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## SORGHUM FLOUR BRS 305 HYBRID HAS THE POTENTIAL TO MODULATE THE INTESTINAL MICROBIOTA OF RATS FED WITH A

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## Abstract

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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 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 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) ar 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 experir 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 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 alph dissimilarity index and between sample diversity, using unweighted UniFrac. The metagenome functional predictive analysis of any variations in the genetic capacity of the microbiota w 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 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  $\alpha$ -diversity and  $\beta$ -diversity. 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 Bacteroidetes and abundance of SCFA-producing bacteria, wh



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