

Title: COMPARATIVE STUDY OF GUT CLINICAL RESISTOME AMONG EUTROPHIC, OVERWEIGHT AND OBESE INDIVIDUALS

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Abstract:

Antibiotic resistance is a major health threat and the intestinal microbiota is considered to be an important reservoir of antibiotic resistance genes. Although it is accepted that obesity may be related to intestinal microbiota changes, little is known on the extent of such phenomena on gut selective pressures and antimicrobial resistance. Add to that, in overweight patients, gut microbes may be exposed to different selective pressures and xenobiotics. The aim of this study was to identify antimicrobial resistance genetic markers in fecal metagenome of eutrophic, overweight and obese individuals recruited in Juiz de Fora, MG, with no antimicrobial chemotherapy in the prior 30 days. Healthy volunteers (n=39) were selected and classified as eutrophic (E), overweight (OW) and obese (OB), according to their BMI (Body Mass Index). From 200 mg of fresh fecal samples, metagenomic DNA was extracted and antimicrobial resistance genetic markers were screened by PCR. The most frequently detected genetic marker was *mef*, found in 24.32% of the samples (E=33%, OW= 25.92%, OB= 40%), followed by *aacA-aphD* detected in 24% (E=16.66%, OW=29.16%, OB=54.16%) and *bla*TEM detected in 23.42% (E=19.23%, OW= 30.76%, OB= 50%). Genetic markers also detected were: *mphA*, 7.20% (E=25%, OW=25%, OB=50%), *ereB* 6.30% (E=28.57%, OW=14.28%, OB=57.14%), *ampC* 4.50% (E=20%, OW=40%, OB=40%), *bla*SHV 3.6% (E= 0%, OW= 75%, OB=25%), and *mecA* 1.8% (OB=100%). Some genetic markers were detected only in obese individuals: *tet*(M), *vgb* and *bla*Z, detected in 3.6% of the samples. The following markers were not detected in any fecal metagenome: *KPC*, *ermA*, *ermB*, *ermC*, *tet*(K), *tet*(M), *mrsB*, *linA*, *vga*, *vatA*, *vatB*, *vatC*, *mexB*, *mexD*, *mexF*, *mexY* and *OXA58*. Overall the genetic markers related to antimicrobial resistance were mostly detected in the fecal metagenome from obese group, suggesting a higher gut selective pressure in these individuals. According to the literature, changes in the gut microbiota associated to the overweight and obesity could lead to an increase in potentially toxic metabolites, not only due to the microbial metabolism, but the individual physiology. Further prospective studies are needed to better address such interesting phenomena which could have implications in the health prognosis and co-morbidities of overweight and obese individuals.

Keywords: Intestinal microbiota, Intestinal resistome, Antibiotic resistance, Obesity.

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