Analyses of single nucleotide polymorphisms in selected nutrient-sensitive genes in weight-regain prevention: the DIOGENES study\textsuperscript{1–4}

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ABSTRACT

Background: Differences in the interindividual response to dietary intervention could be modified by genetic variation in nutrient-sensitive genes.

Objective: This study examined single nucleotide polymorphisms (SNPs) in presumed nutrient-sensitive candidate genes for obesity and obesity-related diseases for main and dietary interaction effects on weight, waist circumference, and fat mass regain over 6 mo.

Design: In total, 742 participants who had lost \geq 8% of their initial body weight were randomly assigned to follow 1 of 5 different ad libitum diets with different glycemic indexes and contents of dietary protein. The SNP main and SNP-diet interaction effects were analyzed by using linear regression models, corrected for multiple testing by using Bonferroni correction and evaluated by using quantile-quantile (Q-Q) plots.

Results: After correction for multiple testing, none of the SNPs were significantly associated with weight, waist circumference, or fat mass regain. Q-Q plots showed that ALOX5AP rs4769873 showed a higher observed than predicted \( P \) value for the association with less waist circumference regain over 6 mo (\(-3.1 \text{ cm/allele; 95\% CI: } -4.6, \ -1.6; P/\text{Bonferroni-corrected } P = 0.000039/0.076\)), independently of diet. Additional associations were identified by using Q-Q plots for SNPs in ALOX5AP, TNF, and KCNJ11 for main effects; in LPL and TUB for glycemic index interaction effects on waist circumference regain; in GHR, CCK, MLXIPL, and LEPR on weight; in PPARC1A, PCK2, ALOX5AP, PYY, and ADRB3 on waist circumference; and in PPARD, FABP1, PLAUR, and LPIN1 on fat mass regain for dietary protein interaction.

Conclusion: The observed effects of SNP-diet interactions on weight, waist, and fat mass regain suggest that genetic variation in nutrient-sensitive genes can modify the response to diet

INTRODUCTION

Successful weight loss does not only include the weight-loss period and the obtained clinically significant weight loss of 5% to 10%; the weight-maintenance period after the weight loss is pivotal in preventing weight regain and repeated cycles of weight loss and weight regain. Studies have shown that only 20% of US adults are successful in preventing weight regain after a clinically significant weight loss (1, 2).

Several dietary approaches have been investigated with regard to weight loss and maintenance (3). An attractive solution to prevent weight regain is to provide a diet with a macronutrient composition that is satiating at a low caloric density, eg, a diet with a high dietary protein content that increases satiety and decreases ad libitum energy intake compared with diets high in carbohydrate or fat (3) or a diet with a low glycemic index (LGI)\textsuperscript{5} that has been shown to increase weight loss and delay weight regain, even when offered ad libitum (4).

The Diet, Obesity and Genes (DIOGENES) study showed that an ad libitum diet high in dietary protein and with an LGI is significantly better at preventing weight regain over 6 mo than are diets with a high glycemic index (HGI) and low dietary protein (LP) or

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\textsuperscript{5} Abbreviations used: DIOGENES, Diet, Obesity and Genes; GI, glycemic index; HGI, high glycemic index; HP, high dietary protein; LCD, low-calorie diet; LD, linkage disequilibrium; LGI, low glycemic index; LP, low dietary protein; Q-Q, quantile-quantile; rs, reference sequence; SNP, single nucleotide polymorphism.

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high dietary protein (HP), with an LGI and LP, or with the official country-specific diet recommendations (5). The results also showed that an HP diet, compared with an LP diet (difference of 5.4% of energy; \( P < 0.001 \)), produced a smaller weight regain (0.93 kg, 0.31–1.55; \( P = 0.003 \)) and that an LGI diet, compared with an HGI diet (5-GI unit difference; \( P < 0.001 \)), produced a smaller weight regain (0.95 kg, 0.33–1.57; \( P = 0.003 \)).

There were, however, large interindividual differences in weight regain within the diet groups, and it could be possible that these differences are dependent on genetic variation in nutrient-sensitive genes (6). The aim of this study was to examine whether single nucleotide polymorphisms (SNPs) in presumed nutrient-sensitive genes, by main effects or by interaction effects with dietary protein or GI, were associated with weight, waist circumference, or fat mass regain during a 6-mo ad libitum weight-maintenance diet.

**SUBJECTS AND METHODS**

**Study design**

The DIOGENES study is a randomized, controlled 6-mo dietary intervention that examines the effects of dietary protein and GI on weight regain and metabolic and cardiovascular risk factors in overweight and obese families, after an 8-wk weight loss period on a low-calorie diet (LCD), in 8 research centers in Europe (5, 7–9). The study included families with at least one overweight or obese \([27 \geq BMI \text{ (in } kg/m^2) \leq 45] \) parent between 18 and 65 y and at least one healthy child between 5 and 17 y. Adult participants who achieved a weight loss \( \geq 8\% \) of their initial body weight were randomly assigned to 1 of 5 different ad libitum diets: \( l \) LP/LGI, \( 2 \) LP/HGI, \( 3 \) HP/LGI, \( 4 \) HP/HGI, or \( 5 \) control diet (5). The control diet was designed to follow the current official dietary guidelines for each of the countries. The study was approved by the local ethical committees in the respective countries, confirming that the study protocol was in accordance with the Declaration of Helsinki.

For the current analyses, a \( 2 \times 2 \) factorial design was used to compare the LP with the HP group or the LGI with the HGI group for adults who lost \( \geq 8\% \) of their initial body weight, who were randomly assigned to the dietary intervention, and who were successfully genotyped.

**Selection of candidate genes and tagSNPs**

The candidate genes were selected on the basis of prior knowledge of whether the pathway, gene, gene transcript, or SNP was implicated in obesity, weight loss, weight regain, or associated diseases with emphasis on interaction with dietary protein or GI, from the literature, or the IntegraGen database. For the presumed nutrient-sensitive candidate genes, a comprehensive approach was used to ensure genetic coverage of the locus \((\pm 5 \text{ kilobases})\) by selecting tagSNPs for each of the selected genes. The tagSNPs were identified from the International HapMap data for European ancestry (release 20, NCBI build 35), and the LD (linkage disequilibrium) structure was evaluated by using Haploview software, version 3.32 (10). TagSNPs were selected by using Tagger (11) with single-marker option with an LD threshold of \( r^2 = 0.8 \), except for the genes \( APP, TUB, KCNJ11+ABCC8, \) and \( PPARGC1A \) for which tagSNPs were selected with an LD threshold of \( r^2 = 0.7 \). SNPs located in exonic regions, frequently studied, or included in the Illumina HumanHap 300 were preferentially included as tagSNPs, whereas SNPs with an expected low genotyping success rate \([\text{in close proximity to another SNP (60 base pairs) or in a repeat region}]\) were deselected. In total, 768 tagSNPs were selected for genotyping. The candidate gene and tagSNP selection are described in more detail elsewhere (12).

**DNA extraction and genotyping**

For genetic analyses, DNA was extracted from EDTA-blood buffy coats stored at −80°C by K Bioscience. Genotyping of all samples was performed by using the Illumina Bead Station System (Illumina Inc) by IntegraGen. Two Centre d’Etude du Polymorphisme Humain control samples were added on each plate: one was different on each plate and one was identical among the 15 genotyped plates. The reproducibility was 100% and the concordance rate was 99.6%. In total, 651 SNPs (in 69 genes) had a call rate \( \geq 95\% \) and a minor allele frequency \( > 1\% \), and they did not deviate significantly \( (P > 0.001) \) from Hardy-Weinberg equilibrium. All genotype analyses were performed and reported with respect to the minor allele \((<50\%)\), because the functional effects of all the selected SNPs are not known. A complete list of candidate genes and tagSNPs is given elsewhere (see Supplementary Table 1 under “Supplemental data” in the online issue).

**Statistical analyses**

The SNP-diet analyses were performed for interaction with either dietary protein, LP compared with HP, or GI, LGI compared with HGI, with respect to weight, waist circumference, and fat mass regain (outcomes) during the 6-mo (182 d) ad libitum diet. The initial diet variable with 5 levels (5 different diets) was recoded into 3 indicator variables, accounting for HP/LP, HGI/LGI, and control diets. The LP and LGI groups were used as reference for the SNP-dietary protein and SNP-GI interaction analyses, respectively. The control diet analyses were omitted because the dietary advice varied between countries. Only the adults from the DIOGENES study were included in the analyses, and family structure, accounting for shared current environment, was defined as single-parent \((10\% \text{ of the individuals})\), 2-parent with one parent participating \((55\%)\), or 2-parent with 2 parents participating \((35\%)\). The statistical analyses were based on linear regressions founded in the following model formulation:

\[
O = I + t + t^2 + SNP \times DIET + SNP + DIET + SEX + FS + P + \text{Age} + BMI + LCDloss + e
\]

where \( O \) is outcome, \( I \) is intercept, \( t \) is time, \( t^2 \) is time squared; \( SNP \times DIET \) is the SNP-diet interaction effect, \( SNP \) is the SNP main effects, \( DIET \) is the diet main effect, \( SEX \) is the individual’s sex, \( FS \) is family structure, \( P \) is partner (clinical center), \( \text{Age} \) is baseline age, \( BMI \) is baseline BMI, \( LCD \) is weight loss during LCD, and \( e \) is the error term (assumed to be normally distributed). For the weight analyses, multiple available measurements during the maintenance diet were used \([\text{at a maximum of 9 time points (number of observations)}] \text{ per individual, and longitudinal models were fitted allowing within individual-correlations.} \text{ The fitting procedure was quasi-least squares, which is based on the generalized} \]
estimating equations approach, as implemented in Stata through the `xtqls`-function. Covariance matrices were fitted based on the Markovian structure, and robust SEs were estimated, which also led to that all nontime based covariates were updated to be linearly dependent on time to facilitate sensible interpretations. The longitudinal adjustment for weight response also partially accounts, as a side effect of the increased underlying data set, for possible bias caused by different dropout rates. For the fat mass and waist circumference outcomes, standard linear regression analyses were performed with additional adjustment for respective baseline measure. Significance testing was performed and derived with respect to the SNP main effects, and SNP-diet interaction effect variables and corresponding quantile-quantile (Q-Q) plots were created. Corrections for multiple testing were performed by using Bonferroni correction for a total of 1953 tests (651 SNPs for SNP-main, SNP-GI, and SNP-dietary protein) per outcome and the Benjamini-Hochberg false discovery rate. Q-Q plots were used to graphically evaluate the results of the SNP main and interaction effects. If the Q-Q plots showed lower P values than expected from the null distribution, it was interpreted as possible true associations. All analyses were performed using Stata 9.2 (StataCorp LP).

RESULTS

The characteristics of the participants are summarized in Table 1. The list of selected nutrient-sensitive candidate genes and tagSNPs are given elsewhere (see Supplementary Table 1 under “Supplemental data” in the online issue). All results of the main effects of SNPs, interaction effects between SNPs and dietary protein, and interaction effects between SNPs and GI on weight, waist circumference, and fat mass regain, respectively, are given elsewhere (see Supplementary Tables 2–10 under “Supplemental data” in the online issue).

After correction for multiple testing, none of the SNPs were significantly associated with weight, waist circumference, or fat mass regain either by main effects or interaction effects. The Q-Q plots indicated that effects observed for SNP-dietary protein interactions on weight regain, SNP main effects and SNP-dietary protein and SNP-GI interaction effects on waist circumference regain, and SNP-dietary protein interaction effects on fat mass regain could be true associations (see Supplementary Figures 1–3 under “Supplemental data” in the online issue) despite being nonsignificant after correction for multiple testing by using either Bonferroni or Benjamini-Hochberg false discovery rate (see Supplementary Tables 2–10 under “Supplemental data” in the online issue). These SNPs included SNPs in LPL, ALOX5AP, LARSEN ET AL 1256

### Table 1

| Participant characteristics at baseline, after the 8-wk LCD weight-loss period, and after the 6-mo weight-maintenance period

<table>
<thead>
<tr>
<th></th>
<th>Low dietary protein</th>
<th>High dietary protein</th>
<th>Control diet</th>
</tr>
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<tbody>
<tr>
<td></td>
<td>n</td>
<td>n</td>
<td>n</td>
</tr>
<tr>
<td><strong>Baseline</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age (y)</td>
<td>146</td>
<td>146</td>
<td>145</td>
</tr>
<tr>
<td>Sex (% F)</td>
<td>146</td>
<td>150</td>
<td>146</td>
</tr>
<tr>
<td>Weight (kg)</td>
<td>146</td>
<td>150</td>
<td>155</td>
</tr>
<tr>
<td>WC (cm)</td>
<td>146</td>
<td>150</td>
<td>155</td>
</tr>
<tr>
<td>Fat mass (kg)</td>
<td>146</td>
<td>150</td>
<td>155</td>
</tr>
<tr>
<td>After 8-wk LCD</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Δ1Weight (kg)</td>
<td>146</td>
<td>150</td>
<td>155</td>
</tr>
<tr>
<td>Δ1WC (cm)</td>
<td>142</td>
<td>145</td>
<td>150</td>
</tr>
<tr>
<td>Δ1Fat mass (kg)</td>
<td>116</td>
<td>110</td>
<td>111</td>
</tr>
<tr>
<td>After 6-mo ad libitum diet</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Δ2Weight (kg)</td>
<td>106</td>
<td>97</td>
<td>124</td>
</tr>
<tr>
<td>Δ2WC (cm)</td>
<td>101</td>
<td>91</td>
<td>115</td>
</tr>
<tr>
<td>Δ2Fat mass (kg)</td>
<td>86</td>
<td>75</td>
<td>102</td>
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</table>

1 All values are means ± SDs. Age, sex, weight, WC, and fat mass were measured at baseline; Δ1, weight, WC, or fat mass loss from baseline to week 8 of a low-caloric diet (for the participants who were randomly assigned to the ad libitum 6-mo period); Δ2, weight, WC, or fat mass regain from randomization to 6 mo (182 d) of the diet. GI, glycemic index; LCD, low-calorie diet; WC, waist circumference.

Downloaded from https://academic.oup.com/ajcn/article-abstract/95/5/1254/4576920 by guest on 19 February 2019
rs9658119

PPARD

lele loading of the combination of
issue). The pairwise LD between the
plementary Figure 3 under “Supplemental data” in the online
noncarriers.

mass regain of 5.0 kg/6 mo (95% CI: 1.1, 8.8), compared with
LPIN1

interaction with dietary protein comprised SNPs in
increased weight regain of 4.1 kg/6 mo (95% CI: 1.7, 6.7),
in 8% of the participants and resulted in a mean estimated

of dietary protein and GI, we examined SNP main effects and
GENES study, investigating the weight-maintenance properties
of dietary protein and GI, we examined SNP main effects and
SNP-diet interaction effects on weight, waist circumference, or
regain, none of the SNP-diet interaction effects remained sig-
igious of the observed
isons of the observed
significant separation of the LP compared with the HP and GI
groups, and careful monitoring of dietary intake and weight
regain, none of the SNP-diet interaction effects remained sig-
nificant after correction for multiple testing. However, compar-
sions of the observed P values with the null distribution by Q-Q
plots indicated that some of the observed associations were
likely to be true associations.

The rs4769873 in the adipokine ALOX5AP, which has been
linked to atherosclerosis and cardiovascular diseases, showed an
association with waist circumference regain that was possibly
true association based on the Q-Q plots but was still not sig-
nificant after correction for multiple testing. The rs4769873 was
in moderate LD with the rs9578196 and rs9315051, and the SNPs
might therefore represent an ALOX5AP haplotype that interacts
with dietary protein to modify abdominal obesity. ALOX5AP
transfers arachidonic acid to 5-lipogenase in the first step of the
leukotriene biosynthesis in which one of the end products is the
proinflammatory leukotriene B4 (13), a ligand for the PPARA

in 8% of the participants and resulted in a mean estimated
increased weight regain of 4.1 kg/6 mo (95% CI: 1.7, 6.7),
compared with noncarriers.

The SNPs that showed an effect on fat mass regain in in-
teraction with dietary protein comprised SNPs in PPARD, FABP1,
LPIN1, and PLAUR (Figure 2), based on Q-Q plots (see Sup-
plementary Figure 3 under “Supplemental data” in the online
issue). The pairwise LD between the PPARD SNPs is 0.28. Al-
lele loading of the combination of PPARD rs6457816 AG/GG,
PPARD rs9658119 AC/CC, and FABP1 rs2970902 CC was
observed for 5% of the participants and led to an increased fat
mass regain of 5.0 kg/6 mo (95% CI: 1.1, 8.8), compared with
noncarriers.

DISCUSSION

In this large-scale multicenter intervention study, the DIO-
GENES study, investigating the weight-maintenance properties
of dietary protein and GI, we examined SNP main effects and
SNP-diet interaction effects on weight, waist circumference, or
fat mass regain for 651 tagSNPs, covering the genetic variation of
69 presumably nutrient-sensitive candidate genes.

Despite the selection of presumed nutrient-sensitive genes
with complete coverage of genetic variation in the 69 loci,
significant separation of the LP compared with the HP and GI
groups, and careful monitoring of dietary intake and weight
regain, none of the SNP-diet interaction effects remained sig-
nificant after correction for multiple testing. However, compar-
sions of the observed P values with the null distribution by Q-Q
plots indicated that some of the observed associations were
likely to be true associations.

The rs4769873 in the adipokine ALOX5AP, which has been
linked to atherosclerosis and cardiovascular diseases, showed an

<table>
<thead>
<tr>
<th>Gene</th>
<th>SNP</th>
<th>No. of participants</th>
<th>MAF</th>
<th>β (95% CI)</th>
<th>P</th>
<th>P_B</th>
</tr>
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<tbody>
<tr>
<td>ALOX5AP</td>
<td>rs4769873</td>
<td>492</td>
<td>0.07</td>
<td>-3.08 (-4.54, -1.61)</td>
<td>0.00039</td>
<td>0.08</td>
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<td>TNF</td>
<td>rs1041981</td>
<td>480</td>
<td>0.29</td>
<td>-1.33 (-2.10, -0.56)</td>
<td>0.00069</td>
<td>1</td>
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<tr>
<td>ALOX5AP</td>
<td>rs9578196</td>
<td>492</td>
<td>0.09</td>
<td>-2.12 (-3.40, -0.83)</td>
<td>0.0013</td>
<td>1</td>
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<tr>
<td>ALOX5AP</td>
<td>rs9315051</td>
<td>492</td>
<td>0.08</td>
<td>-2.17 (-3.53, -0.80)</td>
<td>0.0019</td>
<td>1</td>
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<tr>
<td>KCNJ11 + ABCC8</td>
<td>rs2074308</td>
<td>492</td>
<td>0.13</td>
<td>1.53 (0.52, 2.54)</td>
<td>0.0030</td>
<td>1</td>
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<tr>
<td>SNP-GI</td>
<td>LPL</td>
<td>rs264</td>
<td>490</td>
<td>0.16</td>
<td>-4.11 (-6.29, -1.93)</td>
<td>0.00022</td>
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<td>TUB</td>
<td>rs1881238</td>
<td>485</td>
<td>0.15</td>
<td>-3.22 (-5.40, -1.03)</td>
<td>0.0039</td>
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<tr>
<td>SNP-dietary protein</td>
<td>PPARGC1A</td>
<td>rs2970848</td>
<td>492</td>
<td>0.33</td>
<td>-3.24 (-4.89, -1.58)</td>
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<td>rs2970853</td>
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<td>rs2932976</td>
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<td>PYY</td>
<td>rs1058046</td>
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<td>0.35</td>
<td>2.53 (0.83, 4.23)</td>
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<tr>
<td></td>
<td>ADRB3</td>
<td>rs4998</td>
<td>491</td>
<td>0.06</td>
<td>-4.76 (-7.97, -1.56)</td>
<td>0.0036</td>
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1. The SNP main, SNP-dietary protein, and SNP-GI effects on waist circumference regain were estimated by linear
regression for the minor allele. P values were derived from linear regression, and P_B values were adjusted by using
Bonferroni correction for 3 × 651 tests. The gene denotes the locus with the closest proximity to the SNP. GI, glycemic
index; MAF, minor allele frequency; P_B, Bonferroni-corrected P; SNP, single nucleotide polymorphism.
to cover the genetic variance of the selected genes plus 500 base pairs up- and downstream from the coding region with an LD threshold of 0.7 to 0.8.

The DIOGENES study has a controlled exposure to the dietary components investigated with evaluation of food intake by repeated 3-d weighted food registration and nitrogen excretion (5).
as recommended for studies on gene-environment interactions (18). For dietary intervention studies of weight regain, significant differentiation between interventions can be difficult to obtain (19); however, the DIOGENES study did obtain a significant difference between the LP and HP and LGI and HGI diets. Also, the study includes several measurements of body weight during the 6-mo ad libitum diet period; thus, we can use longitudinal data that allows us to account for possible bias caused by different dropout rates for the diet and, therefore, the analyses of body weight regain can be regarded as the most robust data of the SNP main and SNP-diet interaction data presented.

Previous studies have investigated SNPs in single genes or a few selected genes in relation to weight loss and regain (19–22). In most of these studies, only the main effects of the SNPs are investigated (20) and not the gene-diet interaction effects. A recent article from the epidemiologic part of the DIOGENES study examined the SNP-diet interaction of 123 SNPs in 15 genes in the hypothalamic pathway in 6566 individuals in a case-cohort design and identified one association \( (P = 2 \times 10^{-7}) \) with weight regain for the interaction between neuromedin B rs7180849 and GI (12). However, we could not replicate this finding in the DIOGENES intervention study \( (P = 0.60) \).

**FIGURE 2.** Effect of interaction between single nucleotide polymorphisms and dietary protein on fat mass regain over 6 mo of an ad libitum weight-loss maintenance diet with either a high or low percentage of dietary protein on PPARD rs6457816 \( (P_B = 0.0004/0.94) \) and rs9658119 \( (P_B = 0.0013) \), FABP1 rs2970902 \( (P_B = 0.0041/1) \), LPIN1 rs1050800 \( (P_B = 0.00431) \), and PLAUR rs2239374 \( (P_B = 0.0046/1) \) according to genotype. \( P \) values were derived from linear regression, and \( P_B \) values were adjusted by using Bonferroni correction for 3 × 651 tests. HP, high dietary protein; LP, low dietary protein; \( P_B \), Bonferroni-corrected \( P \).
In conclusion, the analyses of tagSNPs in the selected 69 candidate genes suggests that genetic variation in nutrient-sensitive genes can affect weight, waist circumference, or fat mass regain by interacting with dietary protein or GI. However, further studies are needed to verify the observed gene-diet interaction effects on regain outcomes and to identify new nutrient-sensitive genes.

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