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Associations of polymorphisms of *LEPr* and *FTO* genes with food consumption in severely obese individuals

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Genetic factors play an important role in the pathogenesis of obesity. This study aimed at assessing the associations of polymorphisms of *LEPr* and *FTO* genes with food consumption in obese. Thus, a cross-sectional study of 222 obese, adult patients was carried out. Two SNPs of *LEPr* (rs1137101 and rs8179183), and one SNP of *FTO* (rs9939609) were genotyped and analyzed. The food consumption was measured through a three-day diet diary; nutrients were calculated using Nutribase software. We used generalized linear models (GLMz) in SPSS 18.0 to analyze the additive effect of each SNP to caloric intake and macronutrients. The main effect was based on the interaction *LEPr* rs1137101 and rs8179183; being the caloric consumption associated to these genes ($p < 0.037$ -GLMz). The mean (\pm standard deviation) of the caloric intake in the *LEPr* rs1137101 (AA) genotype was 2780.2 (\pm 1147.9) kcal/day; while in the *LEPr* rs8179183 (GC) genotype was 2811.2 (\pm 1012.6) kcal/day. In both cases, the caloric intake was higher than the other genotypes. Regarding the macronutrients, only protein intake was associated with the SNPs evaluated ($p = 0.023$ -GLMz). Removing SNP rs9939609 of *FTO* from the model had no impact on the statistical significance. SNPs of the *LEPr* gene seem to play a potential role in the stratification of obese patients, as they may help to predict those individuals who are at higher risk for upper calories intake, and, therefore, for poorer outcomes. These findings have to be confirmed in prospective studies.

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