A genome-wide association study of 4862 subjects from the Wellcome Trust Case Control Consortium (United Kingdom) identified a common sequence variant in the FTO (fatso/fat mass and obesity associated) gene that predisposes its carriers to type 2 diabetes mellitus through an effect on body mass index (BMI). In the same article, the authors reported replication of the association between this variant and BMI in 13 cohorts with a total of 38,759 individuals. Associations of FTO with various obesity traits and insulin resistance/type 2 diabetes has since been replicated in numerous other studies. More recently, an association of FTO with obesity-related dyslipidemia has also been reported.

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The mechanisms through which FTO may increase the risk for obesity and obesity-related metabolic abnormalities are still not clear. The gene encodes 2-oxoglutarate-dependent nucleic-acid demethylase, which is highly expressed in the hypothalamus where it may regulate gene transcription. The hypothalamus is a brain structure involved in the regulation of energy homeostasis. Recent evidence suggests that the FTO-risk variant may promote the development of obesity by increasing energy intake, perhaps through its influence on appetite-regulating regions of the hypothalamus.
The hypothalamus, however, is also a powerful regulator of blood pressure (BP). The paraventricular and dorsomedial nuclei of the hypothalamus, which show particularly high FTO expression, are key modulators of sympathetic outflow to the circulatory system. Despite the known role of the hypothalamus in BP regulation, the role of FTO in BP and its regulation has not been studied.

The aim of this study was to investigate whether FTO is associated not only with increased adiposity, insulin resistance, and dyslipidemia, as shown previously in other populations, but also with increased BP and sympathetic modulation of vasomotor tone. This primary investigation was carried out in 485 adolescents recruited from a French Canadian population with a known founder effect in which fewer gene variants are expected to contribute to the determination of complex traits, such as BP and autonomic function. In addition, a replication study was carried out in an independent sample of 298 adults originating from 69 hypertensive families who were recruited from the same French Canadian founder population.

Methods

Study Populations

Adolescents

White adolescents (n=485), aged 12 to 18 years, were recruited from a population with a founder effect living in the Saguenay-Lac St Jean region of Quebec, Canada, as part of the Saguenay Youth Study. This is an ongoing investigation of the long-term consequences of prenatal exposure to maternal cigarette smoking on cardiovascular and metabolic health and on brain and behavior in adolescence. Recruitment and selection criteria have been described previously. In brief, all subjects are recruited via local high schools. At the time of analysis, ~5000 adolescents were informed about the Saguenay Youth Study at both school and home. All who were exposed prenatally to maternal cigarette smoking, were willing to participate and were free of any exclusion criteria were included in the study. The exclusion criteria were positive medical history of heart disease requiring surgery/medication, diabetes mellitus treated with insulin, meningitis, malignancy, severe mental illness (eg, autism, schizophrenia), mental retardation (intelligence quotient <70), or MRI contraindications. An equal number of willing and eligible nonexposed subjects, matched to the exposed ones by maternal education and the school attended, were also included. With this ascertainment, the investigated cohort is representative of the French Canadian adolescent population, except for the higher proportion of subjects exposed prenatally to maternal cigarette smoking (by design, 50% in our sample versus 25% in the general population) and, associated with this fact and the matching of the nonexposed subjects to the exposed ones by maternal education, overrepresentation of families with lower socioeconomic status. In addition, the Saguenay Youth Study is family based and focused primarily on recruitment of sib pairs. The cohort investigated here included 17 unrelated individuals, 188 sib pairs, 28 sibships of 3 siblings, and 2 sibships of 4 siblings.

Adults

An independent sample of white adults (n=298), aged 18 to 71 years, were recruited as members of 69 hypertensive families from the same French Canadian founder population as the earlier adolescent sample. The families were selected on the basis of having 2 age-matched sibships, and 2 sibships of 4 siblings.

French Canadian Founder Population

Importantly, for the genetic component of these studies, the Saguenay-Lac St Jean population is one of the largest population isolates in North America. It originates from ancestors of French descent who migrated to this region in the early 19th century. The population has experienced high intrinsic growth, from 5200 inhabitants in 1852 to 285 000 at present. Because of the founder effect, the prevalence of several recessive disorders is higher in the Saguenay-Lac St Jean region than in other populations, and limited allelic diversity exists among patients with these disorders.

Written consent of the parents and assent of the adolescents (adolescent sample) and subjects (adult sample) were obtained before the commencement of data collection. The Research Ethics Committee of the Chicoutimi Hospital approved the study protocols.

Quantitative Phenotyping

Adolescents

Body-Fat Quantity and Distribution

Measurements included height, weight, waist circumference, multi-frequency bioimpedance analysis to estimate total body-fat mass (Xitron Technologies Inc, San Diego, Calif), and MRI of the abdomen. A 10-mm thick axial T1-weighted image at the level of the umbilicus was segmented into intra-abdominal and subcutaneous fat, as described previously. Subjects were asked to refrain from caffeine, alcohol, and vigorous activity 24 hours before the measurements.

Biochemical Analyses

A fasting blood sample was drawn between 8:00 and 9:00 AM. Serum levels of glucose, insulin, triglycerides, total cholesterol, and high-density lipoprotein cholesterol were measured. We calculated the homeostasis model assessment (HOMA), an index of insulin resistance.

Cardiovascular Measurements

All subjects underwent a 52-minute cardiovascular protocol, conducted in a hospital setting on Saturdays between 8:00 AM and 12:00 PM. The protocol included a resting period, as well as changes in posture from supine to standing and from standing to sitting, and an arithmetic stress test. Throughout the protocol, a noninvasive hemodynamic monitor, Finometer (FMS Finnare, Amsterdam, The Netherlands), was used to record continuously the finger blood flow. The Finometer derives beat-to-beat brachial systolic BP (SBP) and DBP from the reconstructed and level-corrected finger blood-flow waveform.

Sympathetic Modulation of Vasomotor Tone

Power spectral analysis of DBP was used to estimate noninvasively the sympathetic modulation of vasomotor tone and systemic vascular resistance. The analysis was performed in 2-minute periods with 50% overlaps, using a sliding window routine, over the entire 52-minute protocol. For each period, beat-to-beat time series of DBP were interpolated using a piecewise cubic-spline method, resampled at a frequency of 5 Hz and detrended before being transformed by a 1024-point fast Fourier transform, using standard Matlab functions.
The rs9302652 genotype distribution in the adult cohort was follow-

ting the array that is closest to the

tests, respectively. Means of 2-minute LFDBP estimates during 7 different

sections, that is, supine (10 minutes), sitting (10 minutes), and

sitting (10 minutes) periods, and means of 2-minute LFDBP estimates
during prestress (5 minutes), stress-test explanation (2 minutes),
stress test (2 minutes), and stress-test recovery (10 minutes) periods

were used for statistical analyses of posture and arithmetic stress
tests, respectively.

**Questionnaires**
The subjects completed a questionnaire evaluating stages of pubertal
development.23 Parents completed questionnaires including informa-
tion on family income, which we used here as an index of

socioeconomic status.19

**Adults**

**Body-Fat Quantity**

Measurements included weight and height, and multifrequency

biompedance analysis to estimate total body-fat mass (Xitron

Technologies Inc).

**BP Measurements**

Outpatient measurements of BP were obtained with subjects seated

quietly for at least 10 minutes. Three measurements were obtained in

left arm, 2 minutes apart, with an automated BP monitor (Dinamap,

Johnson & Johnson Medical, Tampa, Fla). The recorded BP value is

an average of the 3 measurements. All personnel who measured BP

were trained and certified by use of the Shared Care method.28

**Genotyping**

**Adolescents**

A single-nucleotide polymorphism (SNP) in intron 1 of FTO

(rs9393609, T/A) with the minor A allele was genotyped using

KASPar. KASPar is a competitive allele specific PCR-based SNP

fluorescent genotyping system that uses fluorescence resonance

energy transfer quencher cassette oligos (KBioscience, Herts, United

Kingdom). The call rate was 98% and the SNP was in Hardy-Weinberg

equilibrium. The rs9393609 genotype distribution in the Saguenay

Youth Study cohort (AA, 12.2%; AT, 44.1%; and TT, 43.7%) was

similar to that reported in other population-based cohorts.1

**Adults**

A SNP in intron 3 of FTO (rs9302652, T/C) with the minor allele C

was genotyped using the GeneChip Human Mapping 50K Array

Xba240 (Affymetrix) at the Centre Hospitalier de l’Université de

Montréal Research Centre, Montreal.29 This FTO SNP is a SNP on

the array that is closest to the FTO SNP genotyped in adolescents.
The rs9302652 genotype distribution in the adult cohort was follow-

ing: CC, 9.7%; CT, 40.6%; and TT, 49.7%.

**Statistical Methods**

**Adolescents**

Descriptive statistics used to characterize the study population that

included means and SEs for continuous variables and proportions for
categorical variables. The main analyses focused on estimating

putative associations between the FTO-risk genotype (AA versus AT

or TT) and various outcomes. In all analyses, we relied on the

multivariable mixed linear model to (1) account for clustering of

observations within families (ie, for the correlations of the outcomes

between siblings), and (2) adjust for potential confounders. The

mixed linear model extends the conventional linear regression of

continuous outcomes to correlated data.30 In all our mixed-model

analyses, the family clustering was accounted for by adding random

intercepts, and the compound symmetry covariance structure of

residuals was assumed to represent the within-family correlations.31

In addition, the mixed linear model analyses of longitudinal data

handle well any randomly missing data, because of subjects’ failure

to complete some of the repeated outcome assessments.32 Finally, for
each outcome, a preliminary analysis involved assessing the normal-

ity assumption, on which the statistical inference about the mixed

linear model estimates relies. Then, the values of those outcomes for

which the empirical distribution showed substantial positive skew-

ness (ie, intraabdominal fat, subcutaneous abdominal fat, insulin,

HOMA, and triglycerides) were log transformed, using logarithm

with basis of 2.0. For each of the log-transformed outcomes, the

effected estimate of the FTO-risk genotype (AA versus AT or TT)

was converted into the adjusted relative increase in (percent),
calculated as (2^β−1)*100%, where β is the estimated regression

coefficient. Using the earlier general mixed-model approach, 2
different types of models were used for (a) single-valued outcomes

and (b) repeated-measures outcomes.

For each single-valued continuous outcome (measures of adiposity

and glucose and lipid metabolism), the multivariate mixed

model estimated the fixed effect of the FTO genotype, while

adjusting for the set of a priori selected covariates. Age, height

(except in the model where height was the dependent variable), and

family income were modeled as continuous covariates, and family

income was log transformed to account for its distribution being

highly skewed to the right. Puberty stage was represented by a set

of dummy variables, with the highest stage 5 as the reference category,

whereas sex and prenatal exposure to maternal smoking were

analyzed as binary variables. In addition, to assess to what extent the

effects of the FTO-risk genotype on selected outcomes may be

mediated through its effect on obesity, we repeated the analyses for

insulin, HOMA, and triglycerides, with an additional adjustment for

BMI. Finally, the analysis for intraabdominal fat was repeated with

an additional adjustment for subcutaneous abdominal fat to examine

whether the FTO-risk genotype predisposes to preferentially intra-

abdominal obesity.

The mixed-models analyses of repeated measures of SBP, DBP, and

LFDBP required a more complex approach. First, in addition to

accounting for sibling clustering within families, these analyses had

to account for the interdependence of repeated outcome measures

for the same subject. This was achieved by specifying the assessment

time as a repeated factor in the mixed model and assuming

autoregressive order 1 covariance structure of the within-subject

residuals, which implies that measurements that are closer in time

correlate more strongly.31

Second, analytic complexity was due to the fact that repeated

measures corresponded to different experimental conditions, so that

the resulting time series was composed of 7 different “sections”

(supine, standing, sitting, prestress, stress-test explanation, stress

test, and stress-test recovery). A priori considerations suggested that

the values of SBP, DBP, and LFDBP could systematically differ

between some sections. Therefore, the mixed models for each of the

3 repeated-overtime measures included the binary indicators of each

section, in addition to aforementioned subjects’ characteristics con-

sidered in the analyses of single-valued outcomes, as independent

variables. Finally, similar to selected single-valued outcomes (see

earlier), we repeated the analyses of SBP and LFDBP with an

additional adjustment for BMI to examine whether the effect of

the FTO-risk genotype on these outcomes is dependent on its

effect on obesity.

Furthermore, we considered a possibility that the putative effects

of the FTO-risk genotype might also differ among the 7 sections.

Therefore, in preliminary analyses of each repeated-measures out-

come, we have expanded the multivariable mixed model by includ-

ing a series of 2-way interactions between the FTO genotype and
each of the section indicators. Then, an “omnibus” Wald-like test, on

6 df, was used to test the significance of the joint effect of the 6

interaction terms. If the omnibus test yielded a 2-tailed

P value below 0.05, this was considered as an evidence of significant

differences between the section-specific effects of the FTO genotype

on a given outcome. In such a case, the final analyses of the

particular outcome were stratified by sections, using the same
general mixed-model approach, and separate adjusted effects of the
**Results**

**Descriptive Characteristics of the Adolescent Sample**

In this study, a total of 485 adolescents were included. Individuals with the FTO-risk genotype (AA genotype) compared with the rest of the cohort did not differ significantly in any of the potentially confounding variables, including the proportion of males and females, age, height, puberty stage, the proportion of subjects exposed prenatally to maternal cigarette smoking, and family income (Table 1).

**Single-Valued Outcomes in the Adolescent Sample**

Tables 2 and 3 summarize the results of multivariable mixed-model analyses of 12 single-valued outcomes of body-fat quantity and distribution and glucose and lipid metabolism. For each outcome, adjusted difference in mean values between subjects with AA (risk) genotype and those with AT or TT (nonrisk) genotypes is reported together with 95% CI and a 2-tailed $P$ value.

**Body-Fat Quantity and Distribution**

Even after accounting for family clustering and potentially confounding variables (sex, age, puberty stage, height, prenatal exposure to maternal cigarette smoking, and family income), subjects with the FTO-risk genotype when compared with the rest of the cohort demonstrated significantly higher body weight and BMI ($P<0.01$ for both). For these outcomes, the differences between the risk and nonrisk genotypes were clinically highly relevant, as body weight was higher by $>4$ kg and BMI by 1.5 kg/m$^2$. Subjects with the risk genotype also demonstrated higher fat mass (by 2.5 kg) and waist circumference (by 2.9 cm, $P<0.05$).

When assessing abdominal adiposity directly with MRI, the FTO-risk genotype was associated with higher amounts of both intra-abdominal fat (by 38%) and subcutaneous abdom-
inal fat (by 44%). Note that, because both outcomes were log transformed, these percent increases were calculated from the respective regression coefficients ($\beta$) shown in Tables 2 and 3, using the formula $(2^{\beta-1})\times100\%$; eg, for intra-abdominal fat: $(2^{0.46-1})\times100\%=(1.38$ to $1)^{100\%}=38\%$. The relationship between the $FTO$-risk genotype and intra-abdominal fat became completely nonsignificant after adjusting for subcutaneous abdominal fat, indicating that the relationships between $FTO$ and these 2 strongly correlated outcomes were quite similar.

### Glucose and Lipid Metabolism

Subjects with the $FTO$-risk genotype compared with the rest of the cohort showed similar plasma glucose levels but higher plasma levels of fasting insulin (by 21%, $P=0.007$) and HOMA index (by 21%, $P=0.008$; Table 3). In contrast, no statistically significant differences between the 2 groups were observed in plasma triglycerides, total cholesterol, and high-density lipoprotein cholesterol, although the variation in plasma triglycerides was in the predicted direction (ie, higher by 4% in individuals with the risk genotype; Table 3). Similar to previous studies, the differences in fasting insulin and HOMA index lost their significance after the additional adjustment for BMI ($P=0.09$ and 0.10, respectively), indicating that the association of the $FTO$-risk genotype with insulin resistance is mediated mostly through its effect on BMI, as suggested by others.1,6

### Repeated-Measure Outcomes in the Adolescent Sample

Table 4 summarizes the results of the multivariable mixed linear analyses of these 3 repeated-measure outcomes.

#### BP

Analyses of data pooled across all 7 sections of the protocol demonstrated that SBP is significantly higher (4.4 mm Hg, $P=0.0024$) in subjects with the $FTO$-risk genotype than in those with nonrisk genotypes (Table 4 and Figure 1). The omnibus test of interactions between sections and $FTO$, however, was statistically significant ($P=0.01$), indicating that the association between the $FTO$-risk genotype and SBP varies across specific experimental conditions implemented in different sections. Accordingly, Table 4 reports adjusted differences in SBP between subjects with the risk and nonrisk genotypes separately for each section. For all sections, the risk variant of $FTO$ was associated with higher SBP, and these differences were statistically significant ($P<0.05$) in almost all experimental conditions. The only exception was the section of stress-test explanation during which the difference was only 2.5 mm Hg and was statistically nonsignificant ($P=0.22$). For most other sections (and experimental conditions), adjusted mean SBP differences between subjects with and without the $FTO$-risk genotype varied between 4 and 5 mm Hg, but for the section of the stress-test, the difference reached 6.4 mm Hg (Figure 1).

### Table 3. Glucose and Lipid Metabolism in Adolescents

<table>
<thead>
<tr>
<th></th>
<th>AA (n=59)</th>
<th>AT (n=214)</th>
<th>TT (n=212)</th>
<th>Difference (95% CI) for AA vs AT or TT*</th>
<th>$P$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Glucose, mmol/L</td>
<td>4.77 (0.05)</td>
<td>4.72 (0.03)</td>
<td>4.69 (0.03)</td>
<td>0.07 (−0.05 to 0.19)</td>
<td>0.26</td>
</tr>
<tr>
<td>Insulin, pmol/L</td>
<td>90.8 (4.6)</td>
<td>75.6 (2.4)</td>
<td>73.2 (2.4)</td>
<td>0.27 (0.07 to 0.46)†</td>
<td>0.007</td>
</tr>
<tr>
<td>HOMA index</td>
<td>2.79 (0.20)</td>
<td>2.39 (0.10)</td>
<td>2.23 (0.10)</td>
<td>0.28 (0.07 to 0.49)†</td>
<td>0.008</td>
</tr>
<tr>
<td>Triglycerides, mmol/L</td>
<td>1.11 (0.05)</td>
<td>1.02 (0.03)</td>
<td>0.99 (0.03)</td>
<td>0.06 (−0.11 to 0.23)†</td>
<td>0.48</td>
</tr>
<tr>
<td>HDL, mmol/L</td>
<td>1.48 (0.04)</td>
<td>1.46 (0.02)</td>
<td>1.47 (0.02)</td>
<td>0.01 (−0.07 to 0.10)</td>
<td>0.74</td>
</tr>
<tr>
<td>Cholesterol, mmol/L</td>
<td>4.18 (0.10)</td>
<td>4.22 (0.05)</td>
<td>4.18 (0.05)</td>
<td>−0.03 (−0.27 to 0.20)</td>
<td>0.78</td>
</tr>
</tbody>
</table>

Data are shown as unadjusted means (SEs). HDL indicates high-density lipoprotein.

*Estimated differences (95% CI and $P$ values) between AA homozygotes and both AT heterozygotes and TT homozygotes were tested with mixed-model regression analyses, adjusting for family clustering and potentially confounding variables (proportion of males and females, age, height, puberty stage, family income, and prenatal exposure to maternal cigarette smoking).

†The difference between AA homozygotes and both AT heterozygotes and TT homozygotes was estimated for a log-transformed value.
Table 4. BP (SBP and DBP) and an Index of Sympathetic Vasomotor Tone (LF\textsubscript{DBP}) in Adolescents

<table>
<thead>
<tr>
<th>Repeated-Measure Outcome</th>
<th>Difference (95% CI) for AA vs AT or TT, mm Hg</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>SBP, entire protocol</td>
<td>4.4 (1.6 to 7.2)</td>
<td>0.002</td>
</tr>
<tr>
<td>SBP, supine section</td>
<td>4.1 (1.0 to 7.2)</td>
<td>0.01</td>
</tr>
<tr>
<td>SBP, standing section</td>
<td>4.0 (0.2 to 7.6)</td>
<td>0.03</td>
</tr>
<tr>
<td>SBP, sitting section</td>
<td>4.6 (1.0 to 8.1)</td>
<td>0.01</td>
</tr>
<tr>
<td>SBP, pre-stress section</td>
<td>4.2 (0.6 to 7.9)</td>
<td>0.02</td>
</tr>
<tr>
<td>SBP, stress-test expl section</td>
<td>2.5 (1.5 to 6.4)</td>
<td>0.22</td>
</tr>
<tr>
<td>SBP, stress-test section</td>
<td>6.4 (1.5 to 11.3)</td>
<td>0.01</td>
</tr>
<tr>
<td>SBP, stress-test recovery section</td>
<td>4.9 (1.2 to 8.6)</td>
<td>0.009</td>
</tr>
<tr>
<td>DBP, entire protocol</td>
<td>1.2 (0.8 to 3.2)</td>
<td>0.23</td>
</tr>
<tr>
<td>LF\textsubscript{DBP}, entire protocol, mm Hg\textsuperscript{2}</td>
<td>632 (332 to 931)</td>
<td>&lt; 0.0001</td>
</tr>
</tbody>
</table>

\textsuperscript{*}Estimated differences (95% CI) between AA homozygotes and both AT heterozygotes and TT homozygotes were tested with mixed-model regression analyses, adjusting for family clustering and potentially confounding variables (proportion of males and females, age, height, puberty stage, family income, and prenatal exposure to maternal cigarette smoking). For these analyses, we used all 52 one-minute means of SBP and DBP and all 7 section means of LF\textsubscript{DBP}.

In contrast to SBP, the interaction between different sections of BP time series and the \textit{FTO}-risk genotype was nonsignificant (P = 0.47), indicating that the \textit{FTO} effect on DBP was similar across all 7 experimental conditions. Although there was also a trend for a higher DBP in adolescents with the risk variant, the overall adjusted difference between subjects with and without the variant, estimated by pooling data from all 7 sections was 1.22 mm Hg and did not reach statistical significance (P = 0.23, Figure 1).

**Sympathetic Modulation of Vasomotor Tone**

The interaction among different sections of the protocol and the \textit{FTO}-risk genotype was completely nonsignificant for LF\textsubscript{DBP} (P = 0.86), indicating that the \textit{FTO} effect was similar across all experimental conditions implemented in our protocol. Therefore, we estimated the overall adjusted difference between subjects with and without the risk genotype by pooling data from all the 7 sections. These analyses showed that the risk variant of \textit{FTO} is associated with a mean LF\textsubscript{DBP} increase of \(\approx632 \text{ mm Hg}^2\) and that this difference is statistically highly significant even after adjusting for family clustering and potentially confounding variables (P < 0.0001, Figure 2).

Analyses with additional adjustment for BMI demonstrated that, for LF\textsubscript{DBP}, the adjusted difference between adolescents with and without the \textit{FTO}-risk genotype remained essentially unchanged (637.2 mm Hg\textsuperscript{2}) and highly significant (P < 0.0001). Although the adjustment for BMI reduced the mean difference in SBP to \(\approx3.7 \text{ mm Hg}\), it remained significant (P = 0.01).

**Descriptive Characteristics of the Adult Sample**

**Body-Fat Quantity**

Adults with the rs9302652 genotypes did not statistically significantly differ by sex, age, or height (Table 5).

**Single-Valued Outcomes in the Adult Sample**

**Body-Fat Mass**

Adults with CC or CT genotypes when compared with adults who have TT genotype demonstrated higher body weight, body-fat mass, and BMI, even after adjusting for family clustering and potential confounders (sex, age, and height [not included in case of BMI]). The differences among genotypes were clinically relevant (body weight was higher by 3.8 kg, BMI by 1.3 kg/m\textsuperscript{2}, and fat mass by 2.7 kg) and marginally significant, with 0.01 < P < 0.05 (Table 5).

**BP**

Analyses of sitting BP showed statistically significant associations between \textit{FTO} and BP. Specifically, SBP and DBP were higher in adults with CC or CT genotype than those with TT genotype by 7.5 (P = 0.0008) and 3.5 mm Hg (P = 0.01), respectively (Table 5). Similar to adolescents, analyses with additional adjustment for BMI reduced modestly the differences in SBP and DBP to 6.2 (P = 0.003) and 2.9 mm Hg (P = 0.03), respectively. Finally, 86 of 298 individuals were treated with antihypertensive medication during the time of BP measurement. When these individuals were excluded, the differences in SBP and DBP remained significant (6.1 [P = 0.01] and 3.0 mm Hg [P = 0.04], respectively).

**Hypertension**

Consistent with the quantitative analyses of BP, Generalized Estimating Equations analysis examining the proportion of individuals with hypertension, while adjusting for family clustering and potential confounders (age and sex), showed that the disease is more frequent among individuals with CC or CT genotype than among individuals with TT genotype (odds ratio, 1.9 [1.0 to 3.7], P < 0.05; Table 5).

**Discussion**

The results of this study suggest that, in a French Canadian population isolate, \textit{FTO} increases not only the risk for obesity and insulin resistance, as demonstrated previously in other populations, but also for hypertension. The results also suggest that the latter may be related, at least in part, to higher sympathetic modulation of vasomotor tone associated with this genotype. As such, the current study has a 2-fold outcome: (1) it replicates the \textit{FTO} associations with adiposity and insulin resistance, and (2) it identifies novel \textit{FTO} associations with increased BP and sympathetic vasomotor tone; the latter may be a mechanism that contributes to BP elevation. Because \textit{FTO} association with BP was identified in an adolescent sample (age, 12 to 18 years) and confirmed in an independent adult sample (age, 18 to 71 years), suggests a possibility that individuals at risk for hypertension may be recognized early during development of the disease.

The relationships that we observed between \textit{FTO} and adiposity measures were similar or even more pronounced than those reported previously in a study of close to 40,000 participants.\textsuperscript{1} There, the authors estimated that adult homozygotes of the risk allele weigh \(\approx3\) kg more (4% of body weight in a 75-kg individual) than homozygotes of the nonrisk allele.\textsuperscript{1} In the current study assessed in adolescence and thus earlier during progression of obesity, this difference was already \(>4\) kg (7% of body weight in a 57-kg adolescent).

To the best of our knowledge, the current study is the first to evaluate the relationship of \textit{FTO} with abdominal adiposity measured directly with MRI. These analyses showed that, although the risk genotype compared with the nonrisk geno-
types is associated with a greater amount of intra-abdominal fat (by 38%) the difference is proportionally similar to that in the amount of subcutaneous-abdominal fat, suggesting that the FTO-risk genotype predisposes to general (whole body) rather than preferentially intra-abdominal obesity. This finding supports previous observations made with DEXA.9

In this study, we identified novel associations between the FTO-risk genotype and both increased BP and LFDBP, an index of sympathetic modulation of vasomotor tone. SBP was higher in carriers of the risk genotype compared with the rest of the cohort throughout the protocol, with the difference reaching 6 mm Hg during an arithmetic stress test. Like-wise, LFDBP was higher throughout most of the protocol, suggesting that the FTO-risk allele may increase BP via its influence on sympathetic vasomotor tone. Interestingly, unlike obesity-related insulin resistance, associations between FTO and both BP and the index of sympathetic vasomotor tone seem to be independent of the association between FTO and adiposity. Our analyses demonstrated that additional adjustment for BMI did not alter the difference between subjects with and without the FTO-risk genotype for the index of sympathetic modulation of vasomotor tone, and for SBP, it reduced the difference from 4.4 to 3.7 mm Hg, which remained significant. These results suggest that FTO may influence adiposity and BP/sympathetic vasomotor tone independently.

Importantly, we replicated the novel association between FTO and BP observed in adolescents in an independent sample of adults recruited from the same French Canadian founder population.18 In that sample, we showed that SBP and DBP were higher in individuals with the FTO CC/CT versus TT genotype by 7.5 and 3.5 mm Hg, respectively. Consistent with these BP differences, we also showed that the CC/CT- versus TT-genotype individuals are more likely to have hypertension (odds ratio, 1.9 [1.0 to 3.7]). Moreover, as in the adolescent sample, additional adjustment for BMI made a minimal impact on the BP differences between the genotypes, thus providing further support for the possibility
that FTO may influence BP and adiposity independently. Although FTO as such has not been investigated previously in the relationship to BP, it is of note that a genome-wide linkage study carried out previously identified a region of chromosome 16 including FTO as a region of suggestive linkage to BP.18

Indirect evidence exists suggesting that FTO may be involved in the regulation of sympathetic vasomotor tone. Thus, sympathetic vasomotor tone is powerfully modulated by the paraventricular and dorsomedial nuclei of the hypothalamus,14,35 which are 2 regions of the hypothalamus that showed particularly high FTO expression.10 The paraventricular nucleus of the hypothalamus is thought to exert tonic influences under basal conditions,36 whereas the dorsomedial nucleus of the hypothalamus is mainly involved in the regulation of phasic responses during stress.14,35 FTO encodes 2-oxoglutarate-dependent nucleic acid demethylase that is evolutionarily highly conserved, indicating its biological importance.37 Throughout the body, the highest expression of the gene was detected in the brain and, within the brain, in the hypothalamus.10 It has been proposed that the FTO demethylase may regulate gene transcription in the regions of high expression. This may involve not only genes of energy homeostasis, as suggested previously,10 but also genes of sympathetic modulation of vasomotor tone. This, however, requires further studies in experimental animals.

In the adolescent sample, we used Finometer to measure BP. In the past, precision of SBP measurements with this device exceeded the limits recommended by the American Association for the Advancement of Medical Instruments.38,39 But, more recently, the precision of SBP measurements has improved by the implementation of waveform filtering, level correction, and return-to-flow calibration, and it now meets the Association for the Advancement of Medical Instruments requirements.40,41

Table 5. Descriptive Characteristics, Body-Fat Quantity, and BP in the Adult Sample

<table>
<thead>
<tr>
<th>Description</th>
<th>CC (n=29)</th>
<th>CT (n=121)</th>
<th>TT (n=148)</th>
<th>Difference (95% CI) for CC or CT vs TT*</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Male/female</td>
<td>17/12</td>
<td>48/73</td>
<td>78/70</td>
<td>2.6†</td>
<td>0.11</td>
</tr>
<tr>
<td>Age, y</td>
<td>42.3 (2.2)</td>
<td>42.0 (1.1)</td>
<td>44.3 (1.0)</td>
<td>−2.2 (−5.3 to 0.9)</td>
<td>0.16</td>
</tr>
<tr>
<td>Height, cm</td>
<td>166.7 (1.9)</td>
<td>164.4 (0.9)</td>
<td>167.6 (0.8)</td>
<td>−0.9 (−3.3 to −1.6)</td>
<td>0.48</td>
</tr>
<tr>
<td>Outcome variables</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Weight, kg</td>
<td>73.4 (3.2)</td>
<td>74.4 (1.5)</td>
<td>73.8 (1.4)</td>
<td>3.8 (0.4 to 7.2)</td>
<td>0.03</td>
</tr>
<tr>
<td>Body mass index, kg/m²</td>
<td>26.4 (0.9)</td>
<td>27.3 (0.4)</td>
<td>26.1 (0.4)</td>
<td>1.3 (0.1 to 2.5)</td>
<td>0.04</td>
</tr>
<tr>
<td>Fat mass, kg</td>
<td>20.2 (1.8)</td>
<td>22.2 (0.9)</td>
<td>19.9 (0.8)</td>
<td>2.7 (0.4 to 5.0)</td>
<td>0.02</td>
</tr>
<tr>
<td>SBP, mm Hg</td>
<td>129.6 (3.3)</td>
<td>130.2 (1.6)</td>
<td>123.0 (1.5)</td>
<td>7.5 (3.5 to 11.5)</td>
<td>0.008</td>
</tr>
<tr>
<td>DBP, mm Hg</td>
<td>85.8 (2.1)</td>
<td>83.8 (1.0)</td>
<td>81.4 (0.9)</td>
<td>3.5 (0.9 to 6.1)</td>
<td>0.01</td>
</tr>
<tr>
<td>Hypertension, yes/no</td>
<td>21/8</td>
<td>60/61</td>
<td>58/90</td>
<td>1.9 (1.0 to 3.7)‡</td>
<td>0.049</td>
</tr>
</tbody>
</table>

Data are shown as unadjusted mean (SE).
*Estimated differences (95% CI and P values) between CC homozygotes or CT heterozygotes and TT homozygotes were tested with mixed-model regression analyses, adjusting for family clustering and potential confounders (sex, age, and, when appropriate, weight and fat mass) height.
†Analyzed with χ² statistic.
‡Analyzed with generalized estimating equations to account for the family clustering and potential confounders (age and sex), with odds ratio (95% CI) presented. Office SBP and DBP measurements were obtained while subjects were seated quietly for at least 10 minutes.
A potential limitation of the current study is our use of BP variability as an indirect measure of sympathetic vasomotor tone. Direct measures, such as muscle sympathetic nerve activity, are not suitable for population-based studies of adolescents. Importantly, cardiovascular variability has been validated against this method.24–26

Finally, we have tested the effect of the FTO-risk genotype on several outcomes and, thus, we have to deal with possible inflation of type I error because of multiple testing. Specifically, in both the original and replication studies, we have carried out 19 tests for different single-valued outcomes, 3 tests for the main effects on each of the repeated-measures outcomes, 3 tests of the interactions between the FTO genotype and sections, and 7 tests of section-specific effects of the FTO genotype. With a total of 32 tests, we would expect 1 to 2 statistically significant effects at $P<0.05$ because of chance alone and not $>1$ result with $P<0.01$. In contrast, our analyses yielded $P<0.05$ for 24 of the total of 32 tests, and among the 24 with $P<0.05$, 11 tests showed $P<0.01$. This clearly indicates that most statistically significant results reported in this study represents true rather than spurious effects of the FTO genotypes that would be the result of a sampling error or multiple testing. The replication of the main finding, ie, an association between BP and FTO, in an independent (adult) sample supports further the true nature of our observations.

In summary, the current results suggest that, in a French Canadian population isolate, the FTO increases not only risk for obesity and insulin resistance, as demonstrated previously in other populations, but also for hypertension. The results also suggest that the latter may be related, at least in part, to higher sympathetic modulation of vasomotor tone associated with this genotype. As such, the current study replicated the FTO association with adiposity and insulin resistance reported previously, and identified a novel association of the gene with BP and a potential underlying mechanism. The FTO association with BP was identified in an adolescent sample and confirmed in an independent adult sample, indicating that individuals at risk for hypertension may be recognized early during development of the disease when preventive measures may still be effective. We believe that the current study illustrates the value of genetic studies that focus on extensive, detailed phenotyping carried out in populations characterized by genetic and environmental homogeneity.

Acknowledgments
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Disclosures
None.

References

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CLINICAL PERSPECTIVE

**FTO and Hypertension**

**FTO** is one of several genes associated with common forms of obesity. The gene is highly expressed in the hypothalamus, where it is thought to mediate this effect through its influence on appetite-regulating regions. The hypothalamus, however, is also a powerful regulator of sympathetic outflow to the circulatory system and maintenance of blood pressure (BP).

Consistent with possible influence of **FTO** on both adiposity and BP, the results of this study carried out in a French Canadian founder population suggest that **FTO** may increase not only likelihood of developing obesity, as demonstrated previously in other populations, but also hypertension. The results also suggest that **FTO** may influence BP and adiposity independently and that the **FTO** influence on BP may be mediated, at least in part, by its association with sympathetic tone.

**FTO** is an ancient, up-regulated during food deprivation and expressed in neurons of feeding-related nuclei of the brain, indicating a role in the control of energy balance. Comparison with analysis of intra-arterial recordings. **J Hypertens**. 1993;22:26–33.


**Pausova et al**
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