Positive impact of *Lactobacillus acidophilus* La5 on composition and metabolism of the intestinal microbiota of type 2 diabetics and health individuals using microbiome model

Mateus Kawata Salgaço¹, Fellipe Lopes de Oliveira¹, Adilson Sartoratto², Victoria Mesa³, Katia Sivieri¹

¹ Graduate Program in Food, Nutrition, and Food Engineering, São Paulo State University-UNESP, Araraquara-SP, Brazil
² Pluridisciplinary Center for Chemical, Biological and Agricultural Research - CPQBA-UNICAMP - Paulínia/SP
³ Food and Human Nutrition Research Group, University of Antioquia, Medellín, Colombia.

**Keywords:** probiotic, metabolites, Short Chain Fat Acids

**Summary:** The gut microbiota refers to the microorganisms that inhabit the intestinal tract and live in symbiosis with the host. A microbiota in dysbiosis, as is the case in type 2 diabetics (T2D), can induce inflammation in different parts of the human body. Therefore, the use of probiotics can help modulate the microbiota in dysbiosis. The aim of this study was to verify the impact of *Lactobacillus acidophilus*-La5 on the gut microbial composition and metabolism of adults (40-50 years old) with and without type 2 diabetes using the Human Gut Microbial Ecosystem Simulator (SHIME®). The experimental period in SHIME® was 5 weeks (Stabilization = 2 weeks, Control Period =1 week and Treatment = 2 weeks), for each group (Control Group: NormoGlycemic; Treatment Group: T2D). After 7 and 14 days of colonic fermentation, the gut microbiota (16S rRNA gene sequencing) and metabolites (short chain fatty acids - SCFAs) were analyzed. Statistical analyses were performed using ANOVA and Tukey’s multiple comparison test, as well as bioinformatics analyses for microbiota diversity. The effect of La5 on the composition of the microbiota occurred during the 14 days of treatment for both groups, as an increase in the abundance of Bacteria and a decrease in Firmicutes in the NormoGlycemic, and with an increase in *Faecalibacterium*. Analysis of the relative abundance of the major genera showed a change during treatment, for the Normoglycemic there was an increase (p<0.05) as *Bacteroides* and *Mitsuokella* and a decrease in *Achromobacter* and *Catabacter*. T2D showed an increase (p<0.05) in *Faecalibacterium* and a decrease in *Bacteroides. Megasphaera* spp. stimulated with La-5 treatment in NormoGlycemic has already been reported to produce gut metabolites and recognized to contribute to increased anti-inflammatory and immune responses, *Faecalibacterium*, on the other hand, may modulate the gut epithelium as well as being an important butyrate product in the microbiota. The SCFAs, in the control group only after 14 days of treatment with La5 was observed an increase (p<0.05) in the production of acetic and propionic acids when compared to the control period. However, in the diabetic group, after 14 days of...
treatment there was a significant increase in butyric acid production. Therefore, this study using a dynamic colonic model showed positive and promising results in modulating the composition and metabolism of the intestinal microbiota due to the use of *L. acidophilus*-La5 in the microbiota of healthy adult individuals and especially in the microbiota in dysbiosis, in this case the microbiota of T2D, thus being a promising probiotic to promote intestinal homeostasis of the host.

This work was carried out with the support of CAPES-Funding Code 001 and FAPESP (2019/17794-6)