

Analyses of single nucleotide polymorphisms in selected nutrient-sensitive genes in weight-regain prevention: the DIOGENES study^{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 cm/allele; 95% CI: -4.6 , -1.6 ; *P*/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 *GHRL*, *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. This trial was registered at clinicaltrials.gov as NCT00390637. *Am J Clin Nutr* 2012;95:1254–60.

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)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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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 difference 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 over weight 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 [$27 \geq \text{BMI (in kg/m}^2) \leq 45$] 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: 1) 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 2×2 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 (± 5 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 *PPARG-CIA* 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 [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 KBioscience. 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% 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:

$$O = I + t + t^2 + \text{SNP} \times \text{DIET} + \text{SNP} + \text{DIET} + \text{SEX} + \text{FS} + \text{P} + \text{Age} + \text{BMI} + \text{LCDloss} + e \quad (1)$$

where O is outcome, I is intercept, t is time, t^2 is time squared; $\text{SNP} \times \text{DIET}$ 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), age is baseline age, BMI is baseline BMI, LCD loss 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 [at a maximum of 9 time points (number of observations)] per individual, and longitudinal models were fitted allowing within individual-correlations. 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 by 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 *ALOX5AP* rs4769873, rs9578196, and rs9315051; *TNF* rs1041981; and *KCNJ11+ABCC8* rs2074308, which showed main effects on waist circumference regain (**Table 2**). The pairwise LDs between the *ALOX5AP* SNPs are 0.73 for rs4769873+rs9578196, 0.69 for rs4769873+rs9315051, and 0.49 for rs9578196+rs9315051.

The SNPs that showed effects of interaction with GI or protein on waist circumference regain were in *LPL* and *TUB* and *PPARGC1A*, *PCK2*, *ALOX5AP*, *ADRB3*, and *PYY* (Table 2). The pairwise LDs between the *PPARGC1A* SNPs are 0.48 for rs2970848+rs2932976, 0.16 for rs2970848+rs2970853, and 0.07 rs2932976+rs2970853. The pairwise LD between the *ALOX5AP* SNPs is 0.54 for rs4076128+rs10507391. In terms of an increased risk of waist circumference regain, allele loading of the combination of *PPARGC1A* rs2970848 AA, *PPARGC1A* rs2970853 GA/AA, *PCK2* rs11629199 GG, and *ALOX5AP* rs10507391 CC was observed in 9% of the participants, and this combination of alleles led to an increased waist circumference regain of 6.3 cm/6 mo (95% CI: 2.4, 10.2), compared with noncarriers.

The SNPs that showed an effect on weight regain in interaction with dietary protein were SNPs located in or close to *GHRL*, *CCK*, *MLXIPL*, and *LEPR* (**Figure 1**), based on Q-Q plots (see Supplementary Figure 1 under “Supplemental data” in the online issue). The pairwise LD between the *LEPR* SNPs is 0.03. Allele loading of the combination of *GHRL* rs17032621 AG/GG and *CCK* rs3790426 CA/AA and *LEPR* rs1129949 AA was seen

TABLE 1
Participant characteristics at baseline, after the 8-wk LCD weight-loss period, and after the 6-mo weight-maintenance period¹

	Low dietary protein				High dietary protein				Control diet	
	<i>n</i>	Low-GI diet	<i>n</i>	High-GI diet	<i>n</i>	Low-GI diet	<i>n</i>	High-GI diet	<i>n</i>	Value
Baseline										
Age (y)	146	41 ± 6	150	41 ± 6	155	42 ± 7	146	41 ± 6	145	42 ± 7
Sex (% F)	146	65	150	67	155	66	146	60	145	65
Weight (kg)	146	89.4 ± 15.8	150	88.4 ± 14.8	155	88.9 ± 15.6	146	89.5 ± 17.0	145	89.1 ± 15.7
WC (cm)	146	98 ± 12	150	98 ± 12	155	97 ± 12	146	97 ± 13	145	98 ± 13
Fat mass (kg)	146	32.4 ± 9.9	150	32.5 ± 10.4	155	32.5 ± 11.2	146	32.2 ± 10.4	145	32.3 ± 9.8
After 8-wk LCD										
Δ ₁ Weight (kg)	146	−11.2 ± 3.4	150	−11.0 ± 3.7	155	−11.0 ± 3.5	146	−11.0 ± 3.0	145	−11.1 ± 3.8
Δ ₁ WC (cm)	142	−10.1 ± 4.5	145	−9.7 ± 4.7	150	−9.7 ± 4.4	144	−10.3 ± 4.6	141	−9.7 ± 5.0
Δ ₁ Fat mass (kg)	116	−8.4 ± 5.2	110	−7.6 ± 3.0	111	−8.0 ± 5.2	104	−8.6 ± 5.3	107	−8.4 ± 4.2
After 6-mo ad libitum diet										
Δ ₂ Weight (kg)	106	0.3 ± 4.9	97	1.7 ± 5.2	124	−0.4 ± 6.5	107	0.6 ± 5.5	114	0.8 ± 4.8
Δ ₂ WC (cm)	101	0.5 ± 7.1	91	0.9 ± 7.0	115	−0.3 ± 6.4	101	1.1 ± 6.5	105	0.7 ± 5.6
Δ ₂ Fat mass (kg)	86	−1.0 ± 4.6	75	−0.1 ± 4.6	102	−1.0 ± 5.3	87	−0.2 ± 5.9	93	−0.8 ± 4.4

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-caloric diet; WC, waist circumference.

TABLE 2Regression coefficients (and 95% CIs) for SNP main and interaction effects on waist circumference regain during a 6-mo ad libitum diet¹

Gene	SNP	No. of participants	MAF	β (95% CI)	<i>P</i>	<i>P_B</i>
<i>cm/unit per 6 mo</i>						
SNP main effects						
<i>ALOX5AP</i>	rs4769873	492	0.07	-3.08 (-4.54, -1.61)	0.000039	0.08
<i>TNF</i>	rs1041981	480	0.29	-1.33 (-2.10, -0.56)	0.00069	1
<i>ALOX5AP</i>	rs9578196	492	0.09	-2.12 (-3.40, -0.83)	0.0013	1
<i>ALOX5AP</i>	rs9315051	492	0.08	-2.17 (-3.53, -0.80)	0.0019	1
<i>KCNJ11 + ABCC8</i>	rs2074308	492	0.13	1.53 (0.52, 2.54)	0.0030	1
SNP-GI						
<i>LPL</i>	rs264	490	0.16	-4.11 (-6.29, -1.93)	0.00022	0.43
<i>TUB</i>	rs1881238	485	0.15	-3.22 (-5.40, -1.03)	0.0039	1
SNP-dietary protein						
<i>PPARGC1A</i>	rs2970848	492	0.33	-3.24 (-4.89, -1.58)	0.00013	0.25
<i>PPARGC1A</i>	rs2970853	492	0.23	2.96 (1.15, 4.78)	0.0014	1
<i>PPARGC1A</i>	rs2932976	492	0.26	-2.78 (-4.55, -1.00)	0.0022	1
<i>PCK2</i>	rs11629199	492	0.10	-4.03 (-6.65, -1.40)	0.0026	1
<i>ALOX5AP</i>	rs10507391	492	0.31	-2.58 (-4.26, -0.90)	0.0026	1
<i>ALOX5AP</i>	rs4076128	492	0.26	-2.73 (-4.54, -0.91)	0.0032	1
<i>PYY</i>	rs1058046	492	0.35	2.53 (0.83, 4.23)	0.0035	1
<i>ADRB3</i>	rs4998	491	0.06	-4.76 (-7.97, -1.56)	0.0036	1

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.

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 interaction with dietary protein comprised SNPs in *PPARD*, *FABP1*, *LPIN1*, and *PLAUR* (Figure 2), based on Q-Q plots (see Supplementary Figure 3 under “Supplemental data” in the online issue). The pairwise LD between the *PPARD* SNPs is 0.28. Allele 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 significant after correction for multiple testing. However, comparisons 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 a true association based on the Q-Q plots but was still not significant 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-lipoxygenase 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 (14) and inducer of the proinflammatory chemokine (C-C motif) ligand 2 (15). Previously, *ALOX5AP* expression has been shown to be associated with obesity and insulin resistance; however, no associations between *ALOX5AP* haplotypes and obesity were identified (16).

The selection of nutrient-sensitive genes was done by careful evaluation of evidence of nutrient sensitivity and relation to obesity or obesity-related diseases and as such is based on a hypothesis-driven candidate gene approach. Through this selection of genes, we introduced some limitations to our analyses, because it excluded the possibility of discovering new genes involved in regulating weight, waist circumference, or fat mass. Furthermore, by not including SNPs recently identified in genome-wide association studies, we also excluded the examination of the effects of these SNPs on weight regain. In that respect, it could be argued that a genome-wide association study approach should have been used to initially identify nutrient-sensitive SNPs that might not have been discovered previously. However, such a study would require a large population because of an expected small effect size (17), and the design of a gene-diet interaction study would be a compromise between a large population, precision in the measured phenotypes, and the control of other environmental factors (18). Instead, the selected nutrient-sensitive genes tagSNPs were chosen

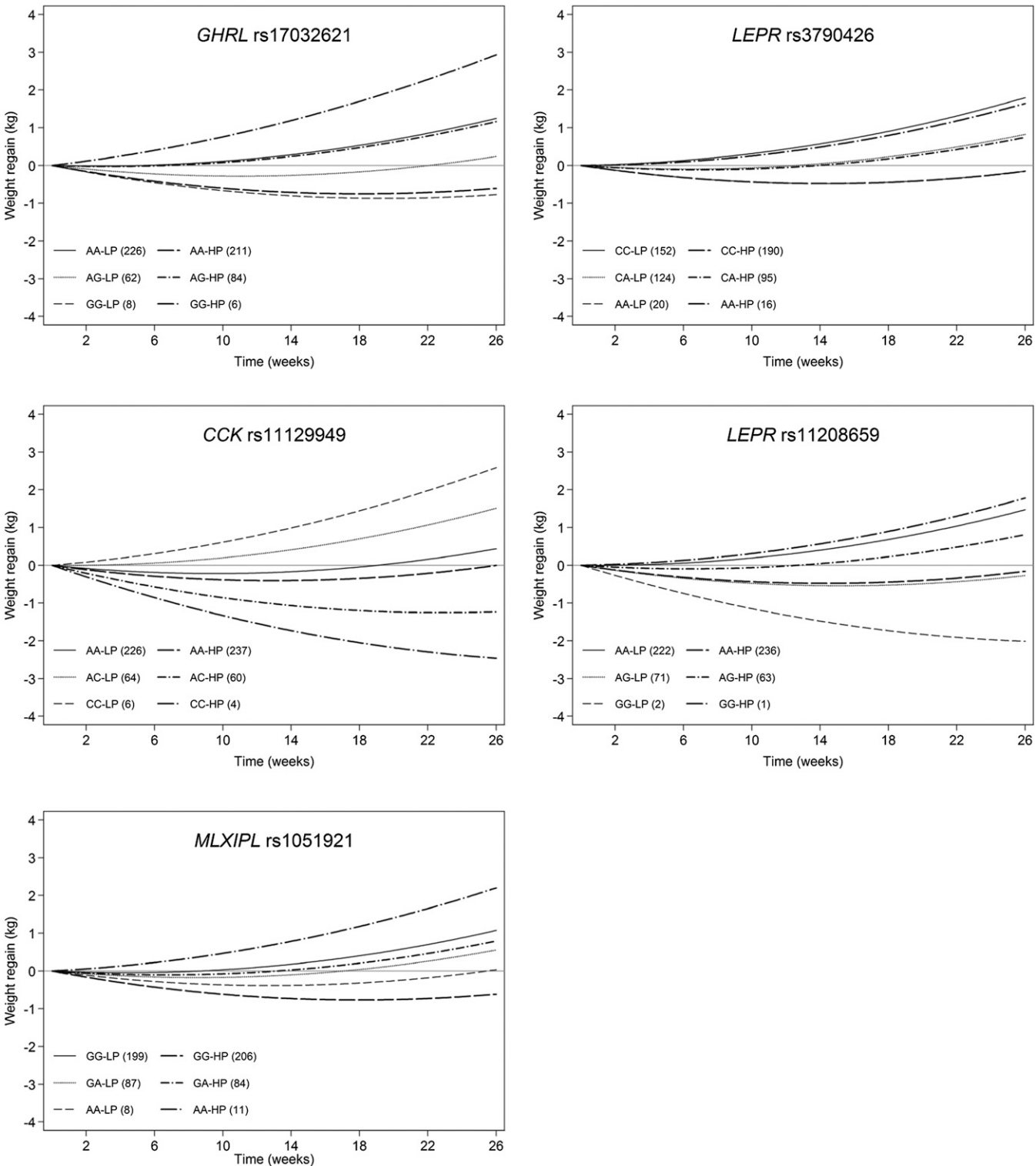


FIGURE 1. Effect of interaction between single nucleotide polymorphisms and dietary protein on weight regain during 6 mo of an ad libitum weight-loss maintenance diet with either a high or low percentage of dietary protein on *GHRL* rs17032621 ($P/P_B = 0.00034/0.66$), *LEPR* rs3790426 ($P/P_B = 0.0024/1$), and rs11208659 ($P/P_B = 0.0044/1$) and on *CCK* rs11129949 ($P/P_B = 0.0042/1$) and *MLXIPL* rs1051921 ($P/P_B = 0.0047/1$) 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 .

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)

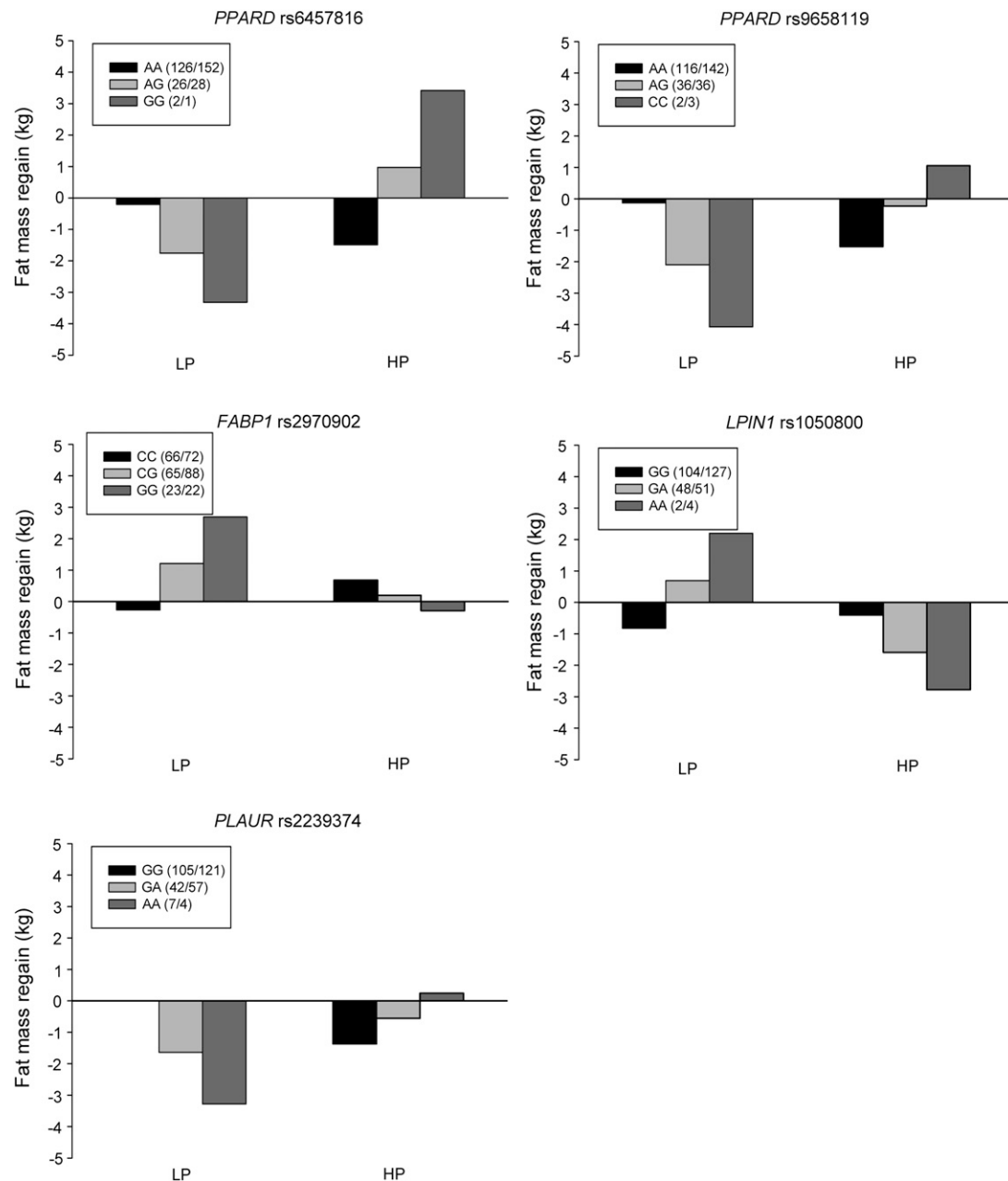


FIGURE 2. Effect of interaction between single nucleotide polymorphisms and dietary protein on fat mass regain over 6 mo of an ad libitum weight-loss maintenance diet with either a high or low percentage of dietary protein on *PPARD* rs6457816 ($P/P_B = 0.00048/0.94$) and rs9658119 ($P/P_B = 0.0013/1$), *FABP1* rs2970902 ($P/P_B = 0.0041/1$), *LPIN1* rs1050800 ($P/P_B = 0.0043/1$), and *PLAUR* rs2239374 ($P/P_B = 0.0046/1$) 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 .

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 ($P = 0.60$).

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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