# SORGHUM FLOUR BRS 305 HYBRID HAS THE POTENTIAL TO MODULATE THE INTESTINAL MICROBIOTA OF RATS FED WITH A HIGH-FAT HIGH-FRUCTOSE DIET

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## Abstract

Sorghum (Sorghum bicolor (L.) Moench) BRS 305 hybrid is a promising cereal, rich in resistant starch and tannins, which are related to antioxidant, anti-inflammatory, and hypoglycemic effects. On the other hand, a diet rich in saturated fat and simple sugar, such as fructose, increases body fat mass and negatively affects many metabolic functions, including damage to the gut barrier function, and induce gut dysbiosis by increasing Firmicutes and reducing Bacteroidetes phylum. Then, the present study aimed to investigate the effect of dry heated whole sorghum BRS 305 hybrid flour on the gut microbiota modulation and gut health of rats fed with a high-fat high-fructose diet (HFHF). In phase I (8 weeks), 45–50-day old, male Wistar rats, were separated into the AIN93-M group (n = 10; fed with normal diet) and HFHF group (n = 20; diet had 31% saturated fat and 20% fructose). In phase II (10 weeks), we maintained the AIN-93M group, and the HFHF group was divided into the HFHF group (n = 10) and HFHF plus sorghum flour group (n = 10; replacing 50% of dietary fiber, 100% starch, 19.8% protein and 22.5% lipids in the experimental diet). Intestinal permeability was analyzed by urinary excretion of lactulose and mannitol by HPLC; short-chain fatty acids in the feces were determined by HPLC; colon histomorphometry analysis was carry-out by colon fragments embedded in paraffin, stained with hematoxylin/eosin, analyzed with 20x objective; genomic DNA was analyzed by Illumina MiSeq platform for paired-end sequencing reactions using PCR amplicon libraries targeting the hypervariable V4-region of the 16S rRNA gene and analysis were performed using the Mothur software, v.1.40.0. The Chao, Shannon and Simpson indexes

was used for estimates of alpha-diversity. Beta-diversity between dietary groups was assessed by Principal Coordinate Analysis (PCoA) based on the Bray-Curtis dissimilarity index and between sample diversity, using unweighted UniFrac. The metagenome functional predictive analysis of any variations in the genetic capacity of the microbiota was carried out using the PICRUSt software system. The data were analyzed by ANOVA and post-hoc of Newman-Keuls ($p<0.05$). No differences were observed in total goblet cell number, crypt thickness and height, circular muscle layer, and butyric acid between all groups ($p>0.05$). The consumption of sorghum flour increased the longitudinal muscle layer and propionic acid when compared to the HFHF group ($p<0.05$), which can be associated with resistant starch and phenolic compounds that had prebiotic effects. The sequencing of the 16S rRNA gene of the cecal microbiota presented no changes in the α-diversity and β-diversity between the groups. However, the sorghum group exhibited higher relative abundance of Firmicutes and higher Firmicutes/Bacteroidetes ratio compared to the other experimental groups, and lower abundance of Bacteroidetes, compared to the HFHF group. Despite, sorghum increased the abundance of the genera Roseburia and Lachnospiraceae_NK4A136_group compared to the HFHF group, which are related to SCFA production. In conclusion, the consumption of an HFHF diet associated with sorghum flour can modulate the gut microbiota composition and abundance of SCFA-producing bacteria, which decreases the effects of an HFHF diet.



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## Track

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- Food and health (AS)

**Keywords**

Sorghum bicolor (L.) Moench

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