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Adiponectin Gene Variants Are Associated with Insulin Sensitivity in Response to Dietary Fat Consumption in Caucasian Men[2]

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Abstract

Adiponectin (*adipoQ*) gene variants have been associated with type 2 diabetes mellitus and insulin resistance. Our aim was to examine whether the presence of several polymorphisms at the *adipoQ* gene locus (-11391 G > A, 11377 C > G, 45 T > G, and 276 G > T) influences the insulin sensitivity to dietary fat. Healthy volunteers (30 men and 29 women) consumed 3 diets for 4 wk each: an initial period during which all subjects consumed a SFA-rich diet (38% total fat, 20% SFA), followed by a carbohydrate-rich diet (CHO) (30% total fat, 55% carbohydrate) or a monounsaturated fatty acid (MUFA)-rich diet (38% total fat, 22% MUFA) following a randomized, crossover design. After participants consumed each diet, we tested peripheral insulin sensitivity with the insulin suppression test and measured plasma adiponectin concentrations. C/C homozygous men for the -11377 C > G single nucleotide polymorphism (SNP) had a significantly greater decrease in the steady-state plasma glucose concentrations when changing from the SFA-rich (8.95 ± 0.6 mmol/L) to the MUFA-rich (6.04 ± 0.31 mmol/L) and CHO-rich (6.35 ± 0.38 mmol/L) diets than did those carrying the minor G allele (SFA, 6.65 ± 0.4 mmol/L; MUFA, 6.45 ± 0.4 mmol/L; CHO, 5.83 ± 0.3 mmol/L) (*P sex × gene × diet interaction* = 0.016). These differences did not occur in female participants. Furthermore, C/C men had lower plasma adiponectin concentrations than did C/C women (*P sex × gene interaction* = 0.015), independently of the dietary fat consumed. None of the variables examined were significantly associated with -11426 A > G, 45T > G, or 276 G > T SNP. In conclusion, C/C homozygous men for the -11377 C > G SNP at *adipoQ* gene were significantly less insulin resistant after consumption of the MUFA- and CHO-rich diets compared with the SFA-rich diet. This information should help in the identification of vulnerable populations or persons who will benefit from more personalized and mechanism-based dietary recommendations.

Introduction

Insulin resistance is a characteristic of abnormal glucose tolerance and it may even be present in subjects with normal glucose tolerance (1). This condition usually precedes clinical expression of type 2 diabetes mellitus (T2DM)[5] by decades and its precise assessment could facilitate the clinical expression of the disease by dietary and lifestyle modifications (2). Observational evidence and intervention studies indicate that the quantity and quality of dietary

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fats influence insulin resistance; in particular, saturated fat worsens, whereas monounsaturated and polyunsaturated fats improve insulin sensitivity (3,4). However, some individuals are insensitive (hypo-responders) to dietary intervention, whereas others (hyper-responders) have an enhanced sensitivity. Therefore, what may be good for the general population may not necessarily be beneficial for an individual. In support of this hypothesis, multiple studies have already shown significant gene × diet interactions; however, the reliability, reproducibility, and practical translation of the current evidence are still rather limited.

Adiponectin is an adipokine that is specifically and abundantly expressed in adipose tissue and sensitizes the body to insulin (5,6). Hypoadiponectinemia, caused by interactions of genetic and environmental factors, appears to play an important causal role in insulin resistance, T2DM, and metabolic syndrome (7-11). Therefore, factors such as diet, which induce increases in adiponectin, might be useful for improving such metabolic abnormalities. However, there is no consistent evidence linking increases in dietary SFA intake with lowering of serum adiponectin concentrations over the long term (12). The adiponectin gene (*adipoQ*) is located on chromosome 3q27, which has been reported to be linked to T2DM and metabolic syndrome (13). Among the single nucleotide polymorphisms (SNP) studied in the a*dipoQ* gene, the one located 276 bp downstream of the translational start site (SNP 276 G > T) has been associated with decreased plasma adiponectin concentrations, greater insulin resistance, and an increased risk of T2DM in Japanese subjects (14). Similar associations of the a*dipoQ* gene with susceptibility to T2DM have been reported in other ethnic groups. In Caucasian German and North American subjects, the 276 G > T SNP, either independently or as a haplotype with the exon 2, 45 G > C SNP, was shown to be associated with obesity and insulin resistance (15, 16). In French subjects, 2 SNP in the promoter region of the a*dipo*Q gene, SNP -11377 C > G and SNP -11391 G > A, were significantly associated with hypoadiponectinemia and T2DM (12). Interestingly, there is some evidence that the -11377 C > G SNP is potentially functional. Taken together, the experimental and observational data support the hypothesis that adiponectin plays an important role in the pathogenesis of T2DM.

In view of the physiological role of adiponectin in glucose homeostasis and the link between insulin resistance and dietary fat, we hypothesized that genetic variations affecting the activity and/or expression of *adipoQ* in humans could be associated with variability in insulin response to dietary fat. Therefore, our aim was to examine whether the genetic variability at the *adipoQ* gene locus (i.e. -11426 A > G, -11377 C > G, 45 T > G, and 276 G > T) influences insulin sensitivity to dietary fat in healthy subjects.

Materials and Methods

Subjects

Fifty-nine healthy volunteers (30 men and 29 women) were recruited from among 250 students at the University of Cordoba. They had a mean age (± SD) of 23.1 ± 1.8 y. Informed consent was obtained from all participants. To avoid potential confounders from other sources, including medication, subjects with clinical metabolic alterations were excluded. Thus, all subjects exhibited no evidence of any chronic disease (hepatic, renal, thyroid, or cardiac dysfunction), obesity, or unusually high levels of physical activity (e.g. sports training). None of the subjects had a family history of premature coronary artery disease or had taken medications or vitamin supplements in the 6 mo prior to the study. Physical activity and diet, including alcohol consumption, were recorded in a personal log for 1 wk and the data were

[5]Abbreviations used: *adipoQ*, adiponectin gene; Apo, apolipoprotein; CHO-rich diet, carbohydrate-rich diet; HDL-C, HDL cholesterol; LDL-C, LDL cholesterol; MUFA-rich diet, monounsaturated fatty acid-rich diet; NEFA, nonesterified FFA; SNP, single nucleotide polymorphism; SSPG, steady-state plasma glucose; SSPI, steady-state plasma insulin; TG, triacylglycerol; T2DM, type 2 diabetes mellitus.

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used to calculate individual energy requirements following the program Dietsource v 2.0 (Novartis Consumer Health). Mean BMI was <25 kg/m^2 at the onset of the study and remained constant throughout the experimental period. Subjects were encouraged to maintain their regular physical activity and lifestyle and were asked to record in a diary any event that could affect the outcome of the study, such as stress, changes in smoking habits and alcohol consumption, or intake of foods not included in the experiment design. The experimental protocol and secondary analyses of the data were approved by the Human Investigation Review Committee at the Reina Sofia University Hospital and the Tufts-New England Medical Center Institutional Review Boards.

Diets

The study design included an initial 28-d period during which all subjects consumed an SFA-enriched diet, with 15% protein, 47% carbohydrate, and 38% fat [20% SFA, 12% monounsaturated fatty acid (MUFA), and 6% PUFA]. We used the SFA diet period as a baseline regimen, because this diet is frequently consumed in Western countries, including most areas of Spain. The fixed order of administration of the diets was based on the findings from the KANWU study (17) that saturated fat is associated with worsening of insulin sensitivity. Our purpose was to analyze the substitution of this type of diet with 2 others (high-carbohydrate or high-monounsaturated fat diets). After the SFA diet period, 30 subjects ate a MUFA-enriched diet and 29 consumed the carbohydrate-rich diet (CHO) for 28 d in a randomized, crossover design. The MUFA-enriched diet contained 15% protein, 47% carbohydrates, and 38% fat (<10% SFA, 6% PUFA, 22% MUFA). The CHO diet contained 15% protein, 55% carbohydrates, and <30% fat (<10% SFA, 6% PUFA, 12% MUFA). The dietary cholesterol content was constant at <300 mg/d during the 3 periods. Eighty percent of the MUFA diet was provided by virgin olive oil, which was used for cooking, salad dressing, and as a spread. Carbohydrate intake from the CHO diet was based on the consumption of biscuits, jam, and bread. Butter and palm oil were used during the SFA dietary period.

The composition of the experimental diets was calculated using the USDA (18) food tables and Spanish food composition tables for local foodstuffs (19). All meals were prepared in the hospital kitchen and were supervised by a dietitian. Lunch and dinner were eaten in the hospital dining room, whereas breakfast and an afternoon snack were eaten in the medical school cafeteria. Fourteen menus were prepared with regular solid foods and rotated during the experimental period.

Duplicate samples from each menu were collected, homogenized, and stored at -70°C. The protein, fat, and carbohydrate contents of the diet were analyzed by standard methods (20). Dietary compliance was verified by analyzing the fatty acids in LDL cholesterol (LDL-C) esters at the end of each dietary period (21). The study took place during January and March to minimize seasonal effects and academic stress.

Lipid analysis and biochemical determinations

Venous blood samples for glucose, lipid, and lipoprotein analysis were collected into EDTA-containing (1 g/L) tubes from all subjects after a 12-h overnight fast at the beginning of the study and at the end of each dietary period. Plasma was obtained by low speed centrifugation at 2500 × *g*; 15 min at 4°C within 1 h of venipuncture. We measured plasma cholesterol and triacylglycerol (TG) concentrations using enzymatic techniques (22). HDL cholesterol (HDL-C) was measured after precipitation with fosfowolframic acid (23). Apolipoprotein (Apo) A-I and B concentrations were determined by immunoturbidimetry (24). The LDL-C concentration was calculated using the Friedewald formula (25). We measured nonesterified FFA (NEFA) concentrations using an enzymatic colorimetric assay (Enzymun-Test FFA, Boehringer Mannheim) (26). Plasma adiponectin was measured by ELISA human adiponectin/

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Acrp30 immunoassay (R&D System). The quantikine adiponectin immunoassay is a solid-phase ELISA designed to measure total (low, middle, and high molecular weight) human adiponectin in cell culture supernatants, serum, and plasma.

Insulin suppression test

A modified insulin suppression test was carried out on all the subjects at the end of the dietary period (27). The study began at 0800 after 12 h of fasting. A continuous infusion of somatostatin (214 nmol/h), insulin (180 pmol·m^{-2}·min^{-1}), and glucose (13.2 mmol·m^{-2}·min^{-1}) was infused in the same vein. Somatostatin was used to inhibit endogenous insulin secretion and glucagon release from pancreatic islets. Blood was sampled every 30 min for the first 2.5 h, by which time steady-state plasma glucose (SSPG) and steady-state plasma insulin (SSPI) concentrations were achieved. Blood was then sampled at 10-min intervals for the last 30 min (at 150, 160, 170, and 180 min) for measurement of plasma glucose and insulin concentrations. Because SSPI concentrations were similar in all subjects, SSPG concentrations provided a measure of the ability of insulin to promote the disposal of infused glucose. Subjects with high SSPG are relatively more insulin resistant than those with lower SSPG.

Genetic analysis

The genotyping study was carried out in the Nutrition and Genomics Laboratory at the Jean Mayer USDA Human Nutrition Research Center on Aging. Genomic DNA was isolated from white blood cells and DNA extraction was performed by standard procedures. Four SNP at the a*dipoQ* gene locus were genotyped [-11391 G > A (rs17300539), -11377 C > G (rs266729), 45 T > G (rs2241766), and 276 G > T (rs1501299)] using the 5' nuclease allelic discrimination Taqman assay with ABI 7900HT system (Applied Biosystems). Standard good laboratory practices were undertaken to ensure the accuracy of genotype data. We used internal controls and repetitive experiments. Any sample that yielded a weak signal was repeated. In addition, 20% of samples were repeated at random to verify the reproducibility.

Statistical methods

The Statistical Package for the Social Sciences version 14 was used for the statistical comparisons. ANOVA was used to test the association between genotype groups and total plasma cholesterol, LDL-C, HDL-C, TG, Apo A-1, Apo B, and fasting glucose concentrations at baseline and repeated-measures ANOVA was used at the end of each dietary period. These analyses were performed for the whole sample and for men and women separately to test the homogeneity of genetic effects in men and women. When there were no differences due to gender, men and women were analyzed together. To test the interaction between diet, genotype, and gender, a 3-way repeated-measures ANOVA was used. When there were no effects of diet, we used 2-way repeated measures ANOVA to test effects of gender, genotype, and their interaction. When F-tests were significant, Tukey's post hoc test was used to identify differences between groups. The Kolmogorov-Smirnov 1-sample test was used to test the normality of the distributions. $P < 0.05$ was considered significant. All data presented in text and tables are expressed as means ± SD.

Results

Fifty-nine healthy volunteers (34 C/C, 20 C/G, and 5 G/G for -11377 C > G; 41 G/G, 17 G/A, and 1 A/A for -11391 G > A; 31 G/G, 24 G/T, and 4 T/T for 276 G > T; and 45 T/T, 12 T/G, and 2 G/G for 45 T > G) participated in the study. Genotype distributions did not deviate from Hardy-Weinberg expectations for any of the SNP. The frequency of the C allele for -11377 G > C, the A allele for -11391 G > A, the T allele for 276 G > T, and the G allele for 45 T > G was consistent with prior reports in other Caucasian populations (15). At baseline, none of the traits examined differed between genotype groups (Table 1) or genders (data not shown).

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SSPI concentrations at 150, 160, 170, and 180 min of the insulin suppression test did not differ between participants who were homozygous for the C allele (C/C) and in those carrying the minor G allele (C/G and G/G). SSPI concentrations (mmol/L) were 10.30 ± 2.40 and 7.70 ± 1.50, respectively, during the SFA diet period; 10.20 ± 1.80 and 9.50 ± 1.30, respectively, during the CHO diet period; and 11.10 ± 2.50 and 8.10 ± 1.50, respectively, during the MUFA diet period. SSPG concentrations did not differ after MUFA, CHO, or SFA diet periods due to the genotype for the -11377 C > G polymorphism (Fig. 1*A*). However, the SSPG concentrations were affected by a sex × genotype × diet interaction ($P = 0.016$). Thus, men homozygous for the C allele in the -11377 C > G polymorphism had lower SSPG concentrations when they switched from the SFA-rich diet to the MUFA- and CHO-rich diets than did the carriers of the minor allele G ($P = 0.018$, 2-way repeated measures ANOVA) (Fig. 1*B*). This effect did not occur in women (Fig. 1*C*).

We further examined the association of this SNP -11377 C > G and dietary effects on plasma adiponectin concentrations. Effects of the diets on plasma adiponectin did not differ due to genotype ($P = 0.489$). However, the sex × gene interaction affected the plasma adiponectin concentration ($P = 0.015$, 2-way repeated-measures ANOVA), so that men homozygous for the C allele in the -11377 C > G polymorphism had significantly lower concentrations of plasma adiponectin than did women carrying the same genotype (C/C). Men and women with the C/G and G/G genotypes did not differ (Fig. 2). Plasma concentrations for total cholesterol, LDL-C, HDL-C, TG, Apo A-I, and Apo B after the 3 diet periods were not affected by genotype (Table 2) or gender (not presented).

Plasma NEFA concentrations were lower when participants switched from the SFA-rich diet to the CHO- and MUFA-rich diets ($P = 0.003$). However, genotype and gender did not affect plasma NEFA. We also investigated the potential associations between -11391 G > A, 276 G > T, and 45 T > G SNP and dietary effects on SSPG and adiponectin concentrations. None of the variables examined were significantly correlated with these 3 SNP.

Discussion

The C/C men homozygous for the -11377 C > G SNP had a significant decrease in insulin resistance after the consumption of MUFA- and CHO-rich diets compared with the SFA-rich diet. These findings were not observed among female participants. We also investigated the potential associations between -11391 G > A, 276 G > T, and 45 T > G SNP and insulin sensitivity to dietary fat. However, there were no correlations between any of the variables examined and these 3 SNP.

Epidemiological evidence and intervention studies strongly support the hypothesis that the quality of dietary fat influences insulin sensitivity in humans. The majority of the epidemiological studies show that a higher intake of saturated fat is associated with the worsening of insulin sensitivity, whereas the contrary is true for unsaturated fat (19,28). In agreement with these results, our group has shown that shifting from the SFA-rich to a MUFA olive oil-rich diet also improved insulin sensitivity in healthy subjects (3). On the other hand, some studies have shown that a high-CHO diet is an adequate alternative for improving glucose metabolism in healthy subjects (29,30). However, these findings could be related to the individual genetic background.

The proximal promoter region of the *adipoQ* gene includes the 5' -untranslated region, exon 1, and intron 1. The minor allele at the -11377 C > G SNP has been previously associated with higher BMI in T2DM patients than with C/C T2DM subjects, suggesting that this SNP may contribute to the genetic risk for obesity in T2DM (31). Another study in a French population reported that this SNP was associated with low adiponectin concentrations and contributed to

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the genetic risk for T2DM, even though they did not detect an association between this SNP and insulin resistance (13). Moreover, Buzzetti et al. (32) observed that subjects carrying the -11377G variant had lower insulin sensitivity and plasma adiponectin concentrations than noncarriers. However, other studies did not find any association between this *adipoQ* gene variant and insulin sensitivity as evaluated by hyperinsulinemic-euglycemic clamp (16,33). There are multiple inconsistencies regarding the outcome of these studies, which could be due to the limited coverage of the genetic variability at this locus but also to different interactions with environmental factors, such as diet. Our data indicate that only men homozygous for the C allele of the -11377 C > G polymorphism had a greater decrease in SSPG concentrations when changing from the SFA-rich diet to MUFA- and CHO-rich diets than did those carrying the minor G allele (C/G and G/G). The presence of steroid hormone receptors in adipose tissue suggests that sex hormones may have some role in modulating adipokine expression and insulin sensitivity. Further support for this concept is the gender difference in insulin sensitivity and the variation in insulin sensitivity throughout the estrous cycle in rodents (34) and throughout the menstrual cycle in women (35). Our finding suggests a role of sex hormones in the biological expression of the effects associated with the presence of this polymorphism; for example, there may be a region in the *adipoQ* gene promoter that is regulated by hormones. At the cellular level, estrogens regulate mRNA production for particular proteins, among which are proteins involved in lipid and glucose metabolism. Thus, it is likely that in young women, the -11377 C > G polymorphism in the *adipoQ* gene promoter would not affect insulin resistance. Another hypothesis to explain our findings could be if the presence of the SNP -11377 C > G in the promoter region of the *AdipoQ* could modulate postprandial lipemia, as has previously been observed for other genotypes (36). This should be tested in future studies. On the other hand, functional analyses have not been performed in our study and it is difficult to predict whether this polymorphism would affect the expression and/or activity.

In a previous study, Vasseur et al. (16) observed that carriers of the minor allele for the -11377 C > G SNP had significantly lower serum adiponectin concentrations, supporting a relation between the promoter region and adiponectin secretion. However, few studies have explored the relation between dietary factors and adiponectin concentrations. In our study, we did not observe genotype-related differences in plasma adiponectin concentrations following the consumption of 3 diets differing in fatty acid constituents. This is consistent with another report that found no significant association between macronutrient intake and plasma adiponectin concentrations in a cross-sectional analysis of 114 students (37). Likewise, Arvidsson et al. (38) found no differences in adiponectin concentrations between obese women who consumed a hypocaloric moderate-fat, moderate-carbohydrate diet and those who consumed a low-fat, high-carbohydrate diet for 10 wk. Also consistent with these findings are data from Peake et al. (39), who reported no changes in plasma adiponectin concentrations during the 6 h after intake of a high-fat, low-carbohydrate meal. In contrast, a recent study indicates that the adherence to a Mediterranean-type dietary pattern for 10 y is associated with higher plasma adiponectin concentrations in diabetic women (40). Taken together, these data suggest that adiponectin concentrations are unlikely to be affected by acute dietary changes, but rather reflect dietary intakes over longer time periods (41). In our study, the lack of a gene × diet interaction affecting plasma adiponectin concentrations could be due to the health status of our young subjects that could have minimized the impact of the gene. Other possibilities include the small sample size. Interestingly, we observed that men homozygous for the C allele in the -11377 C > G polymorphism had a significantly lower plasma adiponectin concentration than did women carrying the same genotype (C/C), independently of the quality of dietary fat. This difference was not observed between men and women carrying the C/G and G/G genotypes. In this context, our data suggest that the presence of the SNP -11377 C > G modulates plasma adiponectin concentrations according to gender. Overall, our findings indicate that men homozygous for the C allele have a higher risk profile consisting of hypoadiponectinemia and higher insulin resistance; however, they are hyper-responders to MUFA- and CHO rich-diets

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with induction of enhanced insulin sensitivity. This study supports the idea that diet may play a major role in triggering insulin resistance by interacting with genetic variants of candidate genes for dyslipidemia and insulin resistance. However, we should be cautious when extrapolating these results to the general population or subjects at higher risk for metabolic syndrome.

In conclusion, genetic variability at the -11377 C > G polymorphism may be a factor in the interindividual differences in insulin sensitivity response after MUFA- and CHO-rich diets in healthy men. A more complete understanding of these factors and a thoughtful use of this information should help in the identification of vulnerable populations or persons who will benefit from more personalized and mechanistic-based dietary recommendations.

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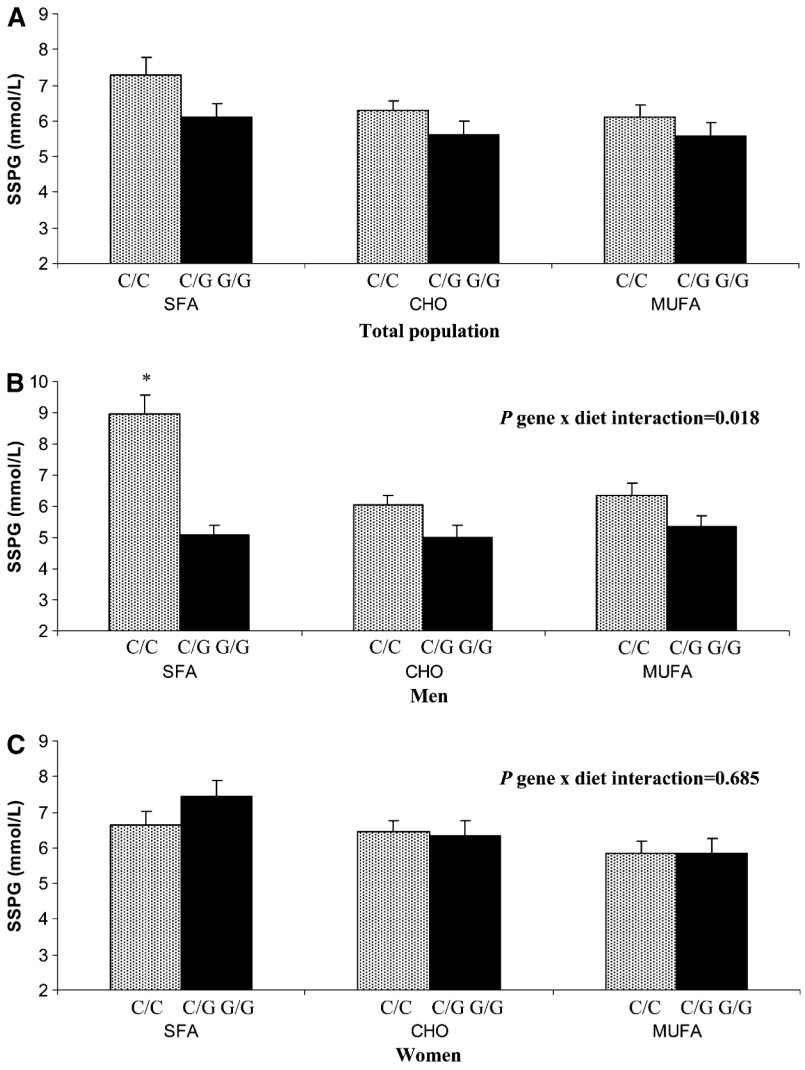

FIGURE 1.

SSPG concentrations during the insulin suppression test according to the -11377 G/C polymorphism at the *adipoQ* gene promoter after participants consumed the SFA-rich diet followed by the CHO- or MUFA-rich diet, each for 4 wk, in the total population (34 C/C and 25 C/G+G/G) (*A*), men (17 C/C and 13 C/G+G/G) (*B*), and women (17 C/C and 12 C/G+G/G) (*C*). Values are means ± SD *P* sex × gene × diet interaction = 0.016 by 3-way repeated-measures ANOVA. *Different from C/G+G/G, $P < 0.05$.

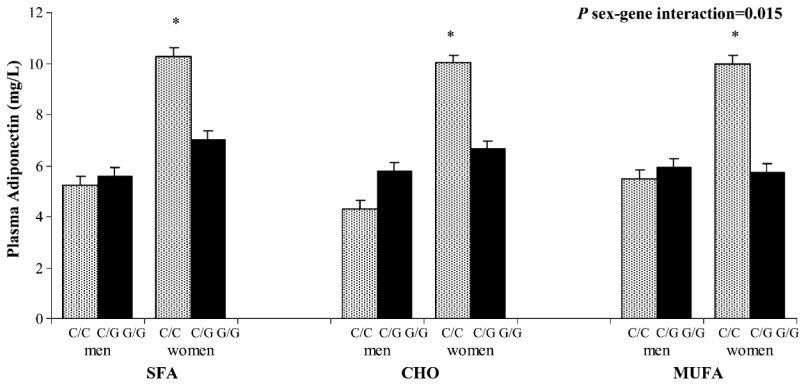

FIGURE 2.

Plasma adiponectin concentrations according to the -11377 G/C polymorphism at the *adipoQ* gene promoter after participants consumed the SFA-rich diet followed by the CHO- or MUFA-rich diet, each for 4 wk, in men (17 C/C and 13 C/G+G/G) and women (17 C/C and 12 C/G+G/G). Values are means + SD. *Different from C/C men, $P < 0.05$.

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TABLE 1

Baseline anthropometrics, plasma lipid, and fasting plasma glucose concentrations in healthy volunteers, according to -11377 C/G, -11391 G/A, 276 G/T, and 45 T/G polymorphisms at the *adipoQ* gene[1,2]

	-11377 C > G		-11391 G > A		+276 G > T		+45 T > G	
	C/C	C/G+G/G	G/G	G/A+A/A	G/G	G/T+T/T	T/T	T/G+G/G
n	34	25	41	18	31	28	45	14
Males/females, *n*	17/17	13/12	20/21	10/8	18/13	12/16	23/22	7/7
BMI, kg/m^2	21.72 ± 3.29	21.00 ± 2.86	21.00 ± 3.23	22.44 ± 2.48	21.87 ± 2.74	20.98 ± 3.43	21.29 ± 3.14	21.85 ± 2.80
Plasma total cholesterol, *mmol/L*	4.32 ± 0.61	4.01 ± 0.56	4.19 ± 0.68	4.20 ± 0.45	4.25 ± 0.60	4.12 ± 0.63	4.16 ± 0.60	4.31 ± 0.64
Plasma LDL-C, *mmol/L*	2.69 ± 0.59	2.44 ± 0.48	2.57 ± 0.62	2.63 ± 0.42	2.66 ± 0.54	2.51 ± 0.60	2.55 ± 0.56	2.71 ± 0.55
Plasma HDL-C, *mmol/L*	1.27 ± 0.30	1.25 ± 0.24	1.27 ± 0.31	1.25 ± 0.17	1.22 ± 0.31	1.29 ± 0.23	1.27 ± 0.25	1.26 ± 0.34
Plasma TG, *mmol/L*	0.78 ± 0.33	0.69 ± 0.28	0.76 ± 0.30	0.68 ± 0.32	0.78 ± 0.32	0.68 ± 0.30	0.73 ± 0.29	0.74 ± 0.36
Plasma Apo A-1, *g/L*	1.51 ± 0.17	1.44 ± 0.15	1.48 ± 0.17	1.48 ± 0.13	1.48 ± 0.16	1.46 ± 0.14	1.47 ± 0.15	1.52 ± 0.19
Plasma Apo B, *g/L*	0.75 ± 0.11	0.70 ± 0.13	0.75 ± 0.13	0.70 ± 0.13	0.74 ± 0.13	0.71 ± 0.13	0.72 ± 0.12	0.75 ± 0.15
Plasma glucose (fasting), *mmol/L*	4.85 ± 0.31	4.75 ± 0.36	4.85 ± 0.34	4.76 ± 0.35	4.84 ± 0.37	4.80 ± 0.33	4.83 ± 0.34	4.79 ± 0.37

[1] Values are means ± SD.

[2] There were no effects of genotype (ANOVA).

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TABLE 2

Plasma lipid and Apo concentrations in healthy volunteers, according to -11377 G/C polymorphism at the *adipoQ* gene, after they consumed the SFA-rich diet followed by the CHO- or MUFA-rich diet, each for 4 wk[1]

	Diet					
	SFA-rich		CHO-rich		MUFA-rich	
	C/C	C/G+G/G	C/C	C/G+G/G	C/C	C/G+G/G
n	34	25	34	25	34	25
Plasma total cholesterol, *mmol/L*	4.32 ± 0.61	4.01 ± 0.56	3.70 ± 0.54	3.52 ± 0.70	3.81 ± 0.69	3.60 ± 0.72
Plasma LDL-C, *mmol/L*	2.69 ± 0.59	2.44 ± 0.48	2.19 ± 0.52	2.06 ± 0.59	2.22 ± 0.62	2.11 ± 0.59
Plasma HDL-C, *mmol/L*	1.27 ± 0.30	1.25 ± 0.24	1.15 ± 0.28	1.11 ± 0.24	1.20 ± 0.30	1.16 ± 0.28
Plasma TG, *mmol/L*	0.78 ± 0.33	0.69 ± 0.28	0.78 ± 0.29	0.75 ± 0.27	0.82 ± 0.35	0.69 ± 0.27
Plasma Apo A-1, *g/L*	1.51 ± 0.17	1.44 ± 0.15	1.42 ± 0.14	1.35 ± 0.15	1.46 ± 0.19	1.39 ± 0.16
Plasma Apo B, *g/L*	0.75 ± 0.11	0.70 ± 0.13	0.66 ± 0.12	0.63 ± 0.14	0.67 ± 0.15	0.64 ± 0.13

[1] Values are means ± SD. None of the main effects or interactions were significant (ANOVA for repeated measures).