

## **Bacterial Diversity in Human Intestinal Microbiota and Correlations with Nutritional Behavior, Physiology, Xenobiotics Intake and Antimicrobial Resistance in Obese, Overweight and Eutrophic Individuals**

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**Abstract :** Obesity is currently a worldwide public health threat, being considered a pandemic multifactorial disease related to the human gut microbiota (GM). Add to that GM is considered an important reservoir of antimicrobial resistance genes (ARG) and little is known on GM and ARG in obesity, considering the altered physiology and xenobiotics intake. As regional and social behavior may play important roles in GM modulation, and most of the studies are based on small sample size and various methodological approaches resulting in difficulties for data comparisons, this study was focused on the investigation of GM bacterial diversity in obese (OB), overweight (OW) and eutrophic individuals (ET) considering their nutritional, clinical and social characteristics; and comparative screening of ARG related to their physiology and xenobiotics intake. Microbial community was accessed by FISH considering phyla as a taxonomic level, and PCR-DGGE followed by dendrograms evaluation (UPGMA method) from fecal metagenome of 72 volunteers classified according to their body mass index (BMI). Nutritional, clinical, social parameters and xenobiotics intake were recorded for correlation analysis. The fecal metagenome was also used as template for PCR targeting 59 different ARG. Overall, 62% of OB were hypertensive, and 12% or 4% were, regarding the OW and ET individuals. Most of the OB were rated as low income (80%). Lower relative bacterial densities were observed in the OB compared to ET for almost all studied taxa ( $p < 0.05$ ) with Firmicutes/Bacteroidetes ratio increased in the OB group. OW individuals showed a bacterial density representative of GM more likely to the OB. All the participants were clustered in 3 different groups based on the PCR-DGGE fingerprint patterns (C1, C2, C3), being OB mostly grouped in C1 (83.3%) and ET mostly grouped in C3 (50%). The cluster C2 showed to be transitional. Among 27 ARG detected, a cluster of 17 was observed in all groups suggesting a common core. In general, ARG were observed mostly within OB individuals followed by OW and ET. The ratio between ARG and bacterial groups may suggest that ARG were more related to enterobacteria. Positive correlations were observed between ARG and BMI, calories and xenobiotics intake (especially use of sweeteners). As with nutritional and clinical characteristics, our data may suggest that GM of OW individuals behave in a heterogeneous pattern, occasionally more likely to the OB or to the ET. Regardless the regional and social behaviors of our population, the methodological approaches in this study were complementary and confirmatory. The imbalance of GM over the health-disease interface in obesity is a matter of fact, but its influence in host's physiology is still to be clearly elucidated to help understanding the multifactorial etiology of obesity. Although the results are in agreement with observations that GM is altered in obesity, the altered physiology in OB individuals seems to be also associated to the increased xenobiotics intake and may interfere with GM towards antimicrobial resistance, as observed by the fecal metagenome and ARG screening. Support: FAPEMIG, CNPQ, CAPES, PPGCBIO/UFJF.

**Keywords :** antimicrobial resistance, bacterial diversity, gut microbiota, obesity

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