

Corn bran fiber modulates gut microbiota in individuals with overweight and obesity

Nguyen K. Nguyen
Edward C. Deehan
Zhengxiao Zhang
Mingliang Jin
Nami Baskota
Maria Elisa Perez-Muñoz
Janis Cole
Yunus E. Tuncil
Benjamin Seethaler
Ting Wang
Martine Laville
Nathalie M. Delzenne
Stephan C. Bischoff
Bruce R. Hamaker
Inés Martínez
Dan Knights
Jeffrey A. Bakal
Carla M. Prado
Jens Walter

Video Byte

Keywords: Microbiome, arabinoxylan, dietary fiber, gut microbiota, inter-individual variability, overweight adults, short-chain fatty acids, SFCAs, obesity, propionate, randomized control trial, microcrystalline cellulose, ecological framework, α -diversity, multiple linear regression, MLR, fiber fermentation, metabolism, operational taxonomic unit, OTU

Posted Date: November 11th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-106077/v1>

License:  This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Abstract

Increasing evidence links dietary fiber consumption to a reduced incidence of obesity-related diseases, including diabetes, cancer, and cardiovascular disease. That's especially true of fermentable fibers like arabinoxylan, which is derived from whole grains and cereals like corn and stimulates the growth of beneficial gut bacteria. But in clinical studies, the benefits appear to vary between individuals. To understand what drives that variability, researchers recently tested the effects of arabinoxylan versus microcrystalline cellulose (a non-fermentable fiber control) on the communities of microbes colonizing the guts of 31 adults with overweight and obesity. Over 6 weeks, arabinoxylan significantly altered the makeup of the fecal bacteria community and increased fecal concentrations of propionate, a short chain fatty acid linked to beneficial effects on metabolism and the immune system. However, the propionate response was highly individualized and linked to both compositional shifts and baseline composition of the fecal microbiota. These results were made visible by adopting an ecological framework that considered features of the wider gut microbial community. This perspective could provide a basis for personalizing the use of dietary fiber supplements and account for differences in health effects in human clinical trials.