


Abstract

Malting of Barley and Wheat Grains Impacts Their Metabolic Profiles in a Model of In Vitro Colonic Fermentation [†]

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Abstract: Background and objectives: Malting is a germination process that alters the composition of cereal grains and can impact the digestion of various nutrients included in whole-grain cereals. This can have a further impact on the composition of dietary fiber fractions fermented by the gut microbiota. We investigated the impact of malting with barley (*Hordeum vulgare*) and wheat (*Triticum aestivum*) grains on gut microbial metabolites during in vitro colonic fermentation in a model of human gut. Methods: Raw and malted barley and wheat grains went through in vitro gastric and intestinal digestions and a 24 h in vitro colonic fermentation mimicking human intestinal activities. Metabolite analysis was performed using nontargeted gas chromatography-mass spectrometry (GC-MS) optimized for the analysis of in vitro gut fermentation samples. Results: Multiple metabolites, including amino acids and their derivatives (e.g., leucine and γ -aminobutyric acid), biogenic amines (e.g., tyramine, histamine, and putrescine), sugars and their derivatives (e.g., fructose and galactinol), fatty acids and associated metabolites (e.g., glycerol and 2-aminoethanol), and energy metabolism-associated compounds (e.g., lactic acid) from raw and malted cereals were identified. The metabolite profiles differed significantly between cereal species and between raw and malted grains. Furthermore, the metabolite profiles changed during the fermentation. At 0 h, there was less variation between the metabolite profiles of raw cereals than malted cereals. At 24 h, the difference between malted barley and wheat was even more pronounced, but raw barley and wheat differed more from each other than at 0 h. Malting increased the initial sugar and sugar derivative levels in the cereals, as expected. However, levels of most amino acids and their derivatives were significantly increased after the 24 h in vitro colonic fermentation. Discussion: The malting of cereal grains seems to influence the metabolites produced by the gut microbiota during colonic fermentation. Understanding how cereals and different processing methods affect gut microbial metabolism can help shed light on their microbial fermentation-mediated health impacts. The optimized GC-MS method used in this study was able to differentiate the different sample types and is thus an excellent tool for monitoring gut microbial metabolite profiles.

Keywords: metabolomics; microbiota; cereals



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