

TITLE : DIVERSITY IN GUT MICROBIOTA OF OBESE INDIVIDUALS AND THEIR INTERACTION WITH METABOLIC PARAMETERS AND THE DEVELOPMENT OF OBESITY

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ABSTRACT:

The gut microbiota has been linked with chronic diseases such as obesity in humans. Several studies have now attempted to demonstrate the variability of gut microbiota composition in skinny and obese humans, which has led to speculation that the gut microbiota may participate in the pathophysiology of obesity. This study aimed to characterize the fecal microbiota of normal- weight, overweight and obese individuals and its interaction with metabolic parameters and the development of obesity. Samples of blood and feces were collected from 169 patients from São Miguel do Oeste, Santa Catarina, Brazil. Samples were organized in 3 groups based on body mass index (BMI): normal weight (BMI 18-24.9), Overweight (BMI 25-29.9) and Obese (BMI \geq 30) with age between 18 and 30 years. Blood serum of patient was used to characterize the metabolic profile. After, to characterize the fecal microbiota, total DNA was extracted from the feces of representative individuals for each group mentioned above. The extraction was done with PureLink™ Microbiome DNA Purification kit with subsequent sequencing platform using the Ion PGM. In the obese group, glycemia 92 ± 32 mg/dL, total cholesterol 182 ± 40 mg/dL, triglycerides 137 ± 85 mg/dL and BMI 30 ± 6.5 kg/m². In the overweight group, glycemia was 80 ± 17 mg/dL, total cholesterol was 170 ± 47 mg/dL, triglycerides 93 ± 61 mg/dL and BMI 27.9 ± 2 kg/m². In the control group (normal weight) glycemia was 78 ± 6 mg/dL, total cholesterol 132 ± 30 mg/dL, triglycerides 78 ± 22 mg/dL and BMI 21 ± 3 kg/m². Microbial diversity revealed that *Firmicutes* presented the highest proportion (79.57%) of microorganisms for the three group studied (normal weight, overweight and obese). Statistical differences ($P < 0.05$) were observed only from the Order differentiation in which an increase in the Erysipelotrichales class was observed in the obese group. Differences that remained even in the differentiation of genera in which the genus most frequently in the obese was *Catenibacterium*. The other difference observed in genera differentiation was that the amount of *Oscillospira* was higher in skinny individuals. These results allowed us to conclude that there are differences in the microbiota of obese and skinny individuals and that these microorganisms may interfere directly in the metabolic profile.

Keywords: gut microbiota, obesity, metabolic profile.

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