

Short Communication

# Obesity and variants of the *GHRL* (ghrelin) and *BCHE* (butyrylcholinesterase) genes

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### **Abstract**

Ghrelin coded by the *GHRL* gene is related to weight-gain, its deactivation possibly depending on its hydrolyzation by butyrylcholinesterase (BChE) encoded by the *BCHE* gene, an enzyme already associated with the body mass index (BMI). The aim was to search for relationships between SNPs of the *GHRL* and *BCHE* genes with BChE activity, BMI and obesity in 144 obese and 153 nonobese Euro-Brazilian male blood donors. In the obese individuals, a significant association with higher BChE activity, in the *72LM+72MM*; *-116GG* genotype class (*GHRL* and *BCHE* genes, respectively) was noted. No significant differences were found otherwise, through comparisons between obese and control individuals, of genotype and allele frequencies in SNPs of the *GHRL* gene (*Arg51GIn* and *Leu72Met*), or mean BMI between *72LL* and *72LM+72MM* genotypes. Although there appears to be no direct relationship between the examined *GHRL* SNPs and BMI, the association of the *72M* SNP with higher BChE activity in obese subjects probably points to a regulatory mechanism, thereby implying the influence of the *GHRL* gene on BChE expression, and a consequential metabolic role in the complex process of fat utilization.

Key words: BCHE gene, body-mass index, butyrylcholinesterase, ghrelin, GHRL gene, obesity.

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Obesity is a risk factor in many diseases, such as hypertension, coronary artery disease, type II diabetes, breast and colon cancer, constituting a current pandemic disorder.

Ghrelin (Kojima *et al.*, 1999), a peptide related to food intake, is coded by the *GHRL* gene (3p25-p26). The GHS (growth hormone secretagogue) receptor is activated by acylated ghrelin, although not so with des-acyl ghrelin (Hosoda *et al.*, 2000). In rodents, it was shown that the administration of ghrelin leads to a gain in weight by increasing food intake and reducing fat utilization (Tschöp *et al.*, 2000). It was further proposed that the decrease in plasma ghrelin concentration found in obese individuals could represent a physiological adaptation (Tschöp *et al.*, 2001).

Butyrylcholinesterase (BChE; EC 1.1.1.8) plasma activity is positively correlated with weight and BMI (body mass index), in a phenotype (CHE2 C5-) with approximately 90% population frequency (Chautard-Freire-Maia *et al.*, 1991; Alcântara *et al.*, 2003), whereas in another (CHE2 C5+; 10% population frequency), with 20% higher BChE activity than the former, it is associated with lower mean weight (Chautard-Freire-Maia *et al.*, 1991) and lower mean BMI (Alcântara *et al.*, 2001). This shows that individuals with innate high BChE activity tend to be thinner and

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that BChE synthesis is increased in individuals that gain weight, suggesting that BChE activity is important in energy balance. Data from the BChE knockout mouse that became obese and significantly heavier than wild-type littermates after an 11% fat diet indicate a role for BChE in fat utilization (Li *et al.*, 2008). Furthermore, SNPs of the human *BCHE* gene (3q26.1-q26.2) have been associated to BMI (Souza *et al.*, 2005; Furtado-Alle *et al.*, 2008).

Considering that ghrelin desacylation may depend on BChE activity (De Vriese *et al.*, 2004), the search was for relationships between SNPs of the *BCHE* and *GHRL* genes and the variables BChE activity, BMI and obesity.

The study involved 144 obese (BMI  $\geq$  30 kg/m<sup>2</sup>; mean age 36.6 years) and 153 control (20 kg/m<sup>2</sup>  $\leq$  BMI  $\leq$  25 kg/m<sup>2</sup>; mean age 36.3 years) male blood donors from Curitiba, south Brazil, ethnically characterized as Euro-Brazilians on the basis of skin, hair and facial traits. The research was approved by the National's Committee for Ethics in Research (CONEP; registration number 2063).

DNA was extracted by a salting-out method (Lahiri and Nurnberger Jr, 1991). SNPs were examined for the *GHRL* gene (G/A, rs34911341, *p.R51Q*, 346 nt and C/A, rs 696217, *p.L72M*, 408 nt) by PCR and Single Strand Conformation Analysis. The respective primers designed for this study were: GHRL15 (TCTCCCAGAGCACAAA GGAC); GHRL13 (TTCTGCTTGACCTCCATCTTCC); GHRL25 (GGAGTCGAAGAAGCCACCA); and GHRL23 (CAGAAGCATAAAACTGCAGAGG). Data

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on genotypes for exons 1 (G/A, rs1126680, -116 nt) and 4 (G/A; rs1803274, *p.A539T*; 1615 nt) of the *BCHE* gene, and BChE plasma activity (Dietz *et al.*, 1972) were obtained from a previous study (Furtado-Alle *et al.*, 2008).

Statistica for Windows (StatSoft, Inc., 1996) was used for data analysis of: means, frequencies, standard errors, standard deviations, Fisher-exact test, t-test,  $\chi^2$  test, linear correlations, and step-wise multiple regression analysis.

Comparisons by  $\chi^2$  tests showed that genotype and allele frequencies for Arg51Gln and Leu72Met SNPs of the GHRL gene did not statistically differ in obese (51RR = 99.3%, 51RQ = 0.7%; 51Q = 0.35%, and72LL = 88.1%, 72LM = 11.2%, 72MM = 0.3%; 72M = 6.3%in 141 and 143 subjects, respectively) or control (51RR = 98.7%, 51RQ = 1.3%; 51Q = 0.65%, and 72LL = 87.6%, 72LM = 11.8%, 72MM = 0.6%; 72M = 6.5% in 153 subjects) individuals. Ukkola et al. (2002) also did not find any significant difference in 51Q allele frequency when comparing obese with normal individuals, but did show that there was a variation in samples of different ethnic composition. In a previous study, no significant difference was found in 72M frequency between obese and non-obese individuals (Hinney et al., 2002). Although total 72M frequency (6.4%; N = 296) in the present study was no different from that obtained for individuals from Utah (8.3%; p > 0.4), it differs significantly from those found for Han Chinese (15.6%, p < 0.01), Japanese (18.2%; p < 0.001), and African individuals (0.8%; p < 0.05), all of which from the International HapMap Project, thereby showing an ethnic difference involved in the frequency of this variant.

Multiple regression step-wise analysis (Table 1) indicated two values for beta, both significantly different from 0, when compared by t-tests: the -116A variant leads to lower BChE activity whereas the 72M to higher. Although BChE activity tends to be higher in obese than in non-obese individuals (Furtado-Alle et al.. 2008), the 72M variant appears to contribute to elevating this even more. This significant association is a novelty, and may be considered an

**Table 1** - Results from step-wise multiple regression analysis that considered butyrylcholinesterase activity as dependent variable in obese individuals (N = 130).

Independent variables <sup>a</sup>	$Beta^b \pm S.E.   t$		
BCHE gene <sup>c</sup>	$-0.21 \pm 0.09$	2.51 (p < 0.02)	
GHRL gene <sup>d</sup>	$0.18 \pm 0.09$	2.09 (p < 0.05)	
	$F = 5.52 (p < 0.01); r^2 = 0.08$		

<sup>a</sup>Nonsignificant independent variables: age, body-mass index, A539T of the *BCHE* gene. <sup>b</sup>Regression coefficients for the standardized variables to a mean 0 and SD 1, allowing for comparison of the relative contribution of each independent variable in predicting the dependent variable, also comparable across variables. <sup>c</sup>(-116GG = 1, -116GA = 2). <sup>d</sup>(72LL = 1, 72LM+72MM = 2).

**Table 2** - Butyrylcholinesterase mean activity in 130 obese individuals, grouped by genotypes of *GHRL* (*Leu72Met*) and *BCHE* (*G-116A*) genes.

Genotypes	n	Mean BChE activity (KU/L) ± S.D.
72LM+72MM; -116GG <sup>a</sup>	13	$8.42 \pm 4.08$
72LL; -116GG <sup>a</sup>	95	$6.55 \pm 2.80$
72LM+72MM; -116GA	2	$5.22 \pm 1.89$
72LL; -116GA	20	$5.04 \pm 2.11$

 $^{a}$ t-test = 2.18; p < 0.05 when comparing 72LM+72MM; -116GG with 72LL; -116GG.

inference, as significance comes close to the 0.05 error limit. This may be due to a regulatory mechanism by which the presence of the 72M variant of the GHRL gene induces BChE synthesis. The -116GG genotype is characterized by normal BChE activity. However, in the presence of the 72M variant, mean BChE activity is higher (t = 2.18, p < 0.05) (Table 2). High BChE activity (> 8 KU/L) was shown in 33% of obese subjects with the 72M variant, but in only 21% of those homozygous for the 72L SNP. Although the L72M SNP is not located in the coding region for the mature ghrelin peptide, the 72M allele leads to an earlier onset of obesity (Ukkola et. al., 2001; Miraglia del Giudice et al., 2004). According to Ukkola et al. (2002), variation in preproghrelin peptide could theoretically change the structure of one or more of the derived products, this leading to functional consequences.

The association between the -116A variant and lower BChE activity (Table 1) is already known, and has been reported in obese and nonobese individuals (Furtado-Alle *et al.*, 2008).

Genotypes 72LL and 72LM+72MM did not differ significantly (t-test) in mean BMI in either control (23.05  $\pm$  1.29 kg/m² and 23.43  $\pm$  0.96 kg/m²; p > 0.20) or obese (32.95  $\pm$  3.29 kg/m² and 32.90  $\pm$  2.7 kg/m²; p > 0.95) individuals. No difference in mean BMI was found in obese individuals, when genotypes 72LL and 72LM+72MM, identical for genotypes -116GG;539AA, -116GG;539AT or -116GA;539AT of exons 1 and 4 of the BCHE gene, respectively, were compared. Obese individuals with and without the 72M variant have already been compared (Ukkola et al., 2001), with no difference found in mean BMI.

Although the examined *GHRL* SNPs do not appear to be directly related to BMI, the association of the 72M SNP with higher BChE activity in obese subjects although requiring further study, points to a regulatory mechanism, thus indicating the influence of the *GHRL* gene on BChE expression and, consequently, its possible role in the complex process of fat utilization.

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#### Internet Resources

HapMap Project, http://www.hapmap.org/.

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