

Title: BACTERIAL DIVERSITY IN HUMAN INTESTINAL MICROBIOTA OF 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 intestinal microbiota (HIM). However, most of the studies on HIM and obesity are based on small sample size and diverse methodological approaches, which results in difficulties for data comparisons. As regional and social behavior may play an important role in HIM modulation, this study was focused on the investigation of bacterial diversity in Brazilian obese, overweight and eutrophic individuals and its relationships with nutritional, clinical and social characteristics. Volunteers (n=72) were evenly classified according to their body mass index. Nutritional, clinical, social parameters were recorded. Fresh fecal samples were collected and homogenized. Bacterial densities considering phyla as a taxonomic level were evaluated by FISH. Microbial community was accessed by PCR-DGGE followed by dendograms evaluation (UPGMA method). Overall, 62% of obese were hypertensive, whereas only 12% of overweight and 4% of eutrophic were. Most of the obese were rated as low income (80%). Lower relative bacterial densities were observed in the obese compared to the eutrophic for almost all studied taxa ($p < 0.05$) with *Firmicutes/Bacteroidetes* ratio (> 1) increased in the obese. Overweight individuals showed a bacterial density representative of HIM more likely to the obese. All the participants were clustered in 3 different groups based on the PCR-DGGE fingerprint patterns (C1, C2, C3). Obese were predominantly grouped in C1 (83.3%), which also included 66.6% of overweight and 33.3% of the eutrophic. C2 included 4.2% of the obese, 12.5% of the overweight and 16.7% of the eutrophic. C3 included 12.5% of the obese, 20.8% of the overweight and 50% of the eutrophic. The cluster C1 comprised mostly obese, whereas eutrophic individuals were highly representative in C3. The cluster C2 showed to be transitional. As with nutritional and clinical characteristics, our data may suggest that HIM of overweight behave in a heterogeneous pattern, occasionally more likely to the obese or to the eutrophic. Regardless the regional and social behaviour of our population, the methodological approaches in this study were complementary and confirmatory. The imbalance of HIM 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.

Keywords: Obesity; Intestinal microbiota; FISH; DGGE

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