Postprandial responses in hunger and satiety are associated with the rs9939609 single nucleotide polymorphism in FTO\textsuperscript{1–3}

Marcel den Hoed, Margriet S Westerterp-Plantenga, Freek G Bouwman, Edwin CM Mariman, and Klaas R Westerterp

ABSTRACT

Background: The common rs9939609 single nucleotide polymorphism (SNP) in the fat mass and obesity–associated (FTO) gene is associated with adiposity, possibly by affecting satiety responsiveness.

Objective: The objective was to determine whether postprandial responses in hunger and satiety are associated with rs9939609, taking interactions with other relevant candidate genes into account.

Design: Sixty-two women and 41 men [age: 31±14 y; body mass index (in kg/m\(^2\)): 25.0±3.1] were genotyped for 5 SNPs in FTO, DNMT1, DNMT3B, LEPR, and LEPR. Individuals received fixed meals provided in energy balance. Hunger and satiety were determined pre- and postprandially by using visual analog scales.

Results: A general association test showed a significant association between postprandial responses in hunger and satiety with rs9939609 (P = 0.036 and P = 0.050, respectively). Individuals with low postprandial responses in hunger and satiety were overrepresented among TA/AA carriers in rs9939609 (FTO) compared with TT carriers (dominant and additive model: P = 0.013 and P = 0.020, respectively). Moreover, multifactor dimensionality reduction showed significant epistatic interactions for the postprandial decrease in hunger involving rs9939609 (FTO), rs992472 (DNMT3B), and rs1137101 (LEPR). Individuals with a low postprandial decrease in hunger were overrepresented among TA/AA (dominant), CC/CA (recessive), and AG/GG (dominant) carriers in rs9939609 (FTO), rs992472 (DNMT3B), and rs1137101 (LEPR), respectively (n = 39), compared with TT, AA, and/or AA carriers in these SNPs, respectively (P = 0.00001). Each SNP had an additional effect.


INTRODUCTION

Twin studies have shown a heritability of 40–80% for obesity-related phenotypes (1–3). This implies that genetic variation determines to a large extent whether an individual is prone to develop obesity when food availability is not limited. Because obesity is a complex metabolic disorder, a genetic predisposition for obesity is anticipated to consist of many nucleic variants, all of which exert a small effect. So far, candidate gene studies attempting to identify genetic variants that contribute to the susceptibility for obesity have not been very successful. In this respect, the recent realization of genome-wide association studies has provided researchers with the promising opportunity to identify risk variants for obesity without the need to select candidate genes a priori. The first series of genome-wide association studies for body mass index (BMI; in kg/m\(^2\)) and obesity showed strong and consistent associations with variants in the fat mass and obesity–associated (FTO) gene (4–7).

Frayling et al (5) showed that the population attributable risk of obesity and overweight associated with the common rs9939609 in the FTO gene is as high as 20% and 13%, respectively. The A allele in rs9939609 was shown to be associated with body fat growth but with a higher BMI and risk of obesity in children from the age of 7 y onward, persisting into adulthood. In young children, the association of the A allele with body mass is almost exclusively attributable to changes in fat mass. In adults, individuals with the AA genotype weigh 3 kg more on average than those with the TT genotype, and each A allele increases BMI by \(\approx 0.4\) (5). Since then, the association between adiposity and SNPs in FTO has been confirmed in many genome-wide association studies (8–12).

The physiologic pathway by which variation in the FTO gene influences the risk of developing obesity largely remains to be established. Recent studies have shown that FTO is highly expressed in adipose tissue and in hypothalamic areas that are involved in food intake regulation, such as the arcuate, paraventricular, dorsomedial, and ventromedial nuclei (13–15). This suggests that FTO may influence adiposity by affecting appetite. Indeed, energy intake from food is higher in children carrying the TA/AA genotype in rs9939609 than in TT carriers (16, 17). In addition, Wardle et al (18, 19) showed that children aged 8–11 y carrying the TA/AA genotype are characterized by a reduced responsiveness to satiety cues, which thereby increases the risk of overeating and developing obesity (20). Whether or not FTO affects responsiveness to satiety cues in adults is currently unknown. We hypothesized that hunger and satiety responsiveness is reduced in adult TA/AA carriers of the common rs9939609 SNP in FTO.

Gerken et al (14) showed that FTO may regulate the transcription of genes involved in metabolism by catalyzing DNA demethylation. Moreover, Qi et al (21) suggested that FTO likely forms part of a pathway mediating the neuroregulation of
food intake, with blocking of the leptin signal inhibiting downstream changes in adipose tissue that induce the expression of FTO. Given these results, we additionally determined whether postprandial responses in hunger and satiety are characterized by epistatic interactions involving the rs9939609 SNP in FTO and common variants in the genes encoding for DNA methyltransferases (DNMT)1 and 3B as well as for leptin (LEP) and the leptin receptor (LEPR). The rationale for the SNPs chosen is provided in Subjects and Methods.

SUBJECTS AND METHODS

Data were collected from intervention studies on the effect of proteins and/or protein contents on the postprandial responses in (an)orexigenic hormones as well as hunger and satiety (22–25). Participants came to the university in the morning and received fixed meals provided in energy balance and according to energy requirements as calculated by using the formula of Harris and Benedict (26). On average, the meals contained 27%, 45%, and 28% of energy from protein, carbohydrate, and fat, respectively. The study conformed to the standards set by the Declaration of Helsinki, and the local Ethics Committee approved the study. Participants provided written informed consent before participating. Recruitment of participants for the last intervention study included in the present report commenced in September 2005. All intervention studies were completed by August 2006.

Postprandial responses in hunger and satiety were determined in 103 individuals of Western European descent (62 women and 41 men aged 31 ± 14 y with a BMI of 25.0 ± 3.1; mean ± SD) by using visual analog scales. After baseline levels were adjusted for, postprandial responses in hunger and satiety were determined. For both hunger and satiety, participants were divided into high or low responders based on the leptin serum concentration, or protein activity, were favored in the selection process. This resulted in the selection of 5 SNPs (Table 1): the aforementioned intronic A→T SNP in FTO (rs9939609), an intronic A→G SNP in DNMT1 (rs2290684), an intronic C→A SNP in DNMT3B (rs992472) (27, 28), the −2548G→A SNP in the coding region of LEP (rs7799039) (29, 30), and the 668A→G SNP in LEPR, which results in amino acid substitution Gln223Arg (31–33).

Genotyping was performed by using commercially available TaqMan SNP genotyping assays from Applied Biosystems (Foster City, CA). The procedure was performed according to the manufacturer’s protocol and was measured on an Applied Biosystems 7900 HT Fast Real-Time PCR System. Allelic calls were determined semiautomatically by using the allelic discrimination software of Applied Biosystems. On allelic discrimination, 5 samples were randomly selected per genotype for all SNPs to be determined in duplicate. Duplicates were fully concordant with the initial calls.

<table>
<thead>
<tr>
<th>Gene</th>
<th>SNP</th>
<th>Genotype</th>
<th>Frequency</th>
<th>Allele</th>
<th>Frequency</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>FTO</td>
<td>rs9939609</td>
<td>TTT</td>
<td>38 (36.9)</td>
<td>T</td>
<td>60.7</td>
<td>0.97</td>
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<tr>
<td></td>
<td></td>
<td>TAG</td>
<td>49 (47.6)</td>
<td>A</td>
<td>39.3</td>
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</tr>
<tr>
<td></td>
<td></td>
<td>AAG</td>
<td>16 (15.5)</td>
<td>A</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DNMT1</td>
<td>rs2290684</td>
<td>AAA</td>
<td>22 (21.4)</td>
<td>A</td>
<td>46.1</td>
<td>0.97</td>
</tr>
<tr>
<td></td>
<td></td>
<td>AGG</td>
<td>51 (49.5)</td>
<td>G</td>
<td>53.9</td>
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<tr>
<td></td>
<td></td>
<td>GGG</td>
<td>30 (29.1)</td>
<td></td>
<td></td>
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<tr>
<td>DNMT3B</td>
<td>rs992472</td>
<td>AAA</td>
<td>17 (16.5)</td>
<td>A</td>
<td>39.8</td>
<td>0.78</td>
</tr>
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<td></td>
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<td>ACC</td>
<td>48 (46.6)</td>
<td>C</td>
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</tr>
<tr>
<td></td>
<td></td>
<td>CCC</td>
<td>38 (36.9)</td>
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<td>LEP</td>
<td>rs7799039</td>
<td>GGG</td>
<td>29 (28.2)</td>
<td>G</td>
<td>51.0</td>
<td>0.38</td>
</tr>
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<td>2548G→A</td>
<td>GA</td>
<td>47 (45.6)</td>
<td>A</td>
<td>49.0</td>
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<tr>
<td></td>
<td>−2548G→A</td>
<td>AA</td>
<td>27 (26.2)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>LEPR</td>
<td>rs1137101</td>
<td>AGG</td>
<td>23 (22.3)</td>
<td></td>
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</tr>
</tbody>
</table>

DNA isolation and SNP genotyping

Genomic DNA was isolated from peripheral blood leukocytes by using the QIAamp blood kit from Qiagen (Amsterdam, Netherlands). Besides the rs9939609 SNP in FTO, SNPs were selected in the DNMT1, DNMT3B, LEP, and LEPR genes. To ensure that an ample number of participants were homozygous for the minor alleles, SNPs were only considered candidates when the minor allele frequency in Europeans was ≥25%, as indicated by the SNP public database (dbSNP; http://www.ncbi.nlm.nih.gov/SNP). SNPs that were associated earlier with relevant phenotypes, such as gene expression, protein concentrations, or protein activity, were favored in the selection process. This resulted in the selection of 5 SNPs (Table 1): the aforementioned intronic A→T SNP in FTO (rs9939609), an intronic A→G SNP in DNMT1 (rs2290684), an intronic C→A SNP in DNMT3B (rs992472) (27, 28), the −2548G→A SNP in the coding region of LEP (rs7799039) (29, 30), and the 668A→G SNP in LEPR, which results in amino acid substitution Gln223Arg (31–33).

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<table>
<thead>
<tr>
<th>Table 1</th>
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<tbody>
<tr>
<td>Genotypic and allelic distributions according to single nucleotide polymorphism (SNP)</td>
</tr>
<tr>
<td>Gene</td>
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<tr>
<td>--------</td>
</tr>
<tr>
<td>FTO</td>
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<td></td>
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<tr>
<td>DNMT1</td>
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<td>DNMT3B</td>
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<tr>
<td>LEP</td>
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<td></td>
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<tr>
<td>LEPR</td>
</tr>
</tbody>
</table>

1 Obtained by using the chi-square test of Hardy-Weinberg equilibrium. For all SNPs, a 100% success rate was accomplished.
Statistical analysis

Descriptive analysis

Postprandial responses were dichotomized by using sex- and study-specific median values, resulting in an approximately equal number of participants with a high and low postprandial response for each phenotype, meanwhile taking sex and study into account (0 = high postprandial response, 1 = low postprandial response).

Age and BMI were not normally distributed among participants. Therefore, the Kruskal-Wallis and the Mann-Whitney U tests were used to determine the associations between BMI and rs9939609 and between the postprandial responses and BMI, respectively. These variables were subsequently log transformed for further analyses.

Association analysis

Before the association analysis was performed, the effect of potential covariates (age and BMI) was evaluated for the postprandial responses in hunger and satiety. Covariates were incorporated into the model when \( P < 0.05 \). A general association test was performed without assuming a mode of inheritance by entering the genotype in the optimized model (with the significant covariates) as 2 class variables. The mode of inheritance was further investigated by testing an additive, dominant, and recessive model. \( P \) values, odds ratios (ORs), and 95% CIs are provided for the associations shown. All statistical analyses were performed with SPSS 13 for Macintosh OS X (SPSS Inc, Chicago, IL).

To identify epistatic interactions, multifactor dimensionality reduction (MDR) was used. MDR is a frequently used multilocus method that was applied as previously described by Heidema et al (34). Briefly, we applied the MDR software (http://www.epistasis.org) to our data set, which comprised an additional 9 control SNPs for this analysis (35), using 10-fold cross-validation and SNP

RESULTS

The genotypic and allelic distributions of the determined SNPs are provided in Table 1. All SNPs were in Hardy Weinberg equilibrium, and BMI was similar between genotypes for all SNPs, including the rs9939609 variant in FTO. BMI was also similar between responders and nonresponders for the postprandial responses in hunger and satiety. Correction of the associations for age and/or BMI did not change the results.

Single-SNP associations for rs9939609

Baseline values for hunger and satiety were similar between genotypes. ORs for the associations between postprandial responses and the rs9939609 SNP in FTO are shown in Table 2. A general association test showed a significant association between the postprandial decrease in hunger (area under the curve) and the rs9939609 SNP (\( P = 0.036 \)). Although we cannot exclude an additive model (\( P = 0.051 \)), a dominant model fits the data best, with individuals with a low postprandial decrease in hunger being overrepresented among TA/AA carriers compared with TT carriers (\( P = 0.013 \)) (Figure 1A). A significant association was also observed between the absolute postprandial increase in satiety and rs9939609 (\( P = 0.050 \)). An additive model fits the data best, with individuals with a strong postprandial increase in satiety being overrepresented among TA/AA carriers in rs9939609 compared with TT carriers (\( P = 0.020 \)).

TABLE 2

<table>
<thead>
<tr>
<th>Phenotype and SNP</th>
<th>Model</th>
<th>Odds ratio</th>
<th>95% CI</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hunger rs9939609 (FTO)</td>
<td>Dominant</td>
<td>3.02</td>
<td>1.26, 7.24</td>
<td>0.013</td>
</tr>
<tr>
<td>Satiety rs9939609 (FTO)</td>
<td>Additive</td>
<td>2.02</td>
<td>1.12, 3.66</td>
<td>0.020</td>
</tr>
<tr>
<td>Hunger rs9939609 (FTO) and rs992472 (DNMT3B)</td>
<td>Dominant and recessive</td>
<td>5.00</td>
<td>2.11, 11.90</td>
<td>0.00025</td>
</tr>
<tr>
<td>Satiety rs9939609 (FTO) and rs1137101 (LEPR)</td>
<td>Dominant and dominant</td>
<td>5.49</td>
<td>2.30, 15.16</td>
<td>0.00013</td>
</tr>
<tr>
<td>Hunger rs9939609 (FTO) and rs992472 (DNMT3B) and rs1137101 (LEPR)</td>
<td>Dominant, recessive, and dominant</td>
<td>8.06</td>
<td>3.15, 20.41</td>
<td>0.000013</td>
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<tr>
<td>Satiety rs9939609 (FTO)</td>
<td>Dominant</td>
<td>3.83</td>
<td>1.49, 9.80</td>
<td>0.0052</td>
</tr>
<tr>
<td>Hunger rs992472 (DNMT3B)</td>
<td>Recessive</td>
<td>4.03</td>
<td>1.10, 14.9</td>
<td>0.036</td>
</tr>
<tr>
<td>Satiety rs1137101 (LEPR)</td>
<td>Dominant</td>
<td>3.17</td>
<td>1.11, 9.01</td>
<td>0.030</td>
</tr>
</tbody>
</table>

1 The results shown are relative to individuals homozygous for the protective alleles (TT for FTO, AA for DNMT3B, and AA for LEPR).
2 Phenotype, postprandial response in hunger or satiety; hunger, the postprandial area under the curve for hunger; satiety, the absolute postprandial increase in satiety, that is, the absolute difference between the baseline value and the maximal postprandial value obtained.
3 The SNP included in the logistic regression model.
4 The model of inheritance fitting the data best.
5 The odds ratio for having a low postprandial response.
hspectively) (P = 0.065) or recessive (P = 0.049) model cannot be excluded for the latter association.

No significant associations were observed between postprandial responses in hunger and satiety and the SNPs in DNMT1 and LEP. As for the rs992472 (DNMT3B) and rs1137101 (LEPR) SNPs, individuals with a low postprandial decrease in hunger were overrepresented among CC/CA carriers in rs992472 (DNMT3B) compared with AA carriers (recessive model: P = 0.036; OR: 3.395; 95% CI: 1.009, 11.416) and among AG/GG carriers in rs1137101 (LEPR) compared with AA carriers (dominant model: P = 0.013; OR: 3.502; 95% CI: 1.307, 9.382).

Epistatic interactions involving rs9939609

MDR showed 2 significant epistatic interactions for the postprandial decrease in hunger (area under the curve) involving rs9939609. These interactions are in the same direction as the aforementioned univariate associations. One interaction is shown with rs992472 (DNMT3B) and the other with rs1137101 (LEPR) [prediction accuracy: 66% (P = 0.050) and 68% (P = 0.040), respectively]. Logistic regression showed that individuals with a low postprandial decrease in hunger were overrepresented among individuals who carried the TA/AA genotype in rs9939609 (dominant model) as well as the CC/CA genotype in rs992472 (DNMT3B) (recessive model) compared with carriers of the TT (rs9939609) and/or AA (rs992472) genotype in these SNPs (P = 0.00025) (Table 2, Figure 2). Individuals with a low postprandial decrease in hunger are also overrepresented among individuals carrying the TA/AA genotype in rs9939609 (dominant model) and the AG/GG genotype in rs1137101 (LEPR) (dominant model) compared with carriers of the TT (rs9939609) and/or AA (rs992472) genotype in these SNPs (P = 0.00013) (Table 2, Figure 3). An evaluation of the combined effect of the 3 SNPs showed that individuals with a low postprandial decrease in hunger were significantly overrepresented among risk-allele carriers in all 3 SNPs, that is, individuals with the TA/AA, CC/CA, and AG/GG genotypes in rs9939609, rs992472, and rs1137101, respectively, compared with individuals homozygous for at least one protective allele in these SNPs (the TT, AA, or AA genotype in rs9939609, rs992472, or rs1137101, respectively) (P = 0.000013) (Table 2, Figure 4). Each SNP had an additional effect.

DISCUSSION

The main result of the present study was that individuals with low postprandial responses in hunger and satiety are overrepresented among TA/AA carriers in rs9939609 (FTO) compared with TT carriers, independent of BMI. This implies that the results of Wardle et al (18, 19), who showed a reduced sensitivity to satiety cues in children with the AA compared with the TT genotype are replicated in adults in an experimental setting. The increased adiposity associated with the TA and AA genotypes in rs9939609 thus appears to at least partly be a function of reduced postprandial responses in hunger and satiety, thereby increasing the risk of overeating (20). The strength of the present study lays in the valid and accurate measurement of the phenotype, that is, the postprandial responses of hunger and satiety. Future studies with larger sample sizes are required to draw firm conclusions about the appropriate mode of inheritance as well as to narrow down the CIs.

In addition to the univariate associations shown for rs9939609, interactions with candidate genes were evaluated to gain more insight into the possible mechanism by which FTO affects appetite responsiveness. The association between the postprandial decrease in hunger and the rs9939609 SNP in FTO was mediated by the rs992472 variant in DNMT3B. Individuals with a low postprandial decrease in hunger are overrepresented among carriers of the TA/AA genotype in rs9939609 (FTO) when accompanied by the CC/CA genotype in rs992472 (DNMT3B), compared with individuals carrying the TT (rs9939609) and/or AA (rs992472) genotype in these SNPs. DNMT3B was originally thought to be responsible for de novo DNA methylation after embryo implantation (27, 36, 37), but was recently concluded to also be essential for the maintenance of preexisting methylation patterns after DNA replication (36, 38, 39).

DNA methylation is a major epigenetic modification that consists of the addition of a methyl group to the 5'-position of cytosine within a CpG dinucleotide, thereby altering gene activity (36). Hypermethylation of the promoter and coding region of a gene decreases its transcription, thereby silencing the gene. Hypomethylation on the other hand enhances the binding of transcription factors, thereby improving gene transcription (27). DNA methylation probably plays a role in body weight regulation, as providing a hypermethylating dietary supplement to Agouti (A¹⁷) mice prevents the transgenerational increase in body weight that occurs without supplementation (40).
The rs992472 SNP in DNMT3B is located in the same linkage disequilibrium (LD) block as the rs2424913 C→T SNP in the same gene, for which the minor allele (T) is associated with an increased DNMT3B promoter activity (28). Additionally, the minor allele in rs2424913 is associated with the risk of developing various types of cancer, probably by aberrant de novo methylation of CpG islands in some tumor suppressor genes (28). Given the LD between rs992472 and rs2424913, a post hoc analysis was performed to determine whether the epistatic interaction for the postprandial decrease in hunger involving rs9939609 (FTO) and rs992472 (DNMT3B) was confirmed for rs9939609 (FTO) and rs2424913 (DNMT3B). Because this interaction was indeed observed ($P = 0.002$; data not shown), it is tempting to speculate that a genotype-driven decrease in the capacity for de novo DNA methylation/maintenance of DNA methylation patterns underlies the overrepresentation of individuals with a low postprandial decrease in hunger among CC/CA carriers in rs992472 (DNMT3B) compared with AA carriers.

Fischer et al (41), recently showed that $FTO^{2/2}$ mice are characterized by lower adiposity than are their wild-type littermates and concluded that the obesity-predisposing alleles in $FTO$ in humans are probably associated with an up-regulation or deregulation of $FTO$ expression. In addition, Gerken et al (14) previously showed that $FTO$ catalyzes Fe(II) and 2-oxoglutarate-dependent DNA demethylation. These findings suggest that TA/AA carriers in rs9939609 (FTO) are characterized by an increased capacity for DNA demethylation compared with TT carriers. The interaction for the postprandial response in hunger involving SNPs in $FTO$ and $DNMT3B$ could thus result from a decreased capacity for de novo DNA methylation and maintenance of preexisting DNA methylation patterns (CC/CA

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**FIGURE 2.** Epistatic interaction for the postprandial decrease in hunger involving rs9939609 (FTO) and rs992472 (DNMT3B). A: The output obtained with the use of multifactor dimensionality reduction. The gray squares represent possible combinations of genotypes; the bars on the left represent the number of individuals with a strong postprandial decrease in hunger, and the bars on the right represent the number of individuals with a low postprandial decrease. B: The statistical interpretation of the model obtained by using logistic regression. On the basis of the response pattern in panel A, participants carrying the TA/AA genotype in rs9939609 and the CC/CA genotype in rs992472 were pooled and compared with individuals with the TT and/or AA genotype in these single nucleotide polymorphisms, respectively. $P = 0.00025$.

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**FIGURE 3.** Epistatic interaction for the postprandial response in hunger involving rs9939609 (FTO) and rs1137101 (LEPR). A: The output obtained by using multifactor dimensionality reduction. The gray squares represent possible combinations of genotypes; the bars on the left represent the number of individuals with a strong postprandial increase in satiety, and the bars on the right represent the number of individuals with a low postprandial increase. B: The statistical interpretation of the model obtained by using logistic regression. On the basis of the response pattern in panel A, participants carrying the TA/AA genotype in rs9939609 and the AG/GG genotype in rs1137101 were pooled and compared with individuals with the TT and/or AA genotype in these single nucleotide polymorphisms, respectively. $P = 0.00013$. 
The interaction between rs9939609 and rs1137101 probably affects the postprandial decrease in hunger via a mechanism other than DNA methylation. After all, if blocking leptin indeed decreases FTO expression (21), the risk of obesity is anticipated to be reduced (40, 41), which is the exact opposite of what is expected when the postprandial decrease in hunger is low. This implies that the effect of this alternative mechanism on the postprandial decrease in hunger should not be underestimated.

We did not confirm the association between BMI and the rs9939609 variant shown in previous studies. This can be explained by the range in BMI in our population and by the character of the study and its concomitant sample size. In the current experimental study, 103 participants were recruited with a BMI ranging from 19 to 31. Only 5 individuals with a BMI > 30 were included. This contrasts sharply with case-control studies (6, 46) and with cohort studies (5, 7), in which the association between BMI and rs9939609 is observed by Stratigopoulos et al (15), who showed that hypothalamic FTO expression is reduced after fasting. However, the fasting-induced decrease in FTO expression observed by Stratigopoulos et al was not mediated by leptin. Our results suggest that leptin resistance may only functionally affect FTO expression in TA/AA carriers.

In conclusion, evidence shows an association between postprandial responses in hunger and satiety with the rs9939609 SNP in FTO, with the TA/AA genotype predisposing individuals to reduced postprandial responses in hunger and satiety. The effect of the variant in FTO on the postprandial response in hunger appears to be mediated by an epistatic interaction involving variants in DNMT3B and LEPR. The interaction with the rs992472 SNP in DNMT3B suggests that DNA methylation, an epigenetic process, is involved in food intake regulation.
We thank Kristel Diepvens, Manuela Lejeune, Astrid Smeets, Margriet Veldhorst, and Ananda Hochstenbach-Waalen for their contributions in acquiring the data on postprandial responses in hunger and satiety.

The authors’ responsibilities were as follows—MdH: developed the study, performed the genotyping and statistical analyses, and wrote the manuscript; MSW-P, ECMM, and KRW: developed the study and wrote the manuscript; and FGB: performed the genotyping and wrote the manuscript. None of the authors had a conflict of interest.

REFERENCES