

# FTO genotype and weight loss in diet and lifestyle interventions: a systematic review and meta-analysis<sup>1,2</sup>

Lingwei Xiang,<sup>3</sup> Hongyu Wu,<sup>4</sup> An Pan,<sup>5</sup> Bhakti Patel,<sup>3</sup> Guangda Xiang,<sup>6</sup> Lu Qi,<sup>4,7</sup> Robert C Kaplan,<sup>3</sup> Frank Hu,<sup>4,7</sup> Judith Wylie-Rosett,<sup>3</sup> and Qibin Qi<sup>3\*</sup>

<sup>3</sup>Department of Epidemiology and Population Health, Albert Einstein College of Medicine, Bronx, NY; <sup>4</sup>Department of Nutrition, Harvard T.H. Chan School of Public Health, Boston, MA; <sup>5</sup>School of Public Health, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China; <sup>6</sup>Department of Endocrinology, Wuhan General Hospital of Guangzhou Command, Wuhan, China; and <sup>7</sup>Channing Division of Network Medicine, Department of Medicine, Brigham and Women's Hospital and Harvard Medical School, Boston, MA

## ABSTRACT

**Background:** Studies have suggested that the fat mass and obesity-associated (*FTO*) genotype is associated with individual variability in weight loss in response to diet/lifestyle interventions, but results are inconsistent.

**Objective:** We aimed to provide a summary of the literature evaluating the relation between the *FTO* genotype and weight loss in response to diet/lifestyle interventions.

**Design:** A search of English-language articles in the PubMed and Embase databases (through 30 April 2015) was performed. Eligible studies were diet/lifestyle weight-loss intervention studies conducted in adults that reported changes in body weight or body mass index (BMI) by the *FTO* variant rs9939609 (or its proxy). Differences in weight loss between *FTO* genotypes across studies were pooled with the use of fixed-effect models.

**Results:** A meta-analysis of 10 studies (comprising 6951 participants) that reported the results of additive genetic models showed that individuals with the *FTO* TA genotype and AA genotype (those with the obesity-predisposing A allele) had 0.18-kg (95% CI: -0.09-, 0.45-kg;  $P = 0.19$ ; NS) and 0.44-kg (95% CI: 0.09-, 0.79-kg;  $P = 0.015$ ) greater weight loss, respectively, than those with the TT genotype. A meta-analysis of 14 studies (comprising 7700 participants) that reported the results of dominant genetic models indicated a 0.20-kg (-0.43-, 0.04-kg) greater weight loss in the TA/AA genotype than in the TT genotype ( $P = 0.10$ ). In addition, differences in weight loss between the AA genotype and TT genotype were significant in studies with a diet intervention only, adjustment for baseline BMI or body weight, and several other subgroups. However, the relatively small number of studies limited these stratified analyses, and there was no statistically significant difference between subgroups.

**Conclusions:** This meta-analysis suggests that individuals carrying the homozygous *FTO* obesity-predisposing allele may lose more weight through diet/lifestyle interventions than noncarriers. Our data provide evidence for genetic variability in response to diet/lifestyle interventions on weight loss, although clinical applications of these findings need further investigations. *Am J Clin Nutr* 2016;103:1162–70.

**Keywords:** *FTO* genotype, lifestyle intervention, weight loss, meta-analysis, diet

## INTRODUCTION

Obesity and its comorbidity have become major public health problems throughout the world (1). It is well established that diet/lifestyle interventions can achieve weight loss (2). However, individual variability in response to interventions has long been noted in weight-loss trials (3, 4). Besides behavioral and psychological characteristics, genetic factors may explain why diet/lifestyle interventions are more effective for some individuals than for others (2, 5). Thus, a better understanding of the modification effects of genetic variation on weight loss in response to diet/lifestyle interventions may help to develop more effective strategies for weight loss, such as individualized interventions based on one's genetic background (5, 6).

With the advent of genome-wide association studies, many genetic loci have been identified as associated with obesity and related traits (7). Given its strong effect on obesity and possible biological function in regulating energy balance (8), there is great interest in the fat mass and obesity-associated (*FTO*) gene. Recent large-scale analyses found that the obesity-risk allele (A allele) of the *FTO* variant is associated with increased food intake (9, 10), and previous studies also reported that the *FTO* obesity-risk allele was associated with a reduced response in hunger and satiety after the meal in adults and children (11, 12). A number of studies have examined whether diet/lifestyle-induced weight loss differs between the *FTO* genotype groups (13–21). However, results from these previous studies remain contradictory, and discrepancies might be due to small sample size, moderate genetic effect, types of interventions, variation in study duration, and other characteristics. Therefore, to increase statistical power and achieve a more precise estimation

<sup>1</sup> QQ received a Scientist Development Award (K01HL129892) from the NIH National Heart, Lung, and Blood Institute.

<sup>2</sup> Supplemental Figures 1–3 and Supplemental Table 1 are available from the “Online Supporting Material” link in the online posting of the article and from the same link in the online table of contents at <http://ajcn.nutrition.org>.

\*To whom correspondence should be addressed. E-mail: [qibin.qi@einstein.yu.edu](mailto:qibin.qi@einstein.yu.edu).

Received September 11, 2015. Accepted for publication January 20, 2016.

First published online February 17, 2016; doi: 10.3945/ajcn.115.123448.

of effects, we conducted a systematic review and meta-analysis of randomized weight-loss trials in adults to provide a summary of the literature evaluating the relation between *FTO* genotype and weight loss in response to diet/lifestyle interventions.

## METHODS

### Literature search

This meta-analysis was conducted in accordance with the PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-analysis) and MOOSE (Meta-analysis of Observational Studies in Epidemiology) guidelines (22, 23). We searched the PubMed (<http://www.ncbi.nlm.nih.gov/pubmed/>) and Embase (<http://www.embase.com>) databases through 30 April 2015 for diet/lifestyle intervention studies examining the relation between *FTO* genotype and weight loss in adults.

Two search themes are specified. The first theme identified relevant terms for *FTO*, and combined exploded versions of the MeSH terms “fat mass and obesity-associated genes” and “*FTO*.” The second theme identified relevant terms for weight and BMI, and combined exploded versions of the MeSH terms “body weight” and “body mass index.” Two search terms were combined with the use of the Boolean operator “and.” Additional articles were identified from reference lists of selected studies. Our search strategy included terms for BMI because some of these studies also report change in BMI. Details regarding search terms are shown in **Supplemental Table 1**.

### Study selection

Articles were included if they met the following criteria: 1) they were diet/lifestyle weight-loss intervention studies; 2) they were conducted in adults aged  $\geq 18$  y; 3) they did not involve medication interventions; 4) they reported changes in body weight or BMI by *FTO* genotypes; 5) they included peer-reviewed publications with sufficient information for the analysis; and 6) they were in the English language. Two investigators independently screened all of the studies by title or abstract and then by a full-text review. Discrepancies of screening results between the 2 investigators were solved by discussing with a senior investigator.

### Data extraction

We extracted the following information from each identified article: basic information from studies (authors, publication year, study duration, number of participants, and *FTO* variant and its minor allele frequency), demographics of participants (mean age, sex ratio, mean BMI, race, and ethnicity), intervention methods, analysis strategy (statistical models, with covariates included in the models), and mean weight changes and their corresponding SDs. SDs were calculated with the use of SEs or 95% CIs when necessary. For articles with missing SDs for measurement of change (20, 24–26), change-from-baseline SDs were imputed by using the correlation coefficient method presented in the Cochrane Handbook for Systematic Reviews of Interventions (27). We used a correlation coefficient of 0.9 between baseline and follow-up weight because the correlation between body weights at the 2 time points was assumed to be very high. One study presented the results (mean weight

changes) in a figure (24), and we extracted the estimates carefully from the given figure. For studies with an initial weight-loss phase followed by a weight-maintenance phase (16, 17, 24), we used data on long-term weight loss. For studies that reported results of weight change without exactable data (14, 28, 29), we contacted the first or corresponding authors to request detailed data; 2 authors replied with the requested data (14, 28). We also contacted the authors of the studies that only reported data in dominant genetic models and requested data on additive genetic models (13, 15, 25, 26), although none of them replied to our request. Thus, we did not include these 4 studies in our primary meta-analysis of studies reporting data in additive genetic models.

### Data synthesis and statistical analysis

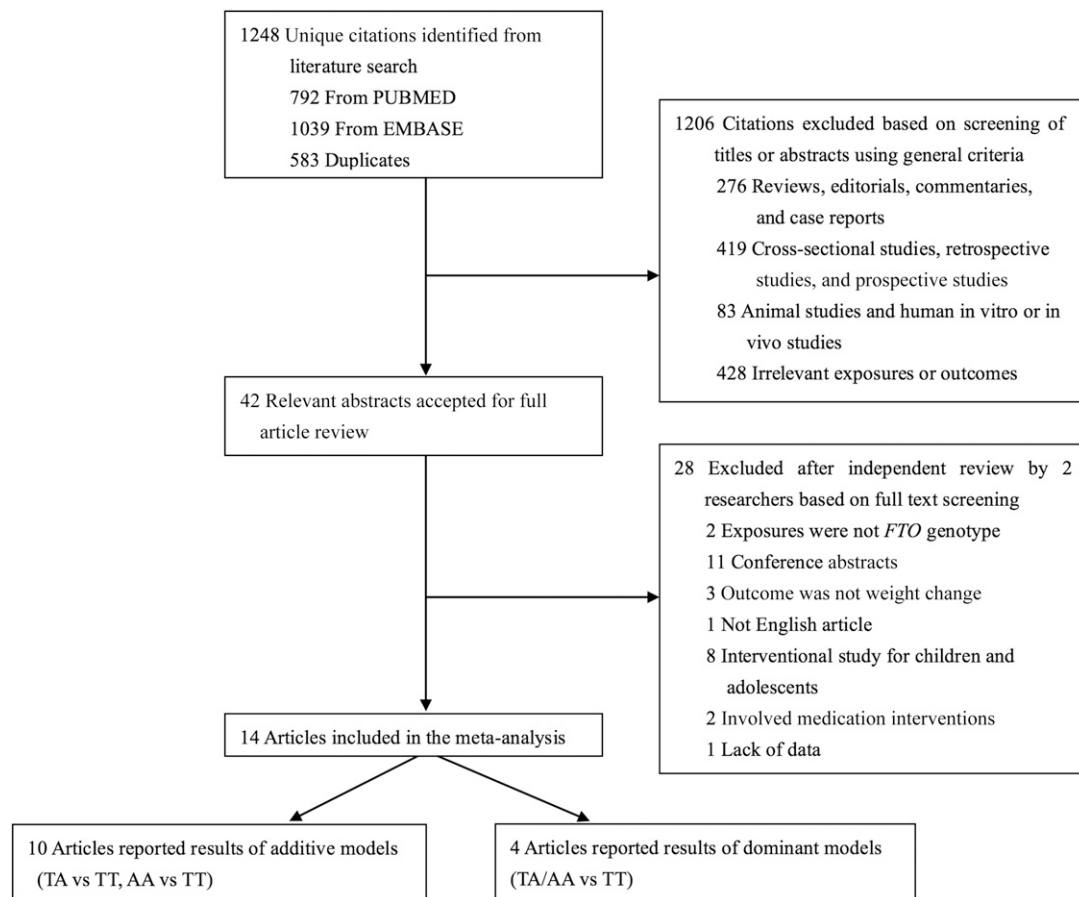
The difference in weight loss (in kg) between the *FTO* genotype groups in response to diet/lifestyle interventions was designated as our principal effect. In this meta-analysis, each selected study was considered to be a single study unit, and mean weight loss by the *FTO* genotype groups in the overall study sample, regardless of intervention differences, was taken into account. For studies that reported weight loss for intervention groups separately (15, 18, 27), we combined the results of different groups with the use of the combining method recommended by the Cochrane Handbook for Systematic Reviews of Interventions (30). We used the same method to combine results of the *FTO* TA and AA genotype groups for studies that provided results of additive genetic models (16–21, 24, 31). All of the data synthesis was conducted after the data collecting and data requesting process.

A heterogeneity test was conducted with the use of 2 different methods, the Cochran's Q test and the  $I^2$  statistic (32, 33). A  $P$  value  $< 0.1$  and  $I^2 > 50\%$  were defined to indicate statistically significant heterogeneity in meta-analysis, in accordance with the Cochrane Handbook for Systematic Reviews of Interventions. Because no significant heterogeneity was detected in our analysis, results were presented in the fixed-effect model. In addition, the possibility of publication bias was evaluated by using a Begg's test and funnel plots (34, 35). Moreover, stratified analyses were performed to evaluate the influence of study characteristics on results. STATA software (version 12.0) was used to perform the meta-analysis.

## RESULTS

### Results of literature search

A total of 1248 unique citations were identified by our search strategy (792 from PubMed and 1039 from Embase, with 583 duplicates), of which 42 were accepted for full text review after screening by titles and abstracts. From the remaining 42 articles, we excluded papers with results stratified by genotypes other than *FTO* ( $n = 2$ ) (36, 37), conference abstracts ( $n = 11$ ) (38–48), studies in children ( $n = 8$ ) (49–56), those that did not have weight or BMI change as the main outcome ( $n = 3$ ) (57–59), those with data not available ( $n = 1$ ) (29), and studies that were not in the English language ( $n = 1$ ) (60). Ultimately, 14 articles were eligible and included in our meta-analysis (13–21, 24–26, 28, 31). A detailed screening flow is shown in **Figure 1**. Of the 14 selected articles, 10 reported the results of an additive genetic



**FIGURE 1** Literature search for the meta-analysis. *FTO*, fat mass and obesity-associated.

model (TA compared with TT, AA compared with TT) (6, 7, 11, 12, 16–21), whereas the other 4 articles reported the results of a dominant genetic model (TA/AA compared with TT) (13, 15, 25, 26), which was mainly the result of limited sample size in these 4 studies. Given the known additive genetic effect of *FTO* variant on BMI and obesity risk, our primary analyses focused on the 10 studies that reported additive genetic model results.

### Study characteristics

The primary characteristics of the 14 studies included in our meta-analysis are shown in **Table 1**. Overall, 7700 participants were included in this meta-analysis, with 33.1% ( $n = 2547$ ) having the TT genotype (reference group). The sample size varied from 75 to 3756 in the 14 studies. Nine studies were conducted in European countries, 3 studies were conducted in the United States, 1 study was conducted in Brazil, and 1 study was conducted in Japan. The age of participants ranged from 18 to 80 y, and the mean baseline BMI (in  $\text{kg}/\text{m}^2$ ) of each study ranged from 28.5 to 41.8. Three studies recruited female participants exclusively (20, 24, 31), and the remaining 11 studies recruited both sexes. Thirteen studies investigated the *FTO* single-nucleotide polymorphism rs9939609, and one study examined a perfect proxy single-nucleotide polymorphism (rs8050136;  $r^2 = 1$ ) (20).

The intervention methods were diverse. Diet modification was used in 12 trials (13–19, 21, 24–26, 28), and 4 of them combined interventions on diet with physical activity (14, 25, 26, 28). One

study only used physical activity modulation (20), and the other study involved only nutritional education to encourage people to consume a balanced and healthy diet (31). The interventions varied in length from 3 mo to 4 y, with a median duration of 9 mo.

In 9 studies, changes in body weight were calculated from multivariable-adjusted models (14, 17–21, 24, 28, 31). One study explicitly mentioned that the model was unadjusted (25). For the other 4 studies (13, 15, 16, 18), no information was provided regarding the statistical adjustment.

### *FTO* genotype and weight loss

We first conducted a meta-analysis of 10 studies (including 6951 subjects) with data from additive genetic models to compare weight loss across the *FTO* genotype groups. Greater weight loss induced by diet/lifestyle interventions was observed in the *FTO* TA genotype [−0.18 kg (95% CI: −0.45, 0.09 kg);  $P = 0.19$ ; NS] and AA genotype [−0.44 kg (95% CI: −0.09, −0.79 kg);  $P = 0.015$ ] groups than in the TT genotype group (Q Qi, unpublished data, 2014) (**Figure 2**). No heterogeneity was observed in either comparison (AA compared with TT:  $I^2 = 0.0\%$ ; TA compared with TT:  $I^2 = 0.0\%$ ).

When carrying out a meta-analysis of 14 studies that reported dominant genetic model results as a secondary analysis, a tendency for greater weight loss was observed in the TA/AA genotype with TT genotype groups [−0.20 kg (95% CI: −0.43, 0.04 kg),  $P = 0.10$ ;  $I^2 = 0.0\%$ ] (**Supplemental Figure 1**).

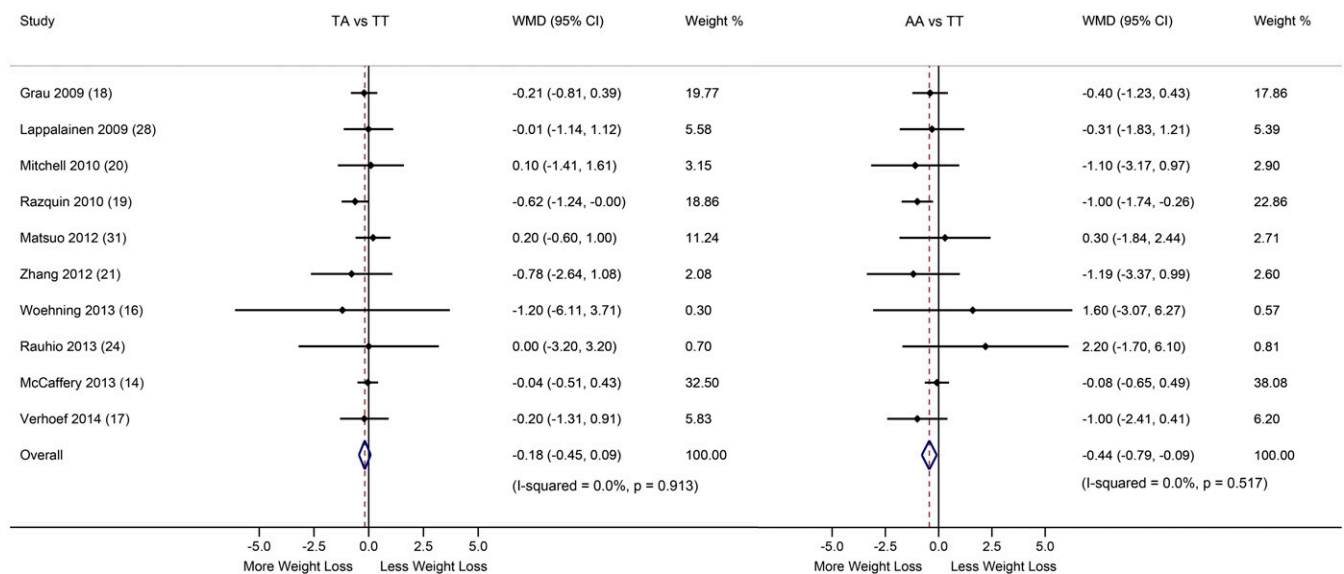
**TABLE 1**  
Characteristics of studies included in the meta-analysis<sup>1</sup>

Study first author and year (ref)	Enrollment or completers, <i>n</i>	Country or region	Age, y	Male, %	BMI, kg/m <sup>2</sup>	Intervention	Energy restricted	Duration	FTO SNP	MAF	Adjustment
Curti 2013 (26) <sup>2</sup>	134	Brazil	56.6 (18–80) <sup>3</sup>	34	30.4 (NA)	Diet and exercise	Yes	9 mo	rs9939609	0.42	NA
de Luis 2012 (15) <sup>2</sup>	305	Spain	43.5 (NA)	26	36.6 (>30)	Diet and exercise	Yes	3 mo	rs9939609	0.44	NA
de Luis 2013 (13) <sup>2</sup>	106	Spain	49.5 (NA)	34	34.8 (>30)	Low-fat hypocaloric diet	Yes	3 mo	rs9939609	0.45	NA
Grau 2009 (18)	618	Europe	NA (20–50)	25	35.5 (≥30)	Two low-energy diets with either low or high fat content	Yes	2 y	rs9939609	0.40	Age, sex, baseline weight, fat-free mass, fat mass, WC, fat oxidation
Haupt 2008 (25) <sup>2</sup>	204	Germany	45.9 (NA)	40	29.1 (>27)	Diet and exercise	Yes	9 mo	rs8050136	NA	Unadjusted
Lappalainen 2009 (28)	412	Finland	55.3 (40–56)	33	31.2 (≥25)	Diet and exercise	Yes	4 y	rs9939609	0.42	Age, sex, baseline BMI
Matsuo 2012 (31)	204	Japan	51.9 (24–66)	0	28.5 (≥25)	Dietary lectures	No	14 wk	rs9939609	0.26	Age, menstrual status, baseline values
McCaffery 2013 (14)	3756	United States	59.0 (45–76)	44	36.2 (>25)	Diet and exercise	Yes	1 y	rs9939609	0.49	Age, sex, study site, ancestry informative markers
Mitchell 2010 (20)	234	United States	58.1 (45–75)	0	31.6 (25–43)	Three groups of different exercise intensity	No	6 mo	rs8050136	0.43	Exercise assignment
Rauhio 2013 (24)	75	Finland	39.6 (25–45)	0	34.0 (>30)	Very low-energy diet followed by weight maintenance	Yes	1 y	rs9939609	0.45	Age, sex
Razquin 2010 (19)	776	Spain	67.8 (55–80)	45	29.2 (NA)	Two Mediterranean diets and one conventional low-fat diet	Yes	3 y	rs9939609	0.45	Age, sex, baseline BMI, diabetes status
Verhoef 2014 (17)	148	Netherlands	NA (20–50)	35	32 (27–38)	Very low-energy diet followed by weight maintenance	Yes	5 mo	rs9939609	0.39	Age, sex, baseline weight, short-term weight loss
Woehning 2013 (16)	125	Germany	44.6 (18–72)	33	41.8 (≥30)	Very low-energy diet followed by weight maintenance	Yes	52 wk	rs9939609	0.48	NA
Zhang 2012 (21)	603	United States	51 (30–70)	40	33 (25–40)	Four low-energy diets with different compositions of macronutrients	Yes	2 y	rs1558902	0.40	Age, sex, race, baseline BMI, intervention group

<sup>1</sup>FTO, fat mass and obesity-associated; MAF, minor allele frequency; NA, not available; ref, reference; SNP, single-nucleotide polymorphism; WC, waist circumference.

<sup>2</sup>Not included in the primary meta-analysis of studies that reported results of additive genetic models because they reported only results of dominant genetic models.

<sup>3</sup>Mean; range in parentheses (all such values).



**FIGURE 2** Differences in weight loss in the *FTO* TA and AA genotype groups compared with the TT genotype group. Data are WMDs and 95% CIs in weight loss between the *FTO* genotype groups across studies, and pooled results were calculated with the use of fixed-effect models. A Cochran's Q test and the  $I^2$  statistic were used to test the heterogeneity between studies. Horizontal lines denote the 95% CIs; solid diamonds represent the point estimate of each study. The open diamond represents the pooled estimate of the lifestyle intervention effect. The dashed lines indicated the point estimate of the pooled result. *FTO*, fat mass and obesity-associated; WMD, weighted mean difference.

### Stratified analysis

Because studies included in the meta-analysis varied in intervention methods and many other characteristics, we then performed subgroup analyses to investigate the influences of study characteristics on pooled results. Studies were classified according to age (mean age <50 or  $\geq$ 50 y), sex (mixed or women only), BMI (mean baseline BMI <35 or  $\geq$ 35), baseline adjustments (adjusted for baseline BMI or body weight, or not adjusted for baseline BMI or body weight), regions in which studies were conducted (America, Europe, or Asia), methods of intervention (diet only or other interventions), and study duration (<1 y or  $\geq$ 1 y).

A total of 10 studies with 6951 participants were included in the stratified analyses. No statistically significant difference between subgroups was observed for any of these stratified analyses (Table 2), although some significant results were observed in several subgroups. Specifically, a significantly greater weight change was observed in those with the TA genotype [-0.40 kg (95% CI: -0.79, -0.01 kg);  $P = 0.04$ ] and AA genotype [-0.72 kg (95% CI: -1.21, -0.23 kg);  $P = 0.004$ ] than in those with the TT genotype group in studies that used diet intervention only (all energy-restricted). In studies with adjustment for baseline BMI or body weight, we also found significantly greater weight loss in the AA genotype group than in the TT genotype group [-0.70 kg (95% CI: -1.16, -0.23 kg);  $P = 0.003$ ]. In addition, significantly greater weight change was observed in the AA genotype group than in the TT genotype group in studies with participants who were  $\geq$ 50 y old [-0.44 kg (95% CI: -1.12, -0.28 kg);  $P = 0.033$ ], those with participants who had a baseline mean BMI <35 [-0.70 kg (95% CI: -1.16, -0.23 kg);  $P = 0.003$ ], studies with men and women combined (mixed) [-0.46 kg (95% CI: -0.83, 0.10 kg);  $P = 0.013$ ], and studies conducted in Europe [-0.42 kg (95% CI: -0.79, -0.05 kg),  $P = 0.026$ ].

### Sensitivity analysis

We conducted a sensitivity analysis in the 10 primary studies by excluding one study at a time to examine the individual effect of each study on the overall results. The estimates (differences in weight loss) comparing the *FTO* AA and TT genotypes ranged from -0.66 kg to -0.27 kg, with the biggest influence coming from the study by McCaffery et al. (14) (Supplemental Figure 2). The results became even more significant after the exclusion of this study [AA compared with TT, -0.66 kg (95% CI: -1.10, -0.21 kg);  $P = 0.004$ ].

In addition, we repeated the meta-analysis by excluding studies without reporting SDs for measurements of weight change, and the results were similar [TA compared with TT: -0.19 kg (95% CI: -0.46, 0.08 kg);  $P = 0.19$ . AA compared with TT: -0.44 kg (95% CI: -0.80, -0.08 kg);  $P = 0.016$ ].

### Publication bias

On the basis of funnel plots (Supplemental Figure 3) and Egger's tests, no significant publication bias was observed in this meta-analysis (TA compared with TT:  $P = 0.78$ ; AA compared with TT:  $P = 0.75$ ).

### DISCUSSION

In this meta-analysis of weight-loss trials, we found that individuals carrying the homozygous *FTO* obesity-predisposing allele (AA genotype) had greater weight loss than did non-carriers (TT genotype) after diet/lifestyle interventions. Furthermore, differences in weight loss between the *FTO* AA and TT genotype groups became more significant in several subgroups stratified by various study and participant characteristics.

To the best of our knowledge, no previous meta-analysis has been conducted to investigate the effect of the *FTO* variant on

**TABLE 2**  
Stratified analysis of *FTO* genotype and weight-loss according to study characteristics<sup>1</sup>

Subgroups	Sample size, <i>n</i>	Studies, <i>n</i>	TA vs. TT			<i>P</i> between groups	AA vs. TT			<i>P</i> between groups
			WMD	95% CI	<i>I</i> <sup>2</sup> value		WMD	95% CI	<i>I</i> <sup>2</sup> value	
Mean age						0.88				0.95
<50	966	4	-0.21	(-0.73, 0.31)	0.0		-0.42	(-1.12, 0.28)	3.2	
≥50	5985	6	-0.17	(-0.48, 0.15)	0.0		-0.44	(-0.85, -0.04)	1.4	
Mean BMI at baseline						0.61				0.08
<35	2452	7	-0.25	(-0.64, 0.14)	0.0		-0.79	(-1.33, -0.26)	0.0	
≥35	4499	3	-0.11	(-0.48, 0.26)	0.0		-0.17	(-0.63, 0.30)	0.0	
Duration						0.51				0.74
<1 y	1204	4	-0.07	(-0.49, 0.35)	0.0		-0.53	(-1.18, 0.12)	0.0	
≥1 y	5747	6	-0.25	(-0.60, 0.09)	0.0		-0.40	(-0.82, 0.02)	25.1	
Intervention						0.12				0.11
Diet intervention only	2345	6	-0.40	(-0.79, -0.01)	0.0		-0.72	(-1.21, -0.23)	0.0	
Other <sup>2</sup>	4606	4	0.02	(-0.35, 0.39)	0.0		-0.15	(-0.65, 0.49)	0.0	
Sex						0.28				0.61
Mixed	6438	7	-0.24	(-0.53, 0.05)	0.0		-0.46	(-0.83, -0.10)	0.0	
Female	513	3	0.17	(-0.52, 0.86)	0.0		-0.09	(-1.48, 1.30)	15.5	
Region						0.40				0.38
America	4593	3	-0.07	(-0.51, 0.37)	0.0		-0.22	(-0.75, 0.32)	0.0	
Europe	2154	6	-0.34	(-0.72, 0.03)	0.0		-0.66	(-1.14, -0.18)	0.0	
Asia	204	1	0.20	(-0.60, 1.00)	NA		0.30	(-0.79, -0.09)	NA	
Adjusted for baseline BMI or body weight						0.66				0.19
Yes	2761	6	-0.26	(-0.60, 0.08)	0.0		-0.70	(-1.16, -0.23)	0.0	
No	4190	4	-0.04	(-0.51, 0.43)	0.0		-0.09	(-0.63, 0.46)	0.0	

<sup>1</sup>Differences in weight loss after intervention between *FTO* genotypes across studies were pooled with the use of fixed-effect models. The heterogeneity between studies for each group was tested by *I*<sup>2</sup>. *P* values between groups were tested with the use of Cochran's Q test. *FTO*, fat mass and obesity-associated; NA, not available; WMD, weighted mean difference.

<sup>2</sup>Includes studies with exercise interventions, both exercise and diet interventions, or nutritional education.

weight loss in response to diet/lifestyle interventions. All previous meta-analyses were based on observational studies investigating interrelations between *FTO* variant, diet/lifestyle factors, and obesity. For example, a large meta-analysis suggested that greater physical activity attenuates the association of *FTO* genotype and obesity in adults (61). Moreover, our prior meta-analysis indicated that the obesity-predisposing allele of *FTO* is associated with higher total energy intake in adults and higher protein intake in children (9, 10), although whether there is an interaction between *FTO* genotype and dietary intake on obesity remains controversial. In the current meta-analysis, we examined the *FTO* genetic effect on weight loss in randomized intervention trials, which provided more reliable evidence because the study conditions were prescribed and the confounding effects were maximally reduced. Taken together, these findings support the interactive roles of the *FTO* gene and diet/lifestyle factors in the regulation of body weight.

It is not surprising that the observed difference in weight loss between the *FTO* genotype groups is modest, which is consistent with the modest effect of the *FTO* variant on BMI (~0.35/allele) (61). In addition, although the result was not significant when comparing the TA and TT genotype groups, the trend of weight loss increased across the 3 genotype groups, which is in line with the additivity of the *FTO* genetic effect. Admittedly, the observed difference in weight loss between the *FTO* genotype groups may not translate into a clinically important benefit; however, the true effect might be underestimated because of

heterogeneity of intervention modality. For example, the effect size is greater with diet interventions [-0.72 kg (95% CI: -1.21, -0.22 kg) between the AA and TT genotypes] than with other interventions [-0.15 kg (95% CI: -0.65, -0.49 kg)], although there is no statistically significant difference between subgroups, which might be due to the limited number of studies and participants in this stratified analysis. Thus, more studies are needed to examine whether intervention modality may influence the *FTO* genetic effect on weight loss, and the clinical relevance of our findings needs further investigations.

It is interesting that the homozygous *FTO* obesity-predisposing genotype is associated with greater weight loss induced by diet/lifestyle interventions. Several other previous studies also reported that individuals carrying risk alleles exhibited greater improvement of respective traits than did noncarriers after diet interventions (62-65). One may argue that this may reflect baseline weight difference for different genotypes: heavier people (the risk allele carriers) tend to lose more weight. However, the significant *FTO* genotype effect on weight loss was observed in the meta-analysis of 6 studies with adjustment for baseline BMI or body weight [-0.70 kg (95% CI: -1.16, -0.23 kg) between the AA and TT genotypes], and there was no significant difference between groups with and without adjustment for baseline BMI or body weight. In addition, it is possible that individuals carrying the *FTO* obesity genotype may have attempted more frequently to lose body weight and are therefore more successful in weight loss, at least in the short term.

However, in the long term, their genetic predisposition to obesity could result in a cycle of weight loss and regain. This might explain a previously reported association between the *FTO* genotype and variation in BMI (66). Nevertheless, further studies are needed to investigate whether the observed genetic influence on diet/lifestyle-induced weight loss could be maintained in the long term.

The mechanisms underlying our findings are unknown but might be related to the potential role of *FTO* in regulating energy homeostasis. *FTO* expression in the hypothalamus is regulated by feeding, fasting, and energy restriction (67–73). Both animal and human studies support the association between *FTO* and food intake (9, 10, 74), and *FTO* also has been linked to habitual appetitive behaviors (11, 12) and appetite-related hormones (ghrelin and leptin) (75, 76). Moreover, a recent study reported that the obesity-predisposing allele of the *FTO* variant was associated with a reduction in food cravings and appetite during an intervention with hypocaloric weight-loss diets (44). Consistently, our subgroup analysis also indicates a stronger effect of *FTO* on weight loss in response to energy-restricted diet interventions than with other interventions. In addition, it should be noted that the *FTO* variants may affect the functions of other genes rather than the *FTO* itself. A recent study reported that the *FTO* obesity-associated variants are associated with expression of the homeobox gene Iroquois-class homeobox protein 2 (*IRX3*) (77).

Several limitations of this meta-analysis should be acknowledged. First, we were unable to include 4 studies (13, 15, 25, 26) in our primary analysis because of difficulty in obtaining additive genetic model results. However, a secondary meta-analysis of 14 studies based on the dominant genetic model showed similar but nonsignificant results. Second, studies included in our meta-analysis varied in intervention methods and duration, sample size, study setting, race/ethnicity, and other participant characteristics, although there was no significant heterogeneity in results across individual studies or subgroups. We had a limited sample size in the stratified analyses, and more studies are needed. Third, we examined the *FTO* genetic effect on weight loss regardless of the various diets and other interventions applied in the individual trials, although some specific *FTO*–diet intervention interactions have been reported (19, 21). However, there are insufficient numbers of published studies with a similar design for the meta-analysis. Moreover, we only included papers published in the English language, and may have missed some eligible studies published in other languages.

In conclusion, this study provides some evidence from a meta-analysis that weight loss varies between the *FTO* genotypes in response to diet/lifestyle interventions. Our findings provide some support for considering genetic variability in response to diet/lifestyle interventions in the development of more effective strategies for weight loss. Nevertheless, more studies are needed to explore which types of diet/lifestyle interventions most powerfully facilitate the *FTO* genetic effect on weight loss.

We thank Jeanne McCaffery, from the Miriam Hospital and the Warren Alpert School of Medicine at Brown University, and Tiina Jääskeläinen, from the Department of Clinical Nutrition, Institute of Public Health and Clinical Nutrition, University of Eastern Finland, for providing unpublished data.

The authors' responsibilities were as follows—LX and QQ: conceived of and designed the research, performed the statistical analysis, and wrote the manuscript; LX, BP, and QQ: conducted the literature review and data collection; and all authors: revised the manuscript for intellectual content and

read and approved the final version of the manuscript. None of the authors reported a conflict of interest related to the study.

## REFERENCES

1. James WP. WHO recognition of the global obesity epidemic. *Int J Obes (Lond)* 2008;32(Suppl 7):S120–6.
2. MacLean PS, Wing RR, Davidson T, Epstein L, Goodpaster B, Hall KD, Levin BE, Perri MG, Rolls BJ, Rosenbaum M, et al. NIH working group report: Innovative research to improve maintenance of weight loss. *Obesity (Silver Spring)* 2015;23:7–15.
3. Espeland MA, Bray GA, Neiberg R, Rejeski WJ, Knowler WC, Lang W, Cheskin LJ, Williamson D, Lewis CB, Wing R, et al. Describing patterns of weight changes using principal components analysis: results from the Action for Health in Diabetes (Look AHEAD) research group. *Ann Epidemiol* 2009;19:701–10.
4. Sacks FM, Bray GA, Carey VJ, Smith SR, Ryan DH, Anton SD, McManus K, Champagne CM, Bishop LM, Laranjo N, et al. Comparison of weight-loss diets with different compositions of fat, protein, and carbohydrates. *N Engl J Med* 2009;360:859–73.
5. Bray GA, Wadden TA. Improving long-term weight loss maintenance: can we do it? *Obesity (Silver Spring)* 2015;23:2–3.
6. Wu H, Wylie-Rosett J, Qi Q. Dietary interventions for weight loss and maintenance: preference or genetic personalization? *Curr Nutr Rep* 2013;2:189–98.
7. Lu Y, Loos RJ. Obesity genomics: assessing the transferability of susceptibility loci across diverse populations. *Genome Med* 2013;5:55.
8. Loos RJ, Yeo GS. The bigger picture of *FTO*: the first GWAS-identified obesity gene. *Nat Rev Endocrinol* 2014;10:51–61.
9. Qi Q, Kilpelainen TO, Downer MK, Tanaka T, Smith CE, Sluijs I, Sonestedt E, Chu AY, Renstrom F, Lin X, et al. *FTO* genetic variants, dietary intake and body mass index: insights from 177,330 individuals. *Hum Mol Genet* 2014;23:6961–72.
10. Qi Q, Downer MK, Kilpelainen TO, Taal HR, Barton SJ, Ntalla I, Standl M, Boraska V, Huikari V, Kieft-de Jong JC, et al. Dietary intake, *FTO* genetic variants, and adiposity: a combined analysis of over 16,000 children and adolescents. *Diabetes* 2015;64:2467–76.
11. den Hoed M, Westerterp-Plantenga MS, Bouwman FG, Mariman EC, Westerterp KR. Postprandial responses in hunger and satiety are associated with the rs9939609 single nucleotide polymorphism in *FTO*. *Am J Clin Nutr* 2009;90:1426–32.
12. Wardle J, Carnell S, Haworth CM, Farooqi IS, O'Rahilly S, Plomin R. Obesity associated genetic variation in *FTO* is associated with diminished satiety. *J Clin Endocrinol Metab* 2008;93:3640–3.
13. de Luis DA, Aller R, Conde R, Izaola O, Sagrado MG, Sanz JC. The rs9939609 gene variant in *FTO* modified the metabolic response of weight loss after a 3-month intervention with a hypocaloric diet. *J Investig Med* 2013;61:22–6.
14. McCaffery JM, Papandonatos GD, Huggins GS, Peter I, Kahn SE, Knowler WC, Hudnall GE, Lipkin EW, Kitabchi AE, Wagenknecht LE, et al. *FTO* predicts weight regain in the Look AHEAD clinical trial. *Int J Obes (Lond)* 2013;37(12):1545–52.
15. de Luis DA, Aller R, Izaola O, de la Fuente B, Conde R, Sagrado MG, Primo D. Evaluation of weight loss and adipocytokines levels after two hypocaloric diets with different macronutrient distribution in obese subjects with rs9939609 gene variant. *Diabetes Metab Res Rev* 2012;28:663–8.
16. Woehning A, Schultz JH, Roeder E, Moeltner A, Isermann B, Nawroth PP, Wolfmuller C, Rudofsky G. The A-allele of the common *FTO* gene variant rs9939609 complicates weight maintenance in severe obese patients. *Int J Obes (Lond)* 2013;37(1):135–9.
17. Verhoef SP, Camps SG, Bouwman FG, Mariman EC, Westerterp KR. Genetic predisposition, dietary restraint and disinhibition in relation to short and long-term weight loss. *Physiol Behav* 2014;128:247–51.
18. Grau K, Hansen T, Holst C, Astrup A, Saris WHM, Arner P, Rossner S, MacDonald I, Polak J, Oppert JM, et al. Macronutrient-specific effect of *FTO* rs9939609 in response to a 10-week randomized hypo-energetic diet among obese Europeans. *Int J Obes (Lond)* 2009;33:1227–34.
19. Razquin C, Martinez JA, Martinez-Gonzalez MA, Bes-Rastrollo M, Fernandez-Crehuet J, Marti A. A 3-year intervention with a Mediterranean diet modified the association between the rs9939609 gene variant in *FTO* and body weight changes. *Int J Obes (Lond)* 2010;34(2):266–72.

20. Mitchell JA, Church TS, Rankinen T, Earnest CP, Sui X, Blair SN. FTO genotype and the weight loss benefits of moderate intensity exercise. *Obesity* (Silver Spring) 2010;18:641–3.
21. Zhang X, Qi Q, Zhang C, Smith SR, Hu FB, Sacks FM, Bray GA, Qi L. FTO genotype and 2-year change in body composition and fat distribution in response to weight-loss diets: The pounds lost trial. *Diabetes* 2012;61:3005–11. Correction published in: *Diabetes* 2013;62:662.
22. Stroup DF, Berlin JA, Morton SC, Olkin I, Williamson GD, Rennie D, Moher D, Becker BJ, Sipe TA, Thacker SB. Meta-analysis of observational studies in epidemiology: a proposal for reporting. Meta-analysis Of Observational Studies in Epidemiology (MOOSE) group. *JAMA* 2000;283:2008–12.
23. Moher D, Liberati A, Tetzlaff J, Altman DG, Group P. Preferred reporting items for systematic reviews and meta-analyses: the PRISMA statement. *J Clin Epidemiol* 2009;62:1006–12.
24. Rauhio A, Uusi-Rasi K, Nikkari ST, Kannus P, Sievanen H, Kunnas T. Association of the FTO and ADRB2 genes with body composition and fat distribution in obese women. *Maturitas* 2013;76:165–71.
25. Haupt A, Thamer C, Machann J, Kirchhoff K, Stefan N, Tschritter O, Machicao F, Schick F, Haring HU, Fritsche A. Impact of variation in the FTO gene on whole body fat distribution, ectopic fat, and weight loss. *Obesity* (Silver Spring) 2008;16:1969–72.
26. Curti MLR, Rogero MM, Baltar VT, Barros CR, Siqueira-Catania A, Ferreira SRG. FTO T/A and peroxisome proliferator-activated receptor-(gamma) Pro12Ala polymorphisms but not ApoA1 -75 are associated with better response to lifestyle intervention in Brazilians at high cardiometabolic risk. *Metab Syndr Relat Disord* 2013;11:169–76.
27. Higgins JPT, Green S, editors. *Cochrane handbook for systematic reviews of interventions version 5.1.0*. The Cochrane Collaboration. Chichester (United Kingdom); Hoboken (NJ): Wiley-Blackwell; 2011.
28. Lappalainen TJ, Tolppanen AM, Kolehmainen M, Schwab U, Lindstrom J, Tuomilehto J, Pulkkinen L, Eriksson JG, Laakso M, Gylling H, et al. The common variant in the FTO gene did not modify the effect of lifestyle changes on body weight: the Finnish Diabetes Prevention Study. *Obesity* (Silver Spring) 2009;17:832–6.
29. Dlouha D, Suchanek P, Lanska V, Hubacek JA. Body mass index change in females after short-time life style intervention is not dependent on the FTO polymorphisms. *Physiol Res* 2011;60(1):199–202.
30. VanderWeele TJ. A unification of mediation and interaction: a 4-way decomposition. *Epidemiology* 2014;25:749–61.
31. Matsuo T, Nakata Y, Murotake Y, Hotta K, Tanaka K. Effects of FTO genotype on weight loss and metabolic risk factors in response to calorie restriction among Japanese women. *Obesity* (Silver Spring) 2012;20:1122–6.
32. Higgins JP, Thompson SG. Quantifying heterogeneity in a meta-analysis. *Stat Med* 2002;21:1539–58.
33. Higgins JP, Thompson SG, Deeks JJ, Altman DG. Measuring inconsistency in meta-analyses. *BMJ* 2003;327:557–60.
34. Begg CB, Mazumdar M. Operating characteristics of a rank correlation test for publication bias. *Biometrics* 1994;50:1088–101.
35. Egger M, Davey Smith G, Schneider M, Minder C. Bias in meta-analysis detected by a simple, graphical test. *BMJ* 1997;315:629–34.
36. Stofan JR, Osterberg KL, Horswill CA, Lacambra M, Eichner ER, Anderson SA, Murray R. Daily fluid turnover during preseason training in U.S. college football. *Int J Sport Nutr Exerc Metab* 2007;17:340–51.
37. Cha S, Koo I, Park BL, Jeong S, Choi SM, Kim KS, Shin HD, Kim JY. Genetic effects of FTO and MC4R polymorphisms on body mass in constitutional types. *Evid Based Complement Alternat Med* 2011;2011:106390.
38. Tiwari HK, Patki A, Lieberman J, Stroup TS, Allison DB, Leibel RL, Chung WK. Association of allelic variation in genes mediating aspects of energy homeostasis with weight gain during administration of antipsychotic drugs (CATIE study). *Front Genet* 2011;2:56.
39. Schmi J, Rai BK, Chambers JC, Kooner JK. Weight change following dietary intervention: the role of common genetic variants in FTO and MC4R. *Eur Heart J* 2009;30:953–4.
40. Moreles A, Rendo T, Campoy C, Zapatera B, Moreno L, Garagorri J, Marcos A, Martinez JA, Azcona-Sanjulian MC, Marti A. Influence of eight obesity-related SNPs with body mass index and weight loss in Spanish adolescents after a lifestyle intervention. *Obes Rev* 2011;12:43–4.
41. Moraes TI, Oliveira R, Kiyokawa RK, Sousa MC, Cerda A, Hirata MH, Fajardo CM, Dorea EL, Damasceno NRT, Jorge MIE, et al. The relationship between FTO polymorphisms and anthropometric and metabolic profile in individuals with ms enrolled in a nutritional orientation program. *J Nutrigenet Nutrigenomics* 2012;5:287.
42. Luglio HF, Aller E, Bowman F, Mariman E, Van Baak M. Genetic risk score as a predictor of weight loss during a lifestyle intervention in obese adults. *J Nutrigenet Nutrigenomics* 2012;5:233–4.
43. Hubacek J, Ceska R, Dlouha D, Zlatohlavek L. Effect of fto and MC4R variants on BMI decrease in children. *Obes Facts* 2012;5:172.
44. Huang T, Qi Q, Li Y, Hu FB, Bray GA, Sacks FM, Williamson DA, Qi L. FTO genotype, dietary protein, and change in appetite: the Preventing Overweight Using Novel Dietary Strategies trial. *Am J Clin Nutr* 2014;99:1126–30.
45. Harbron J, Zaahl M, Kotze M, Van Der Merwe L, Senekal M. Effect of eight polymorphisms on weight loss outcomes in overweight/obese Caucasian adults. *J Nutrigenet Nutrigenomics* 2010;3:120.
46. Ehehalt S, Schum J, Blumenstock G, Weber K, Schweizer R, Ranke MB, Binder G. FTO-risk alleles had no impact on body composition and parameters of metabolism before and after a lifestyle intervention programme in obese children and adolescents. *Horm Res Paediatr* 2011;76:266.
47. Dusatkova L, Zamrazilova H, Sedlackova B, Vcelak J, Hlavaty P, Bendlova B, Kunesova M, Hainer V. BDNF and FTO gene variants modified the response to short-term weight management in overweight and obese adolescents. *Horm Res Paediatr* 2013;80:104–5.
48. Curti MLR, Rogero MM, Barros CR, Siqueira-Catani A, Baltar VT, Ferreira SRG. Indicated for the young investigator award FTO T/A, PPARgamma PRO12ALA but not APOA1-75 polymorphisms are associated with better response to lifestyle intervention in Brazilians at high cardiometabolic risk. *J Nutrigenet Nutrigenomics* 2012;5:252.
49. Lauria F, Siani A, Bammann K, Foraita R, Huybrechts I, Iacoviello L, Koni AC, Kourides Y, Marild S, Molnar D, et al. Prospective analysis of the association of a common variant of FTO (rs9939609) with adiposity in children: results of the IDEFICS study. *PLoS One* 2012;7:e48876.
50. Müller TD, Hinney A, Scherag A, Nguyen TT, Schreiner F, Schafer H, Hebebrand J, Roth CL, Reinehr T. 'Fat mass and obesity associated' gene (FTO): no significant association of variant rs9939609 with weight loss in a lifestyle intervention and lipid metabolism markers in German obese children and adolescents. *BMC Med Genet* 2008;9:85.
51. Reinehr T, Hinney A, Toschke AM, Hebebrand J. Aggravating effect of INSIG2 and FTO on overweight reduction in a one-year lifestyle intervention. *Arch Dis Child* 2009;94:965–7.
52. Scherag A, Kleber M, Boes T, Kolbe AL, Ruth A, Grallert H, Illig T, Heid IM, Toschke AM, Grau K, et al. SDCCAG8 obesity alleles and reduced weight loss after a lifestyle intervention in overweight children and adolescents. *Obesity* (Silver Spring) 2012;20:466–70.
53. Zlatohlavek L, Vrablik M, Motykova E, Ceska R, Vasickova L, Dlouha D, Hubacek JA. FTO and MC4R gene variants determine BMI changes in children after intensive lifestyle intervention. *Clin Biochem* 2013;46:313–6.
54. Moleres A, Rendo-Urteaga T, Zulet MA, Marcos A, Campoy C, Garagorri JM, Martinez JA, Azcona-Sanjulian MC, Marti A. Obesity susceptibility loci on body mass index and weight loss in Spanish adolescents after a lifestyle intervention. *J Pediatr* 2012;161:466–70.e2.
55. Schum J, Blumenstock G, Weber K, Schweizer R, Pfaff C, Schurr N, Ranke MB, Binder G, Ehehalt S. Variants of the FTO gene in obese children and their impact on body composition and metabolism before and after lifestyle intervention. *Exp Clin Endocrinol Diabetes* 2012;120:128–31.
56. Hinney A, Wolters B, Putter C, Grallert H, Illig T, Hebebrand J, Reinehr T. No impact of obesity susceptibility loci on weight regain after a lifestyle intervention in overweight children. *Journal of pediatric endocrinology & metabolism. J Pediatr Endocrinol Metab* 2013;26:1209–13.
57. Matsuo T, Nakata Y, Hotta K, Tanaka K. The FTO genotype as a useful predictor of body weight maintenance: Initial data from a 5-year follow-up study. *Metabolism* 2014;63:912–7.
58. Rankinen T, Rice T, Teran-Garcia M, Rao DC, Bouchard C. FTO genotype is associated with exercise training-induced changes in body composition. *Obesity* (Silver Spring) 2010;18:322–6.
59. Huang T, Qi Q, Li Y, Hu F, Bray GA, Sacks FM, Qi L. FTO genotype, dietary protein, and change in appetite: The pounds lost trial. *Am J Clin Nutr* 2014;99:1126–30.
60. Reinehr T, Hinney A, Friedel S, Muller T, Hebebrand J. Impact of genetic markers on overweight reduction in a lifestyle intervention. *Aktuel Ernahrungsmed* 2008;33:231–6.



61. Kilpeläinen TO, Qi L, Brage S, Sharp SJ, Sonestedt E, Demerath E, Ahmad T, Mora S, Kaakinen M, Sandholt CH, et al. Physical activity attenuates the influence of FTO variants on obesity risk: a meta-analysis of 218,166 adults and 19,268 children. *PLoS Med* 2011;8:e1001116.
62. Qi Q, Bray GA, Smith SR, Hu FB, Sacks FM, Qi L. Insulin receptor substrate 1 gene variation modifies insulin resistance response to weight-loss diets in a 2-year randomized trial: the Preventing Overweight Using Novel Dietary Strategies (POUNDS LOST) trial. *Circulation* 2011;124:563–71.
63. Qi Q, Durst R, Schwarzfuchs D, Leitersdorf E, Shpitzen S, Li Y, Wu H, Champagne CM, Hu FB, Stampfer MJ, et al. CETP genotype and changes in lipid levels in response to weight-loss diet intervention in the POUNDS LOST and DIRECT randomized trials. *J Lipid Res* 2015;56:713–21.
64. Zhang X, Qi Q, Bray GA, Hu FB, Sacks FM, Qi L. APOA5 genotype modulates 2-y changes in lipid profile in response to weight-loss diet intervention: the Pounds Lost Trial. *Am J Clin Nutr* 2012;96:917–22.
65. Marín C, Perez-Martinez P, Delgado-Lista J, Gomez P, Rodriguez F, Yubero-Serrano EM, Garcia-Rios A, Camargo A, Perez-Jimenez F, Lopez-Miranda J. The insulin sensitivity response is determined by the interaction between the G972R polymorphism of the insulin receptor substrate 1 gene and dietary fat. *Mol Nutr Food Res* 2011;55:328–35.
66. Yang J, Loos RJ, Powell JE, Medland SE, Speliotes EK, Chasman DI, Rose LM, Thorleifsson G, Steinthorsdottir V, Magi R, et al. FTO genotype is associated with phenotypic variability of body mass index. *Nature* 2012;490:267–72.
67. Gerken T, Girard CA, Tung YC, Webby CJ, Saudek V, Hewitson KS, Yeo GS, McDonough MA, Cunliffe S, McNeill LA, et al. The obesity-associated FTO gene encodes a 2-oxoglutarate-dependent nucleic acid demethylase. *Science* 2007;318:1469–72.
68. Stratigopoulos G, Padilla SL, LeDuc CA, Watson E, Hattersley AT, McCarthy MI, Zeltser LM, Chung WK, Leibel RL. Regulation of Fto/Ftm gene expression in mice and humans. *Am J Physiol Regul Integr Comp Physiol* 2008;294:R1185–96.
69. Fredriksson R, Haglund M, Olszewski PK, Stephansson O, Jacobsson JA, Olszewska AM, Levine AS, Lindblom J, Schiöth HB. The obesity gene, FTO, is of ancient origin, up-regulated during food deprivation and expressed in neurons of feeding-related nuclei of the brain. *Endocrinology* 2008;149:2062–71.
70. Olszewski PK, Fredriksson R, Olszewska AM, Stephansson O, Alsjö J, Radomska KJ, Levine AS, Schiöth HB. Hypothalamic FTO is associated with the regulation of energy intake not feeding reward. *BMC Neurosci* 2009;10:129.
71. Wang P, Yang FJ, Du H, Guan YF, Xu TY, Xu XW, Su DF, Miao CY. Involvement of leptin receptor long isoform (LepRb)-STAT3 signaling pathway in brain fat mass- and obesity-associated (FTO) down-regulation during energy restriction. *Mol Med* 2011;17:523–32.
72. Boender AJ, van Rozen AJ, Adan RA. Nutritional state affects the expression of the obesity-associated genes *Etv5*, *Faim2*, *Fto*, and *Negr1*. *Obesity (Silver Spring)* 2012;20:2420–5.
73. Tung YC, Ayuso E, Shan X, Bosch F, O’Rahilly S, Coll AP, Yeo GS. Hypothalamic-specific manipulation of *Fto*, the ortholog of the human obesity gene *FTO*, affects food intake in rats. *PLoS One* 2010;5:e8771.
74. Church C, Moir L, McMurray F, Girard C, Banks GT, Teboul L, Wells S, Bruning JC, Nolan PM, Ashcroft FM, et al. Overexpression of *Fto* leads to increased food intake and results in obesity. *Nat Genet* 2010;42:1086–92.
75. Karra E, O’Daly OG, Choudhury AI, Youssef A, Millership S, Neary MT, Scott WR, Chandarana K, Manning S, Hess ME, et al. A link between *FTO*, ghrelin, and impaired brain food-cue responsiveness. *J Clin Invest* 2013;123:3539–51.
76. Benedict C, Axelsson T, Soderberg S, Larsson A, Ingelsson E, Lind L, Schiöth HB. Fat mass and obesity-associated gene (*FTO*) is linked to higher plasma levels of the hunger hormone ghrelin and lower serum levels of the satiety hormone leptin in older adults. *Diabetes* 2014;63:3955–9.
77. Smemo S, Tena JJ, Kim KH, Gamazon ER, Sakabe NJ, Gomez-Marin C, Aneas I, Credidio FL, Sobreira DR, Wasserman NF, et al. Obesity-associated variants within *FTO* form long-range functional connections with *IRX3*. *Nature* 2014;507:371–5.