



BLACK CORN (ZEA MAYS L.) FLOUR CONSUMPTION IMPROVED THE GUT DYSBIOSIS PROMOTED BY A HIGH-FAT DIET ON MICE

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Abstract

High-fat diets are associated with intestinal dysbiosis and a leaky gut leading to intestinal inflammation. Bioactive components, including phenolic compounds, isolated or in the original food matrix, have alleviated intestinal changes promoted by a high-fat diet. Black corn (*Zea mays* L.) is colored corn in which anthocyanins are the most abundant bioactive compound. This study investigated the preventive effects of black corn whole flour on intestinal health and gut microbiota in mice fed a high-fat diet. Thirty C57BL/6 mice were randomly divided into three experimental groups receiving the following diet for eight weeks: NC: normal control (fed a normal diet); HF: high-fat (fed a high-fat diet: 60% of calories from fat); HFC: high-fat corn (fed a high-fat diet added with 20% of black corn whole flour). After the 8 weeks of diet, the cecal microbiota was analyzed by 16S rRNA sequencing analysis in the V3-V4 region, and the cecal short-chain fatty acids (SCFA) were measured by high-performance liquid chromatography. The number of colonic goblet cells was analyzed by histomorphology analyses. The data were analyzed by ANOVA and post-hoc of Duncan ($p < 0.05$) and the study was approved by Ethics Commission of Animal Experimentation of UFV (CEUA/UFV), process n° 10/2019. The black corn whole flour (20%) consumed by mice promoted positive changes in the intestinal homeostasis by enhancing the diversity of cecal bacterial communities through a higher relative abundance of the genus *Ruminococcus*, *Roseburia*, and *Prevotellaceae_UCG-001*, and decreased *Bacteroides* and *Faecalibaculum* in the HFC group. Further, there was no difference in cecal SCFA concentration, but an increase in goblet cell number after the black corn flour intake. The rise in the genus *Roseburia* might be involved in the intestinal metabolism of anthocyanins

due to the β -glucosidase activity of species included in this genus. In addition, the proliferation of Prevotellaceae-UCG 001 is related to the improvement of lipid metabolism by inhibiting fatty acids synthesis. Further, as the consumption of black corn flour stimulated the growth of Roseburia, Ruminococcus, and Prevotellaceae abundance, it might have promoted status of the competition, thus avoiding the growth of Akkermansia. We highlight that even with an increase in the relative abundance of genus responsible for producing SCFA no changes at the colonic SCFA level were observed. Therefore, the reason might be due to the use of the energy produced by SCFA for cell proliferation, as observed enrichment of goblet cell numbers. These findings suggest that black corn whole flour for eight weeks as a source of anthocyanins could partially alleviate the undesirable intestinal modifications associated with a high-fat diet in the animal model. Therefore, finding in our study indicates that black corn as a dietary source of anthocyanins can be a potential candidate as functional food promoting beneficial intestinal effects.



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