prevotella* and *Subdoligranulum*, whereas propionate levels were higher in donor I ($p=0.02$) with high relative abundance of *Bacteroides* and *Escherichia/Shigella*.
- Total gas production was higher in donor II ($p<0.0001$).
- Gas and SCFA levels followed the substrate fibre amount with rye contributing to highest and wheat to lowest levels.
- Some differences in fibre degradation, for example in water-insoluble arabinoxylan, were observed between the donors and substrates.
- Shifts in microbiota composition were observed during fermentation, and were driven by different substrates.

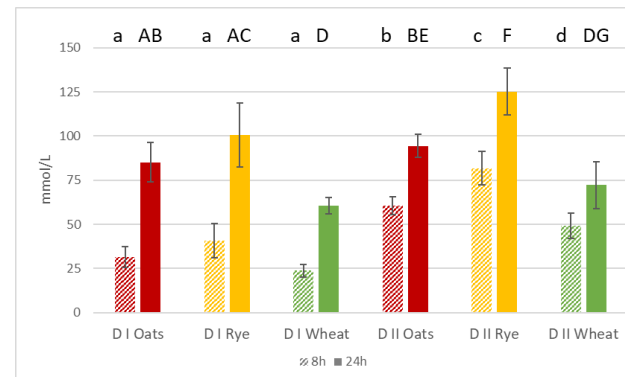


Figure 1. Total short chain fatty acid levels at 8h and 24 h. Different letters indicate significant difference between samples; lowercase 8h, uppercase 24h. D, Donor.

Conclusions

- The results indicate contrasting fermentation capacity and substrate utilisation potential between different microbiota profiles in the human gut.
- Differences in gut microbiota composition could in part explain intra-individual differences in diet-related health outcomes.
- Findings can lead to personalised dietary recommendations on fibre intake, or products containing special fibre composition for different microbiota profiles, but human clinical trials are needed.

References

1. Chen, T., et al., *Fiber-utilizing capacity varies in Prevotella- versus Bacteroides-dominated gut microbiota*. Sci Rep, 2017. 7(1): p. 2594.
2. Wu, Q., et al., *Fermentation properties of isomaltooligosaccharides are affected by human fecal enterotypes*. Anaerobe, 2017. 48: p. 206-214.

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Contact

Laura Pirkola, Industrial PhD student
laura.pirkola@slu.se

