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Abstract

The Impact of Malted Grains on Human Intestinal Microbiota Composition in an In Vitro Model †

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Abstract: Background and Objectives: Malting barley (Hordeum vulgare) and wheat (Triticum aestivum) grains offer various nutritional benefits through controlled germination processes, including an increased fiber content, improved mineral bioavailability, higher levels of vitamins and antioxidants, and enhanced protein digestibility. However, the specific impact of malting on the intestinal microbiota remains unknown. Given the potential of malted grains to enhance fiber content and because they contain beneficial compounds like prebiotics, it is reasonable to speculate that the consumption of malted barley and wheat could positively influence the intestinal microbiota by promoting the growth of beneficial bacteria and supporting a healthy gut environment. Methods: Raw and malted barley and wheat grains were subjected to in vitro gastric and intestinal digestion using the INFOGEST method. After gastrointestinal digestion, samples were centrifuged, and the undigested pellet and 10% of the supernatant were introduced into a bioreactor that mimicked the proximal colon's environmental conditions. The bioreactor was inoculated with human fecal microbiota pooled from six healthy human donors to simulate colonic fermentation. Samples were collected at 0, 6, and 24 h, and DNA was extracted. Whole variable region sequencing using PacBio technology was performed for 16S sequencing. Results: In our in vitro system, malting did not significantly impact microbiota alpha diversity (Shannon index and richness) or beta diversity. The colonic fermentation of malted barley was characterized by a higher relative abundance of *Enterococcus faecalis* ($p = 0.02$), *Weissella cibaria* ($p = 0.04$), and the *Ruminococcus gnavus* group ($p < 0.05$). When comparing malted and non-malted wheat, non-malted wheat fermentation showed a higher relative abundance of *Lactobacillus gasseri* ($p = 0.05$) and lower levels of *Bacteroides* sp. ($p < 0.05$). Discussion: Based on our results, malting has a minimal impact on microbiota composition in vitro. However, considering the changes in nutrients and bioactive compounds, alterations to the microbiota activity may be more substantial. Future analyses using metagenomic sequencing or metabolomics profiling could provide valuable insights into the impact of malting on the functional activity of the microbiota. In vivo studies will be necessary to assess whether the consumption of malted grains over extended periods can have a more significant impact on the intestinal microbiota.

Keywords: malting; cereals; microbiome; colonic fermentation; *Lactobacillus*

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