Association of FTO and PPARG polymorphisms with obesity in Portuguese women

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Purpose: We evaluated the association between risk of obesity in the Portuguese population and two obesity-related single-nucleotide gene polymorphisms: fat-mass and obesity-associated (FTO) rs9939609 and peroxisome proliferator-activated receptor gamma (PPARG) rs1801282.

Patients and methods: A total of 194 Portuguese premenopausal female Caucasians aged between 18 and 50 years (95 with body mass index [BMI] $\geq 30$ g/m², 99 controls with BMI 18.5–24.9 kg/m²) participated in this study. The association of the single-nucleotide polymorphisms with obesity was determined by odds ratio calculation with 95% confidence intervals.

Results: Significant differences in allelic expression of FTO rs9939609 ($P<0.05$) were found between control and case groups, indicating a 2.5-higher risk for obesity in the presence of both risk alleles when comparing the control group with the entire obese group. A fourfold-higher risk was found for subjects with class III obesity compared to those with classes I and II. No significant differences in BMI were found between the control and case groups for PPARG rs1801282 ($P>0.05$).

Conclusion: For the first time, a study involving an adult Portuguese population shows that individuals harboring both risk alleles in the FTO gene locus are at higher risk for obesity, which is in agreement to what has been reported for other European populations.

Keywords: rs9939609, rs1801282, BMI, SNP, odds ratio

Introduction

Obesity prevalence has grown dramatically in recent decades and shows no signs of decline. According to the World Health Organization (WHO), it is estimated that 1.5 billion people are overweight, of which 500 million are obese.¹ Obesity and overweight result from a combination of genetic background, environmental, and lifestyle factors, and are intrinsically associated with increased risk of associated disease, such as hypertension, dyslipidemia, and type 2 diabetes.² Several gene-association studies have led to the identification of different loci (single nucleotide polymorphisms [SNPs]) that contribute to obesity and overweight.³ One of these SNPs, rs9939609, in the fat-mass and obesity-associated (FTO) gene, has been described as a risk factor to obesity, and strongly associated with body mass index (BMI) increments in European adults.⁴ Frayling and colleagues⁵ demonstrated that the presence of the risk allele A is cumulative and represent a 20% higher risk for the development of obesity and 13% for the development of overweight. This association was later confirmed by several other studies in different populations.⁵–⁷ Another gene playing an important role in
Obesity is peroxisome proliferator-activated receptor gamma (PPARG), which regulates the adipocyte differentiation, thus influencing BMI, as well as glucose metabolism. In particular, SNP rs1801282 has been associated with obesity in different populations, with a clear identification of the risk allele G. To date, there are no data on the involvement of either of these SNPs in obesity in the adult Portuguese population, and whether the same pattern of risk alleles is present. Here, we report on the first association study between these SNPs and obesity for the adult Portuguese population, which can provide useful data for the clinical management and risk assessment of obesity.

Materials and methods

Subjects

All 194 subjects participating in the study were premenopausal Caucasian Portuguese females between 18 and 50 years old, duly informed about the study and having signed an informed consent.

As a control group were 99 healthy subjects showing a BMI ranging between 18.5 and 24.9 kg/m² with body-weight variation inferior to 10% in the last year. These subjects were either selected during a routine health check or belonged to the staff of Curry Cabral Hospital (Lisbon, Portugal).

The case group was composed of 95 subjects showing a BMI ≥30 kg/m² with body-weight variation inferior to 10% in the last year. These subjects were all attending the Endocrinology Department of Curry Cabral Hospital.

Sample collection

Samples were collected from peripheral total blood and preserved at −80°C. For analysis, 2 mL of blood was transferred to individual FTA (Whatman, Maidstone, UK) microcards, and DNA was purified according to the manufacturer’s protocol.

Polymorphism analysis

Polymerase chain reaction (PCR) amplifications were performed on a Biometra TGradient Thermocycler (Göttingen, Germany) in 25 µL final volume with Master Mix and DNA Surf Hot Taq Polymerase (10 U/µL) (Stab Vida, Lisbon, Portugal) with the following thermal cycling conditions: initial 15-minute denaturation at 96°C, followed by 30 amplification cycles of denaturation at 94°C for 1 minute, annealing at 59°C for 1 minute, elongation at 70°C for 1 minute, and a final elongation at 70°C for 5 minutes. Primers for PPARG locus (GenBank accession no NC_000003.11): PPARG-F 5′-CAATTCAAGCCCAGTCCTTT-3′ and PPARG-R 5′-TTATCTCTGTGATGGCGTCC-3′. Primers for FTO locus (GenBank accession no NC_000016.9): FTO-F 5′-GCATAATGGCAACACACACT-3′ and FTO-R 5′-AACACCATCTTTGGCGCTG-3′.

SNP identification was performed via direct sequencing. Sequencing reactions were carried out with 100 ng/100 bp of the previously PCR-amplified product using Big Dye version 3.1 technology (Life Technologies, Carlsbad, CA, USA) in an Applied Biosystems 3730XL DNA analyzer.

Statistical analysis

To determine the normality of the continuous variables (age), Student’s t-test was used. To determine the differences between genotype groups of each SNP and anthropometric traits, one-way analyses of variance and a post hoc Bonferroni test were used. All odds ratio (OR) analysis was performed using binary logistic regression with 95% confidence interval (CI) to determine the risk of each loci to obesity and the respective P-value. All statistical analyses were carried out using SPSS software version 20 (IBM, Armonk, NY, USA).

Results

Table 1 presents the descriptive analyses of the subjects subdivided by their phenotype group. Figure 1 shows the population characterization by allele and genotype frequencies for FTO and PPARG SNPs. Significant differences (P<0.05) were found only among the different genotypes of FTO rs9939609 for BMI, fat mass, and waist circumference. No other anthropometric traits were statistically different for FTO rs9939609 or PPARG rs1801282. Genotype frequencies for FTO rs9939609 were 24.74% T/T, 56.70% A/T, and 18.56% A/A. When comparing case and control groups, no significant deviation from the Hardy–Weinberg equilibrium of allele frequencies was observed for this locus (P=0.053), with a majority of individuals being heterozygous (A/T). Data showed that the T allele is more frequent in subjects with BMI values between 18.5 and 24.9 kg/m², whereas the A allele is preeminent in subjects with BMI ≥30 kg/m².

For PPARG rs1801282, the allele frequencies were 80.93% for homozygous C/C, 1.03% for homozygous G/G, and 18.04% for heterozygous C/G. Again, no significant deviation from the Hardy–Weinberg equilibrium of allele frequencies was observed for PPARG rs1801282 (P=0.97).

The presence of the A allele in FTO rs9939609 does not per se confer risk for obesity in the studied population. However, significant differences in allele frequencies between

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What is more striking is the allelic expression of A/A homozygosity in subjects with a BMI $\geq$ 40 kg/m$^2$, i.e., class III obesity. Considering this subgroup of obese women compared to those with class I and class II obesity, an OR = 4.044 (CI 1.099–14.878; $P=0.035$) was found (Table 2B).

Analysis of PPARG rs1801282 showed no association with obesity ($P>0.05$) within the studied population.

**Discussion**

The worldwide prevalence of obesity has been increasing dramatically in the last few decades, and Portugal is no exception, where a 13.8% prevalence of obesity has been recorded. Association studies have highlighted the influence of SNPs in obesity, with particular focus on FTO rs9939609. Thus far, no data on the possible association of this SNP to obesity in the adult Portuguese population has been reported. Here, for the first time, we demonstrate an association between the FTO rs9939609 homozygous AA genotype and increased BMI when compared to homozygous TT. Significant differences were found between control and case group confirming the increased risk for obesity of homozygous AA at this locus. Also, with the post hoc Bonferroni test, it was...

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**Table 1** Anthropometric data of all subjects subdivided by phenotype

<table>
<thead>
<tr>
<th>Anthropometric measures</th>
<th>Total</th>
<th>Phenotype</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Normal</td>
</tr>
<tr>
<td>n</td>
<td>194</td>
<td>99</td>
</tr>
<tr>
<td>Age (years)</td>
<td>34.19 (±8.22)</td>
<td>34.24 (±8.30)</td>
</tr>
<tr>
<td>BMI (kg/m$^2$)</td>
<td>21.42 (±1.69)</td>
<td>43.60 (±7.83)</td>
</tr>
<tr>
<td>Fat mass (kg)</td>
<td>14.32 (±3.61)</td>
<td>54 (±14.88)</td>
</tr>
<tr>
<td>Fat mass (%)</td>
<td>25.30 (±4.67)</td>
<td>47.61 (±5.30)</td>
</tr>
<tr>
<td>Waist (cm)</td>
<td>94.19 (±25.72)</td>
<td>71.75 (±5.85)</td>
</tr>
<tr>
<td>Waist/hip ratio</td>
<td>0.80 (±0.09)</td>
<td>0.74 (±0.05)</td>
</tr>
</tbody>
</table>

Notes: Obesity status: normal (BMI between 18.5 and 24.9 kg/m$^2$); obese (BMI $\geq$ 30 kg/m$^2$); all data presented as means ± standard deviation.

Abbreviation: BMI, body mass index.

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**Figure 1** Population characteristics, in function of the respective genotype (upper). Genotype and allele frequencies (bottom) obtained for each single-nucleotide polymorphism. White bars – all subjects, grey bars – controls and black bars – case. (A) Genotype frequencies for fat mass and obesity-associated (FTO) rs9939609; (B) allele frequencies for FTO rs9939609; (C) genotype frequencies for peroxisome proliferator-activated receptor gamma (PPARG) rs1801282; (D) allele frequencies for PPARG rs1801282.

Note: "Significant differences between groups were found for these cases."
possible to determine that individuals with both A alleles in FTO rs9939609 show 6.37±2.35 (P=0.022) higher BMI, 11.99±4.86 kg (P=0.043) higher body-fat mass and 13.31±4.87 cm (P=0.020) higher waist circumference compared to T-allele carriers. These data are in clear agreement with what has been reported for other populations of European origin.5–7,15,16 Our data show that in the adult Portuguese population, this polymorphism confers an even higher risk for class III obesity (BMI >40 kg/m²). This may allow identification of those individuals at increased risk and target them for an earlier clinical and lifestyle intervention. This idea has been recently reinforced by the report of Albuquerque and colleagues showing a strong association of FTO rs9939609 with obesity in Portuguese children.17 Together, these data may prove useful for a structured public health strategy within the European Union.

Conversely, PPARG rs1801282 showed no association with obesity within the studied population, as no significant difference was found between control and case subjects (P>0.05). In European populations, PPARG rs1801282 has shown association with obesity and higher BMI for homozygous carriers of the G allele (P<0.05).18 Nevertheless, no association was found in other studies,18–20 indicating that this SNP may differ between populations and probably should not be considered as a strong genetic marker to evaluate risk for obesity as FTO rs9939609 is. Despite reports on a relation between PPARG rs1801282 and diabetes type 2,21 we observed no relation in our study (P>0.05). The relevance of PPARG rs1801282 as a genetic marker to assess risk for obesity and high insulin levels in premenopausal Portuguese women is, therefore, negligible.

**Conclusion**

Thus far, this is the first association study involving obesity-related genetic polymorphisms in the adult Portuguese population. Data show that FTO rs9939609 could be useful for the clinical management of obese women. Nevertheless, additional data are required, namely inclusion of males and youth subjects, to fully characterize the involvement of these loci in the development of obesity within the Portuguese population.

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**Disclosure**

The authors report no conflicts of interest in this work.

**References**