Gene-nutrient interactions in the metabolic syndrome: single nucleotide polymorphisms in ADIPOQ and ADIPOR1 interact with plasma saturated fatty acids to modulate insulin resistance

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ABSTRACT

Background: Progression of the metabolic syndrome (MetS) is determined by genetic and environmental factors. Gene-environment interactions may be important in modulating the susceptibility to the development of MetS traits.

Objective: Gene-nutrient interactions were examined in MetS subjects to determine interactions between single nucleotide polymorphisms (SNPs) in the adiponectin gene (ADIPOQ) and its receptors (ADIPOR1 and ADIPOR2) and plasma fatty acid composition and their effects on MetS characteristics.

Design: Plasma fatty acid composition, insulin sensitivity, plasma adiponectin and lipid concentrations, and ADIPOQ, ADIPOR1, and ADIPOR2 SNP genotypes were determined in a cross-sectional analysis of 451 subjects with the MetS who participated in the LIPGENE (Diet, Genomics, and the Metabolic Syndrome: an Integrated Nutrition, Agro-food, Social, and Economic Analysis) dietary intervention study and were repeated in 1754 subjects from the LIPGENE-SU.VI.MAX (SUPplementation en Vitamines et Minéraux Antioxydants) case-control study (http://www.ucd.ie/lipgene).

Results: Single SNP effects were detected in the cohort. Triacylglycerols, nonesterified fatty acids, and waist circumference were significantly different between genotypes for 2 SNPs (rs266729 in ADIPOQ and rs10920533 in ADIPOQ). Minor allele homozygotes for both of these SNPs were identified as having degrees of insulin resistance, as measured by the homeostasis model assessment of insulin resistance, that were highly responsive to differences in plasma saturated fatty acids (SFAs). The SFA-dependent association between ADIPOQ rs10920533 and insulin resistance was replicated in cases with MetS from a separate independent study, which was an association not present in controls.

Conclusions: A reduction in plasma SFAs could be expected to lower insulin resistance in MetS subjects who are minor allele carriers of rs266729 in ADIPOQ and rs10920533 in ADIPOQ. Personalized dietary advice to decrease SFA consumption in these individuals may be recommended as a possible therapeutic measure to improve insulin sensitivity. This trial was registered at clinicaltrials.gov as NCT00429195. Am J Clin Nutr 2010;91:794–801.

INTRODUCTION

The metabolic syndrome (MetS) is a complex disorder characterized by abdominal obesity, insulin resistance, hyperglycemia, dyslipidemia, and inflammation. It is associated with severe health complications, such as an increased risk of type 2 diabetes and cardiovascular disease (CVD). Development of the MetS is influenced by genetic as well as environmental factors, with dietary fat being a major environmental factor. Adiponectin is the most quantitatively abundant adipokine secreted by adipocytes. Concentrations of circulating adiponectin are reduced in obese and type 2 diabetes subjects. It is proposed that this hormone is a key player in the etiology of the MetS, because it may be an important regulator of insulin sensitivity and inflammation. Thus, polymorphisms in the ADIPOQ gene and its receptors, ADIPOR1 and ADIPOR2, may play a role in the pathogenesis of the MetS. Functional studies in animal models have shown that adiponectin attenuates insulin resistance by reducing the triacylglycerol content in muscle and liver. Adiponectin knockout mice develop insulin resistance in response to a high-fat, high-sucrose diet, whereas mice with increased plasma adiponectin exhibit improved insulin sensitivity. The precise roles of the adiponectin receptors are not yet fully known, and they may have diverse and even contradictory effects. The mouse Adipor1 receptor appears to act via the AMPK pathway, whereas the Adipor2 receptor has greater involvement in peroxisome proliferator–activated receptor α (PPARα) signaling. Adipor1 knockout mice die via the AMPK pathway, whereas the Adipor2 receptor has greater involvement in peroxisome proliferator–activated receptor α (PPARα) signaling.
velop obesity and decreased glucose tolerance, whereas Adipor2 knockout mice appear protected against diet-induced obesity and have better glucose tolerance and reduced cholesterol (11). However, Adipor2 deletion leads to inadequate pancreatic β cell function and type 2 diabetes in the longer term (12). In humans, associations have been found between many polymorphisms in ADIPOQ, ADIPOR1, and ADIPOR2 and adiponectin concentrations, insulin resistance, and MetS phenotypes (13, 14). Inconsistencies in the reported associations of polymorphisms in these genes and metabolic measures could be due to environmental interactions, particularly dietary factors. Gene-nutrient interactions can modulate the effect of certain polymorphisms in MetS-related traits (15). Although, thus far, there has been little focus on gene-nutrient interactions with ADIPOQ and its receptors, one study conducted in obese females found that there was an interaction between the rs266729 polymorphism of ADIPOQ and the percentage of dietary-derived energy from fat with the development of obesity (16).

Our present study addressed the hypothesis that interactions between adiponectin and adiponectin receptor gene variants and fatty acids may modulate metabolism of subjects with the MetS, particularly insulin resistance. Thus, we examined interactions between polymorphisms in ADIPOQ, ADIPOR1, and ADIPOR2 and plasma fatty acid composition in relation to metabolic indexes of insulin resistance, dyslipidemia, hypertension, obesity, and plasma adiponectin in 451 subjects with the MetS. A second MetS case-control population (n = 1754) was used to attempt to replicate the gene-nutrient interactions.

SUBJECTS AND METHODS

Subjects

Subjects aged 35–70 y with a body mass index (BMI; in kg/m²) of 20 to 40 were recruited for the LIPGENE (Diet, Genomics, and the Metabolic Syndrome: an Integrated Nutrition, Agro-food, Social, and Economic Analysis) dietary intervention study, details of which have been published (17). In the present study, the preintervention data for 451 subjects were analyzed. Subjects were recruited from 8 European countries: Ireland (n = 59), United Kingdom (n = 58), Norway (n = 63), France (n = 39), the Netherlands (n = 45), Spain (n = 70), Poland (n = 67), and Sweden (n = 50). See Supplemental Table 1 under “Supplemental data” in the online issue for the clinical characteristics of the subjects. All centers conformed to the Helsinki Declaration of 1975 as revised in 1983. Subject eligibility was determined by using a modified version of the National Cholesterol Education Program (NCEP) criteria for MetS (18), and subjects were required to fulfill ≥3 of the following 5 criteria: waist circumference >102 cm (men) or >88 cm (women), fasting glucose 5.5–7.0 mmol/L, triacylglycerol ≥1.5 mmol/L, HDL cholesterol <1.0 mmol/L (men) or <1.3 mmol/L (women), and blood pressure ≥130/85 mm Hg or treatment of previously diagnosed hypertension. Anthropometric measurements and samples taken in the supine position were recorded according to a common standardized protocol for the LIPGENE study, and blood pressure was measured according to the European Society of Hypertension Guidelines (19). Subjects for the LIPGENE-SU.VI.MAX (SUPplementation en VItamines et Minéraux AntioXydants) population were selected from the existing French SU.VI.MAX cohort, a prospective population-based study (13,000 subjects studied over 7 y, 1995–2002) (20). Baseline and 7-y follow up data were made available to LIPGENE and were used to identify individuals who developed elements of the MetS over the 7-y follow up period and matched control subjects (n = 1754). MetS cases and controls were selected according to screening criteria and a scoring system, based on World Health Organization and the NCEP-Adult Treatment Panel III criteria for the MetS. Additional ethical approval from the ethical committee (of Paris-Cochin Hospital) included an additional clause (n° Am 2840–12–706) to perform the biochemical analysis and genetic analysis required for the LIPGENE study. LIPGENE-SU.VI.MAX subjects (women aged 35–60 y and men aged 45–60 y) were informed of the study objectives and signed a consent form. Plasma fatty acids, homeostasis model assessment of insulin resistance (HOMA-IR), and SNP genotyping data were analyzed here, and there were complete data for 818 cases and matched controls. There was no overlap in participants between the LIPGENE dietary intervention study and the LIPGENE-SU.VI.MAX population.

Biochemical measurements

In the LIPGENE dietary intervention cohort, plasma, serum, and buffy coat were prepared from 12-h fasting blood samples from each subject. Serum insulin was measured with a solid-phase, 2-site fluoroimmunometric assay on a 1235 automatic immunoassay system (AutoDELFIA kits; Wallac Oy, Turku, Finland). Plasma glucose concentrations were measured by using the IL Test Glucose Hexokinase Clinical Chemistry kit (Instrumentation Laboratories, Warrington, United Kingdom). HOMA-IR was derived from fasting glucose and insulin concentrations [(fasting plasma glucose × fasting serum insulin)/22.5] as determined previously (21). Plasma concentrations of adiponectin were measured by enzyme-linked immunosorbent assay (Duoset ELISA Development System; R&D Systems, Minneapolis, MN). Cholesterol and triacylglycerol were quantified by using the IL Test Cholesterol kit and the IL Test Triacylglycerides kit (Instrumentation Laboratories, Warrington, United Kingdom). The IL Test HDL-C Kit (Instrumentation Laboratories) was used for direct quantification of HDL cholesterol. The WAKO NEFA C enzymatic color kit (Alpha Laboratories, Hampshire, United Kingdom) was used to quantify plasma nonesterified fatty acid (NEFA) concentrations. The plasma fatty acid composition for both study populations was measured on a GC 2010 gas-liquid chromatograph (Shimadzu, Japan), as previously described (22). In the LIPGENE-SU.VI.MAX population, fasting glucose was measured as previously described (20). Fasting insulin concentrations were measured by electrochemiluminescence immunoassays (Roche Diagnostics, Meylan, France), and HOMA-IR was calculated from these concentrations as described previously.

SNP selection and genotyping

Genotype data from HapMap (http://hapmap.org) (ADIPOQ, ADIPOR1, and ADIPOR2) were uploaded into HITAGENE, a combined database and set of genetic analysis tools developed by Hitachi Dublin Laboratory. Haplotype frequencies in each
gene were estimated by implementation of the expectation-maximization algorithm. Using a 5% cutoff for individual haplotype frequency and >70% for the sum of all haplotype frequencies, genotype data were then transferred from HITAGENE to SNP tagger (http://www.broad.mit.edu/mpg/tagger/server.html) to identify haplotype tagged (Ht) SNPs. A combination of Ht SNPs and SNPs previously mentioned in the literature were genotyped providing a total of 11 SNPs in 3 genes: ADIPOQ (rs266729, rs822395, rs17366568, rs2241766, and rs1063538), ADIPOR1 (rs2275737, rs10753929, and rs10920533), and ADIPOR2 (rs6498932, rs1058322, and rs10848571). DNA was extracted from buffy coat samples by using the AutoPure LS automated system (Genta Systems Inc, Minneapolis, MN), and low-yielding samples (<10 ng) were subjected to whole genome amplification by using the REPLI-g kit (Qiagen Ltd, West Sussex, United Kingdom). Genotyping was conducted by Illumina Inc (San Diego, CA). Adherence to Hardy-Weinberg equilibrium at each SNP locus was determined by using the chi-square test with 1 df. All SNPs were found to adhere to Hardy-Weinberg equilibrium. Linkage disequilibrium between SNPs was assessed by using THESIAS version 3.1 (23). Because there was no significant linkage disequilibrium, all SNPs were retained for further analysis.

Statistical analysis

Biochemical variables were assessed for normality of distribution, and skewed variables were normalized by log_{10} or square root transformation as appropriate. Analysis of variance–based models were used to test for associations between individual SNPs and biomarkers of the MetS. Gene-nutrient interactions were tested for by using an SNP–fatty acid interaction term in a univariate general linear model. The effect of each SNP interacting with plasma saturated fatty acids (SFAs) on each biochemical variable was investigated by using SFA as a continuous variable with an SNP–SFA interaction term and with SNP and SFA entered individually, controlling for age, sex, BMI, and LIPGENE center of origin. If a significant interaction was found, the result was verified by analysis of variance in the cohort dichotomized by the median level of SFA by using Tukey’s post hoc test. To correct for multiple testing, the false discovery rate (FDR) procedure was used for each SNP on all variables tested. Statistical analysis was carried out by using SPSS version 14.0 for Windows (SPSS Inc, Chicago, IL) and SAS for Windows (version 9.0, SAS Institute, Cary, NC).

RESULTS

Genotype frequencies and metabolic characteristics

Details of the 11 SNPs characterized in this study and the genotype frequencies in the LIPGENE cohort are presented in Table 1. There were no significant differences in genotype frequencies across the 8 European countries. All SNPs were used in the analysis; however, the results are presented for only the 2 SNPs (rs266729 and rs10920533) that showed a number of interesting significant associations. Characteristics of the subjects with different alleles for ADIPOQ rs266729 and ADIPOQ rs10920533 are summarized in Table 2. Triacylglycerol (P = 0.009) and NEFA (P = 0.003) concentrations were significantly different between the genotype groups for ADIPOQ rs266729, and waist circumference varied significantly for ADIPOQ rs10920533 (P = 0.021). The association with NEFA remained significant (FDR: P = 0.039) when the FDR was used to correct for multiple testing, whereas the association with triacylglycerol was reduced to borderline significance (FDR: P = 0.059), and the association with waist circumference was no longer significant (FDR: P = 0.27).

Effect of SFA-SNP interactions on insulin sensitivity

Because this study was primarily interested in potential interactions between genotypes and nutritional status, the effect of the 2 previously mentioned SNPs on metabolic markers was examined in combination with plasma fatty acid status. Statistically significant gene-nutrient interaction terms between SNPs and plasma SFAs were detected for effects on insulin sensitivity. Similar results were obtained for both fasting insulin and HOMA-IR. HOMA-IR was used for further analysis, because it takes into account both fasting insulin and fasting glucose. From the initial analyses using a univariate general linear model to assess statistical interaction, the overall interaction terms for the effect on HOMA-IR were as follows: rs266729 in ADIPOQ (P = 0.01; adjusted FDR: P = 0.059) and rs10920533

<table>
<thead>
<tr>
<th>Gene</th>
<th>Chromosome</th>
<th>SNP rs number</th>
<th>Location within gene</th>
<th>Genotype frequencies</th>
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<tr>
<td>ADIPOQ</td>
<td>3</td>
<td>rs266729</td>
<td>5’ near-gene</td>
<td>CC/CC/CG = 41/162/248</td>
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<tr>
<td></td>
<td></td>
<td>rs822395</td>
<td>Intron 1</td>
<td>AA/AG/GG = 191/206/54</td>
</tr>
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<td></td>
<td></td>
<td>rs17366568</td>
<td>Intron 1</td>
<td>AA/AG/GG = 787/357</td>
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<tr>
<td></td>
<td></td>
<td>rs2241766</td>
<td>Exon 2</td>
<td>AA/AC/CC = 340/101/9</td>
</tr>
<tr>
<td></td>
<td></td>
<td>rs1063538</td>
<td>3’ UTR</td>
<td>GG/TT/TT = 170/203/78</td>
</tr>
<tr>
<td>ADIPOR1</td>
<td>1</td>
<td>rs2275737</td>
<td>Intron 1</td>
<td>AA/AC/CC = 79/224/154</td>
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<tr>
<td></td>
<td></td>
<td>rs10753929</td>
<td>Intron 1</td>
<td>AA/AG/GG = 8/94/351</td>
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<tr>
<td></td>
<td></td>
<td>rs10920533</td>
<td>Intron 1</td>
<td>AA/AG/GG = 37/192/224</td>
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<tr>
<td>ADIPOR2</td>
<td>12</td>
<td>rs6489323</td>
<td>Intron 1</td>
<td>AA/AG/GG = 232/182/39</td>
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<tr>
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<td></td>
<td>rs1058322</td>
<td>Intron 1</td>
<td>AA/AG/GG = 40/182/230</td>
</tr>
<tr>
<td></td>
<td></td>
<td>rs10848571</td>
<td>Intron 3</td>
<td>GG/TT/TT = 199/150/87</td>
</tr>
</tbody>
</table>

UTR, untranslated region.
Diastolic BP (mm Hg) 87.3
6
6
TAG (mmol/L) 2.2

Figure 1
sensitivity remained relatively stable despite variations in SFAs.

between genotype groups. The minor allele homozygotes dis-
median plasma SFA concentrations. A difference was observed
cohort
SFA concentrations above or below the median of the
Effect of individual SNPs on insulin sensitivity at plasma
fatty acids) and SNPs on insulin sensitivity.

SFA, saturated fatty acid; MUFA, monounsaturated fatty acid; PUFA, polyunsaturated fatty acid. Superscript letters indicate significant differences between groups (Tukey’s post hoc test).

HOMA-IR 2.9
Insulin (l)
Glucose (mmol/L) 5.9

TABLE 2

Combining SNPs into multilocus genotypes can improve
the strength of the association

with plasma SFAs, increased the association with HOMA-IR. A
combined interaction term of the 2 SNPs and plasma SFAs
appeared to have a highly significant association with HOMA-
IR (P < 0.001). Whereas this does not prove a biological in-
teraction, the increased strength of association resulting from
using both SNPs combined rather than individually could in-
dicate that considering combined genotypes at both loci for
individuals would be more informative than analyzing either
locus individually. For both SNPs, the minor allele homozygotes
displayed significant increases in HOMA-IR with high plasma
SFA concentrations. Therefore, these individuals were pooled in
a multilocus genotype and were compared with individuals who
were heterozygous or major allele homozygous for either SNP.
Application of analysis of variance on this multilocus genotype
showed a highly significant effect of plasma SFAs on insulin
sensitivity in individuals who were minor allele homozygotes
for either of the SNPs in the multilocus genotype but not in those
carrying a major allele at both loci, which indicated a significant
gene-nutrient interaction in this multilocus genotype (Figure 2).

Using multilocus SNP combinations to strengthen the
predictive power of the effects of genotype and plasma
SFAs on insulin sensitivity

The predicted HOMA-IR values based on the model were
determined by using a linear regression model for each of the 2
multilocus genotype groups and used for the graphic represen-
tation (Figure 3). A clear difference in HOMA-IR in response to
plasma SFAs can be seen between the 2 multilocus genotype
groups. Such information could theoretically be applied in the
context of nutrigenomics, where an individual’s genotype at

ADIPOR1 (P = 0.004; adjusted FDR P = 0.026). There were no
significant interactions between other plasma fatty acid variables
(monounsaturated fatty acids and n−6 or n−3 polyunsaturated
fatty acids) and SNPs on insulin sensitivity.

Effect of individual SNPs on insulin sensitivity at plasma
SFA concentrations above or below the median of the
cohort

The statistical interactions were probed further for their specific
biological effects by dichotomizing the cohort with respect to
the median plasma SFA concentrations. A difference was observed
between genotype groups. The minor allele homozygotes dis-
played phenotypic variation in response to differences in plasma
SFA concentrations, whereas in the major allele carriers insulin
sensitivity remained relatively stable despite variations in SFAs.
As shown in Figure 1, A and B, there were significant differ-
ces in HOMA-IR between genotype groups for rs266729 and
rs10920533 depending on plasma SFA concentrations. From this,
it is apparent that the degree of insulin sensitivity in individuals
homozygous for the minor allele (CC and AA) is sensitive to the
concentrations of plasma SFAs, whereas the heterozygotes appear
to be insensitive (CG and AG), and the major allele homozygotes
(GG and GG) only showed a small response.

Combining SNPs into multilocus genotypes can improve
the strength of the association

These 2 SNPs (rs266729 in ADIPOQ and rs10920533 in
ADIPOQ) were investigated further to determine whether a
combination of alleles into a multilocus genotype, interacting

ADDITIVE GENES INTERACT WITH SFA ON HOMA-IR 797

<table>
<thead>
<tr>
<th>Sex (M/F)</th>
<th>19/22</th>
<th>72/88</th>
<th>104/143</th>
<th>0.789</th>
<th>20/17</th>
<th>83/108</th>
<th>91/131</th>
<th>0.331</th>
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<tbody>
<tr>
<td>Age (y)</td>
<td>53.7 ± 1.4</td>
<td>54.1 ± 0.7</td>
<td>54.9 ± 0.6</td>
<td>0.609</td>
<td>55.2 ± 1.7</td>
<td>54.7 ± 0.6</td>
<td>54.1 ± 0.6</td>
<td>0.742</td>
</tr>
<tr>
<td>Insulin (mmol/L)</td>
<td>11.0 ± 1.3</td>
<td>10.3 ± 0.5</td>
<td>9.8 ± 0.3</td>
<td>0.596</td>
<td>10.3 ± 1.2</td>
<td>10.6 ± 0.4</td>
<td>9.6 ± 0.3</td>
<td>0.139</td>
</tr>
<tr>
<td>Glucose (mg/dL)</td>
<td>5.9 ± 0.2</td>
<td>5.9 ± 0.1</td>
<td>5.9 ± 0.1</td>
<td>0.567</td>
<td>5.8 ± 0.1</td>
<td>6.0 ± 0.1</td>
<td>5.9 ± 0.1</td>
<td>0.341</td>
</tr>
<tr>
<td>Adiponectin (g/L)</td>
<td>3.4 ± 0.3</td>
<td>3.7 ± 0.2</td>
<td>3.9 ± 0.2</td>
<td>0.137</td>
<td>4.0 ± 0.6</td>
<td>3.9 ± 0.2</td>
<td>3.7 ± 0.2</td>
<td>0.185</td>
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<tr>
<td>Cholesterol (mg/dL)</td>
<td>5.6 ± 0.1</td>
<td>5.3 ± 0.1</td>
<td>5.3 ± 0.1</td>
<td>0.265</td>
<td>5.2 ± 0.1</td>
<td>5.3 ± 0.1</td>
<td>5.4 ± 0.1</td>
<td>0.383</td>
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<tr>
<td>LDL (mg/dL)</td>
<td>3.5 ± 0.1</td>
<td>3.2 ± 0.1</td>
<td>3.3 ± 0.1</td>
<td>0.286</td>
<td>3.2 ± 0.1</td>
<td>3.2 ± 0.1</td>
<td>3.3 ± 0.1</td>
<td>0.715</td>
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<tr>
<td>HDL (mg/dL)</td>
<td>1.2 ± 0.1</td>
<td>1.1 ± 0.0</td>
<td>1.1 ± 0.0</td>
<td>0.303</td>
<td>1.0 ± 0.1</td>
<td>1.1 ± 0.0</td>
<td>1.1 ± 0.0</td>
<td>0.405</td>
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<tr>
<td>TAG (mg/dL)</td>
<td>2.2 ± 0.2</td>
<td>1.8 ± 0.1</td>
<td>1.7 ± 0.1</td>
<td>0.009</td>
<td>1.7 ± 0.1</td>
<td>1.8 ± 0.1</td>
<td>1.8 ± 0.1</td>
<td>0.659</td>
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<tr>
<td>NEFA (μmol/L)</td>
<td>713.1 ± 41.2</td>
<td>578.2 ± 16.5</td>
<td>622.6 ± 15.2</td>
<td>0.003</td>
<td>594.6 ± 41.5</td>
<td>612.9 ± 16.2</td>
<td>619.9 ± 15.9</td>
<td>0.955</td>
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<td>BMI (kg/m²)</td>
<td>32.6 ± 0.7</td>
<td>32.4 ± 0.3</td>
<td>32.4 ± 0.3</td>
<td>0.938</td>
<td>32.6 ± 0.7</td>
<td>32.9 ± 0.3</td>
<td>31.9 ± 0.3</td>
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<td>Waist circumference (cm)</td>
<td>110.3 ± 2.6</td>
<td>105.6 ± 0.9</td>
<td>105.9 ± 0.7</td>
<td>0.180</td>
<td>106.2 ± 1.9</td>
<td>107.9 ± 0.8</td>
<td>104.7 ± 0.7</td>
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<td>Diastolic BP (mm Hg)</td>
<td>87.3 ± 1.9</td>
<td>86.8 ± 0.8</td>
<td>86.1 ± 0.6</td>
<td>0.499</td>
<td>85.0 ± 1.3</td>
<td>86.7 ± 0.8</td>
<td>86.5 ± 0.6</td>
<td>0.673</td>
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<td>Systolic BP (mm Hg)</td>
<td>140.5 ± 2.5</td>
<td>139.6 ± 1.2</td>
<td>138.7 ± 1.0</td>
<td>0.739</td>
<td>137.6 ± 2.2</td>
<td>140.21 ± 1.1</td>
<td>138.6 ± 1.1</td>
<td>0.588</td>
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<tr>
<td>Plasma SFA (% of total lipids)</td>
<td>32 ± 0.9</td>
<td>33.1 ± 0.6</td>
<td>33.2 ± 0.4</td>
<td>0.137</td>
<td>31.8 ± 0.9</td>
<td>32.96 ± 0.5</td>
<td>32.2 ± 0.4</td>
<td>0.623</td>
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<tr>
<td>Plasma MUFA (% of total lipids)</td>
<td>29.3 ± 0.7</td>
<td>27.8 ± 0.4</td>
<td>28.1 ± 0.3</td>
<td>0.192</td>
<td>28.8 ± 0.8</td>
<td>28.8 ± 0.8</td>
<td>27.7 ± 0.3</td>
<td>0.250</td>
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<tr>
<td>Plasma PUFA (% of total lipids)</td>
<td>39.7 ± 0.5</td>
<td>38.8 ± 0.6</td>
<td>39.7 ± 0.4</td>
<td>0.428</td>
<td>38.9 ± 1.0</td>
<td>38.7 ± 0.5</td>
<td>39.9 ± 0.5</td>
<td>0.187</td>
</tr>
</tbody>
</table>

1 HOMA-IR, homeostasis model assessment of insulin resistance; TAG, triacylglycerol; NEFA, nonesterified fatty acid; BP, blood pressure; SFA, saturated fatty acid; MUFA, monounsaturated fatty acid; PUFA, polyunsaturated fatty acid. Superscript letters indicate significant differences between groups (Tukey’s post hoc test).
2 ANOVA for differences between genotype groups.
3 Mean ± SEM (all such values).

ADIPOR1 (P = 0.004; adjusted FDR P = 0.026). These 2 SNPs
(rs266729 and rs10920533) only showed a small response.

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plasma SFAs can be seen between the 2 multilocus genotype
groups. Such information could theoretically be applied in the
context of nutrigenomics, where an individual’s genotype at
these 2 SNPs might predict whether their degree of insulin resistance may be modulated by alterations in plasma SFAs.

**Repllication of the effect of the rs10920533 SNP and plasma SFAs on HOMA-IR in a second population**

To determine whether the gene-nutrient interactions observed in the LIPGENE dietary intervention cohort could be replicated in an independent population, data from the LIPGENE-SU.VI. MAX MetS case-control cohort were analyzed. As presented in Figure 4, the rs10920533 SNP in ADIPOR1 had a significant plasma SFA-dependent effect on HOMA-IR within MetS cases only. This association was not seen when looking at both cases and controls combined or in the control population alone. Specifically, the minor allele homozygotes (AG) again showed significant variation in HOMA-IR, depending on whether plasma SFA concentrations were above or below the median, whereas carriers of the major allele (AG and GG) appeared less sensitive to differences in plasma SFAs. The association with rs266729 was not replicated in the second population.

**DISCUSSION**

**Single SNP associations with MetS traits**

Adiponectin is an important insulin-sensitizing adipokine. Thus, polymorphisms in the adiponectin gene and its receptors are likely candidates for playing a role in the development of insulin resistance and the MetS. In obese subjects, SNPs in ADIPOQ were associated with adiponectin concentrations and type 2 diabetes (24–26). Adiposity-dependent associations with insulin resistance have also been reported (27–29). In the LIPGENE cohort, significant associations between rs266729 and both triacylglycerols and NEFAs were observed. This SNP is located in the 5’ near-genre promoter region and has been shown to alter the binding site of the transcriptional stimulatory protein (SP1), representing a potential pathway for downstream effects (30). Data from previous studies suggest a possible involvement of many SNPs in the adiponectin receptors with potential importance to the MetS (31–36); however, there remains a lack of reliable replication of associations. In the present study, an association with waist circumference was also observed, albeit with a different SNP in ADIPOR1 (rs10920533) to those mentioned in the literature. The SNPs investigated have not been the same in each population, making direct comparisons with previous work more difficult.

**SFA is an important mediator of the association between SNPs in adiponectin and its receptors and insulin sensitivity and plasma adiponectin**

Few studies have investigated gene-nutrient interactions involving SNPs in ADIPOQ, ADIPOR1, or ADIPOR2. One study showed reduced adiponectin concentrations after x-linolenic acid supplementation in overweight individuals, although polymorphisms in 2 ADIPOQ SNPs did not appear to have any effect (37). However, this study was conducted in a small number of individuals, and adiponectin concentrations were different in the intervention group and controls before dietary intervention. A potential gene-nutrient interaction was found between the rs266729 polymorphism of ADIPOQ and the percentage of energy derived from fat in the diet for the development of obesity (16). In the present study, this SNP interacted with plasma SFAs to determine HOMA-IR, thus replicating the potential sensitivity of this SNP to dietary factors. In subjects with suboptimal dietary fat intakes. Many studies reported associations between the rs2241766 and rs1501299 SNPs in ADIPOQ with postprandial adiponectin and lipoprotein profiles (38). Individuals with susceptible genotypes were more sensitive to an oral fat load, which might suggest greater susceptibility to suboptimal dietary fat intakes. Many studies reported associations with rs2241766 dependent on adiposity (27, 28), and it is
Many reported associations are notoriously difficult to replicate in different study populations; therefore, data from a second population were analyzed to determine whether similar effects could be observed. The association with the rs266729 SNP was not observed in this population; however, the association with the rs10920533 SNP was replicated within MetS cases only. Differences in population stratification and environmental factors possibly that, in these patients, obesity may be linked to dietary patterns, for example, by high saturated fat consumption linked to higher lipogenic activity. A recent study reported a significant interaction between an ADIPOQ SNP and insulin resistance and hyperadiponectinemia in relation to glycemic load (39). This indicates, once again, that evaluation of the importance of SNPs in adiponectin should take dietary factors into account, especially in diseases with strong metabolic components. On the basis of the results observed for the rs266729 and rs10920533 SNPs in the LIPGENE cohort, one can speculate that it is indeed likely that endogenous fatty acids modulate the involvement of the adiponectin gene and its receptors in downstream pathways. In the present study, the association seen with plasma SFAs can be attributed mainly to palmitic acid, because this fatty acid constituted the majority of total SFAs. Plasma measures of fatty acids are imperfect biomarkers of dietary intake, because the plasma contains both diet-derived and endogenously synthesized fatty acids. Thus, whereas dietary fatty acids are easier to manipulate, it is likely that plasma measurements more accurately describe the bioactive state.

**FIGURE 2.** Homeostasis model assessment of insulin resistance (HOMA-IR) in the LIPGENE (Diet, Genomics, and the Metabolic Syndrome: an Integrated Nutrition, Agro-food, Social, and Economic Analysis) cohort in relation to the multilocus genotype of ADIPOQ rs266729 and ADIPOR1 rs10920533 and stratified by preintervention median plasma saturated fatty acid (SFA) concentrations. Values are expressed as group means ± SEs. Bars not sharing a common letter or symbol are significantly different at P < 0.05 (ANOVA and Tukey’s post hoc test). The group comprising the CC or AA allele homozygotes from both single nucleotide polymorphisms showed significant differences in HOMA-IR depending on whether their plasma SFA concentration was above or below the median. The individuals with this “high responder” genotype and below-median fatty acid profile had a significantly lower HOMA-IR than did individuals with a below-median fatty acid profile combined with a CG/GG and AG/GG “low responder” genotype. Individuals with a “high responder” genotype and plasma SFA concentration above the median had a significantly higher HOMA-IR than did individuals with a “low-responder” genotype and an above-median SFA concentration. For CC or AA, n = 39 for below the median and n = 31 for above the median. For CG+GG and AG +GG, n = 181 for below the median and n = 180 for above the median.

**FIGURE 3.** Predicted values for homeostasis model assessment of insulin resistance (HOMA-IR) for the multilocus genotype of rs266729 and rs10920533. A clear difference was seen between the genotype groups, with the minor allele homozygote group (triangles) appearing to be “high responders” to plasma saturated fatty acid (SFA) concentrations and the major allele genotype group (circles) appearing to be “low responders.”

**SNP combination into multilocus genotypes improves the strength of association and predictive capacity**

Evaluation of the interactions between SNPs may be advantageous, and detection of these interactions can indicate significant associations with a far greater effect than any one SNP individually. Combining SNPs that each contribute a small effect to the same trait can have a cumulative effect, greatly increasing predictive power, even in the absence of a direct interaction between the genes (40). In our present study, the combination of 2 SNPs, interacting with the same fatty acid variable to influence a shared trait, facilitated a greater predictive capacity to identify individuals likely to be more responsive to modification of dietary saturated fatty acid intake. In this case, sample size constraints limited the multilocus genotype to 2 SNPs; however, larger sample sizes would allow for additional SNPs to be included in a similar way, inviting the possibility to generate a database of robust multilocus-SNP-nutrient associations.

**Effect of the rs10920533 SNP interacting with plasma SFA was replicated in MetS subjects from a separate population**

Many reported associations are notoriously difficult to replicate in different study populations; therefore, data from a second population were analyzed to determine whether similar effects could be observed. The association with the rs266729 SNP was not observed in this population; however, the association with the rs10920533 SNP was replicated within MetS cases only. Differences in population stratification and environmental factors

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was attributable to the lack of replication of the effect of rs266729, with the original cohort being of mixed European origin and the independent replication population being entirely of French origin. For confirmation, this must be verified by analysis in additional populations. It was particularly interesting that the effect of the rs10920533 SNP was only observed in MetS cases and not in the healthy controls. This may indicate that dietary advice based on this genotype should only be applied to individuals already exhibiting risk symptoms of insulin resistance and not to the population in general.

Potential limitations and issues arising from the study

Whereas the LIPGENE dietary intervention cohort consisted of individuals from 8 European countries, including France, the entire LIPGENE-SU.VI.MAX population was recruited in France, which raised the possibility of confounding effects due to variations in population stratification, admixture, and differences in environmental exposure. This was corrected for to some extent by including the center of origin as a cofactor in all analytic models. Previous studies have been carried out in a large variety of populations, indicating that the effects of SNPs in these genes are not limited to specific populations. Another main issue that posed conceptual problems was that the classic model of a wild-type and a risk allele was not entirely adhered to. Thus, examples were seen in which the homozygote groups were more similar to each other than to either heterozygote group. The various selective pressures in existence, and the mechanisms that determine allele frequencies are varied and not yet all understood (41). Heterozygote advantage is well documented in cystic fibrosis (42) and sickle cell anemia (43), and balancing selection, antagonistic pleiotropy, and overdominance are important evolutionary forces. It is of particular importance in nutrigenomic research to consider all of these possible effects, because it is highly likely that nutrition has been a powerful selective force in human evolutionary history (44). Multiple testing is a recurrent issue in association studies and one that has not yet been successfully resolved. Whereas both unadjusted $P$ values and $P$ values corrected for by using FDR were considered here, standard multiple correction methods are still ill-suited to hypothesis-driven studies such as this one. Thus, at present, replication in other cohorts remains the most reliable method for discerning genuine associations from false-positive ones.

In conclusion, this study suggests that 2 SNPs in genes encoding adiponectin (rs266729) and its receptor 1 (rs10920533) interact with plasma SFAs to alter insulin sensitivity as measured by HOMA-IR. Individuals homozygous for the minor allele and additionally having a high SFA concentration appear to be particularly susceptible. The association with rs10920533 was replicated in a separate population of MetS cases. Within the context of personalized nutrition, the genotype at these polymorphisms may play a role in the responsiveness to dietary fatty acid modification in subjects with the MetS.

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REFERENCES


FIGURE 4. Effect of the rs10920533 single nucleotide polymorphism in ADIPOQ and plasma saturated fatty acid (SFA) concentration on homeostasis model assessment of insulin resistance (HOMA-IR) in metabolic syndrome cases (A) and matched controls (B) from the LIPGENE-SUVIMAX (Diet, Genomics, and the Metabolic Syndrome: an Integrated Nutrition, Agro-food, Social, and Economic Analysis–SUPplementation en Vitamines et Minéraux AntioXydiants) cohort. Values are expressed as group means ± SEs. Letters (a and b) are used for comparisons between SFA concentrations above or below the median within the same genotype group. Symbols (∗ and #) are used for comparisons between different genotype groups in the same plasma SFA category. Bars not sharing a common letter or symbol are significantly different at $P < 0.05$ (ANOVA and Tukey’s post hoc test). The AA minor allele homozygotes showed significant differences in HOMA-IR depending on whether their plasma SFA concentration was above or below the median. Within individuals with plasma SFA concentrations above the median, the minor allele homozygotes had a significantly higher HOMA-IR than did both the heterozygotes and the major allele homozygotes. Below-median SFA concentration: AA ($n = 39$), AG ($n = 159$), and GG ($n = 160$). Above-median SFA concentration: AA ($n = 42$), AG ($n = 206$), and GG ($n = 212$). There were no significant differences in HOMA-IR between genotype groups in the cases with the metabolic syndrome.
ADIPONECTIN GENES INTERACT WITH SFA ON HOMA-IR


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