Association of Morbid Obesity With FTO and INSIG2 Allelic Variants

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Objective: To determine whether 2 single nucleotide polymorphisms (SNPs) in the obesity genes the fat mass and obesity associated gene (FTO) and the insulin induced gene 2 (INSIG2) are associated with class III, or morbid, obesity in patients undergoing bariatric weight loss operations.

Results: The mean BMI in the predominantly white female cohort was 51.2. Approximately 21% of patients were homozygous for the FTO obesity SNP variant, 13% were homozygous for the INSIG2 obesity SNP variant, and 3.4% were homozygous for both. Mean BMIs in the groups homozygous for each of these genes were not significantly different from nonhomozygotes. However, FTO/INSIG2 double homozygotes and homozygote/heterozygote pairs had significantly higher BMIs than the other groups.

Conclusion: Increased BMI in morbid obesity is associated with a combination of FTO and INSIG2 SNPs.

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produced in a variety of populations, whereas this association has not been found in others.10

A second SNP associated with BMI, rs9939609, is found within the fat mass and obesity associated gene (FTO). The FTO SNP was first identified in a genome-wide association study of patients with type 2 diabetes.11 However, subsequent analysis indicated that the FTO variant was actually associated with increased BMI, suggesting that the original relationship found between the FTO SNP and type 2 diabetes risk was mediated through BMI. Independent data reported for other SNPs within FTO in patients with morbid obesity and pediatric obesity corroborated the link to BMI.12

As an initial step in understanding potential genetic influences in patients undergoing bariatric surgery, the association of FTO and INSIG2 SNPs with BMI was determined in a large cohort of morbidly obese patients enrolled in a bariatric surgery program. Because of the role of INSIG2 in lipid and cholesterol metabolism, the effect of the 2 obesity genes on blood-lipid parameters was also analyzed.

METHODS

PATIENTS

Patients undergoing open or laparoscopic Roux-en-Y gastric bypass operations or laparoscopic adjustable gastric banding procedures for morbid obesity or its comorbid medical problems at Geisinger Medical Center, Danville, Pennsylvania, were enrolled in a clinical research program on obesity and metabolic syndrome. All patients undergoing bariatric operations at Geisinger Medical Center are required to participate in a standardized multidisciplinary preoperative program, which includes obtaining standardized clinical and laboratory data at designated times. An accurately measured BMI is obtained at the first visit at the weight management clinic. Blood samples for DNA and lipid measures were obtained approximately 3 weeks before the date of operation. Total cholesterol, high-density lipoprotein cholesterol, low-density lipoprotein cholesterol (calculated), triglyceride levels, and the cholesterol to high-density lipoprotein ratio were also measured using standard clinical laboratory techniques. The institutional review board at the Geisinger Medical Clinic approved the research protocol and all participants provided written informed consent.

DATA ACQUISITION

Demographic, BMI, and laboratory data were obtained through an electronic search of EpicCare electronic medical records (Epic Systems, Verona, Wisconsin). The electronic medical record data were imported into SAS/STAT software (SAS Institute Inc, Cary, North Carolina) and were mapped to predefined fields. The resulting data were available for statistical analysis in SAS or for export into other software applications.

DNA ISOLATION

DNA was extracted from 0.35 mL of EDTA-anticoagulated whole blood using the Qiagen MagAttract DNA Blood Midi M48 Kit and Qiagen BioRobot M48 Workstation (Qiagen, Valencia, California) according to the manufacturer’s directions. The final elution volume was 200 µL. For a few patients, blood was not available, so DNA was extracted from fixed liver tissue. Livers were first treated with proteinase K (1 µg/µL) in 350 µL of Qiagen Tissue Lysis Buffer (Qiagen) and incubated at 55°C overnight. Following digestion, samples were loaded onto the Qiagen BioRobot M48 Workstation and DNA was extracted, as described for blood samples. Quantification of extracted DNA was performed using a NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies, Wilmington, Delaware).

GENOTYPE ANALYSIS

Single nucleotide polymorphism genotyping was performed on an Applied Biosystems 7500 Real-Time Polymerase Chain Reaction System (Applied Biosystems, Foster City, California). Assay reagents for each SNP were obtained from Applied Biosystems (FTO rs9939609, assay C__30090620_10; INSIG2 rs7566605, assay C__29404113_20). DNA was genotyped according to the manufacturer’s protocol. Briefly, the components for each genotyping reaction were as follows: 10 ng of DNA, 5 µL of TaqMan Genotyping Master Mix (Applied Biosystems), 0.25 µL of assay mix (40×), and water up to a total volume of 10 µL. The thermocycler conditions were as follows: 50°C for 2 minutes, 95°C for 10 minutes, and 40 cycles at 95°C for 15 seconds and at 60°C for 60 seconds. The reaction was then analyzed using Applied Biosystems Sequence Detection Software.

STATISTICAL ANALYSIS

Deviation from Hardy-Weinberg equilibrium was tested with the HelixTree software package (Golden Helix, Bozeman, Montana). The HelixTree application was used to determine differences in genotype and allele frequencies to examine the association of SNPs with BMI and laboratory results. Multiple testing corrections were performed using simulations and the Bonferroni method. Significant association was considered likely for a Bonferroni-corrected P < .05.

RESULTS

PATIENT CHARACTERISTICS

The mean age of the patient cohort was 45.9 years, with a mean BMI of 51.2 (Table 1). More than 97% of the patients had white European ancestry, representative of the geographic area, and 81% were women. Mean lipid measurements were as follows: triglyceride level, 177.6 mg/dL (2.01 mmol/L); total cholesterol, 188.8 mg/dL (4.89 mmol/L); high-density lipoprotein cholesterol, 48.1 mg/dL (1.25 mmol/L); total cholesterol to HDL cholesterol ratio, 4.1; and calculated low-density lipoprotein, 106.2 mg/dL (2.75 mmol/L). The distribution of BMI measurements is shown in the Figure. Almost 4% of the population had BMIs higher than 70.

GENOTYPES

A total of 707 DNA samples were genotyped for the FTO (rs9939609) and INSIG2 (rs7566605) SNPs (Table 2). Genotyping consisted of analyzing the DNA from each patient to determine whether he or she carried the A and/or T sequences in FTO and the G and/or C sequences near INSIG2. The FTO A SNP and the INSIG2 C SNP are considered the obesity SNPs. The frequencies of the INSIG2 and FTO SNPs in...
this population are presented in Table 2 and concur with previous studies.12,13

To determine whether the population was genetically skewed through inbreeding or strong founder effects, a statistical test for Hardy-Weinberg equilibrium was performed. Both SNPs were found to be well within Hardy-Weinberg equilibrium (FTO, \( P > .44 \); INSIG2, \( P > .29 \)). Our frequency of SNP sequences is thus consistent with an out-bred, mixed, white European population.

The diploid SNP sequences, or genotypes (ie, AA, AT, and TT for FTO and CC, GC, and GG for INSIG2), of each patient for each gene were also analyzed (Table 3). The homozygous genotype AA in FTO was present in approximately 21% of the population and the homozygous genotype CC in INSIG2 was present in approximately 13%, consistent with previous studies.12,13 These 2 homozygous genotypes are considered the high-obesity risk genotypes. The heterozygous AT and GC genotypes were found in 48% and 44% of the study population, respectively. The homozygous low-obesity risk genotype for FTO (TT) was found in 31% of the population and the low-obesity risk genotype (GG) for INSIG2 was present in 43%.

ASSOCIATION OF BMI WITH SNPs

The relationship of BMI with the INSIG2 and FTO obesity SNP genotypes was analyzed using the HelixTree Genetics Analysis Software (Golden Helix). With this program, data are analyzed by minimizing the sum of squared deviations of each group mean from the remainder of the observations. An \( F \) test was used to generate an unadjusted \( P \) value; an adjusted \( P \) value was calculated by curve-fitting thousands of simulations; and a Bonferroni correction for multiple comparisons of the adjusted \( P \) value

Table 1. Characteristics of Patients Undergoing Roux-en-Y Gastric Bypass

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Body mass index(^a,b)</td>
<td></td>
</tr>
<tr>
<td>Mean (SD)</td>
<td>51.2 (8.5)</td>
</tr>
<tr>
<td>Median (range)</td>
<td>49.5 (40-88.4)</td>
</tr>
<tr>
<td>Triglycerides, mg/dL(^c)</td>
<td></td>
</tr>
<tr>
<td>Mean (SD)</td>
<td>177.6 (105.3)</td>
</tr>
<tr>
<td>Median (range)</td>
<td>153 (36-908)</td>
</tr>
<tr>
<td>Total cholesterol, mg/dL(^c)</td>
<td></td>
</tr>
<tr>
<td>Mean (SD)</td>
<td>188.8 (38.7)</td>
</tr>
<tr>
<td>Median (range)</td>
<td>184 (70-309)</td>
</tr>
<tr>
<td>HDL cholesterol, mg/dL(^c)</td>
<td></td>
</tr>
<tr>
<td>Mean (SD)</td>
<td>48.1 (11.3)</td>
</tr>
<tr>
<td>Median (range)</td>
<td>47 (22-103)</td>
</tr>
<tr>
<td>Total cholesterol to HDL cholesterol ratio(^c)</td>
<td></td>
</tr>
<tr>
<td>Mean (SD)</td>
<td>4.1 (1.1)</td>
</tr>
<tr>
<td>Median (range)</td>
<td>4 (1.5-7.8)</td>
</tr>
<tr>
<td>LDL cholesterol, mg/dL(^d)</td>
<td></td>
</tr>
<tr>
<td>Mean (SD)</td>
<td>106.2 (34)</td>
</tr>
<tr>
<td>Median</td>
<td>102 (5-226)</td>
</tr>
<tr>
<td>Age, y(^b)</td>
<td></td>
</tr>
<tr>
<td>Mean (SD)</td>
<td>45.9 (11.2)</td>
</tr>
<tr>
<td>Median (range)</td>
<td>46.6 (18.6-72.2)</td>
</tr>
</tbody>
</table>

Abbreviations: HDL, high-density lipoprotein; LDL, low-density lipoprotein. SI conversion factors: To convert HDL, LDL, and total cholesterol to millimoles per liter, multiply by 0.0259; triglycerides to millimoles per liter, multiply by 0.0113.

\(^a\)Calculated as weight in kilograms divided by height in meters squared.

\(^b\)N = 707.

\(^c\)n = 679.

\(^d\)n = 661.

Table 2. Frequencies of FTO and INSIG2 Alleles in Morbidly Obese Patients

<table>
<thead>
<tr>
<th>Allele</th>
<th>No. of Alleles</th>
<th>Allele Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>638</td>
<td>0.45</td>
</tr>
<tr>
<td>T</td>
<td>776</td>
<td>0.55</td>
</tr>
<tr>
<td>C</td>
<td>495</td>
<td>0.35</td>
</tr>
<tr>
<td>G</td>
<td>919</td>
<td>0.65</td>
</tr>
</tbody>
</table>

Abbreviations: FTO, fat mass and obesity associated gene; INSIG2, insulin induced gene 2.

Table 3. Frequencies of FTO and INSIG2 Genotypes in Morbidly Obese Patients

<table>
<thead>
<tr>
<th>Genotype</th>
<th>No. of Genotypes</th>
<th>Genotype Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>AA</td>
<td>149</td>
<td>0.21</td>
</tr>
<tr>
<td>AT</td>
<td>340</td>
<td>0.48</td>
</tr>
<tr>
<td>TT</td>
<td>218</td>
<td>0.31</td>
</tr>
<tr>
<td>CC</td>
<td>93</td>
<td>0.13</td>
</tr>
<tr>
<td>CG</td>
<td>309</td>
<td>0.44</td>
</tr>
<tr>
<td>GG</td>
<td>305</td>
<td>0.43</td>
</tr>
</tbody>
</table>

Abbreviations: FTO, fat mass and obesity associated gene; INSIG2, insulin induced gene 2.

Figure. Histogram of body mass index (calculated as weight in kilograms divided by height in meters squared) in morbidly obese patients.
was also calculated. A conservative threshold of <.05 was used for this Bonferroni-corrected P value.

The initial analysis was performed using BMI and the individual FTO and INSIG2 SNP genotypes. Although the mean BMIs increased by approximately 2 kg/m² in FTO and INSIG2 obesity genotypes (Table 4), they were not statistically different (Table 5). With a less stringent statistical threshold (not Bonferroni corrected), the BMIs of the 3 FTO genotypes were found to be significantly different (P < .03). No significant association was found between the FTO or INSIG2 genotypes and any of the lipid parameters (P > .10).

When both the FTO and the INSIG2 genotypes of each patient were considered together as a compound genotype (ie, AA/CC, AA/GC, AA/GG, AT/CC, AT/GC, AT/ GG, AA/CC, AA/GC, and AA/GG), patients who were double homozygotes for the obesity-risk alleles (AA/CC) were found to have significantly higher BMIs (P < .01, Bonferroni corrected). Those who were FTO homozygous and INSIG2 heterozygous (AA/GC) or FTO heterozygous and INSIG2 homozygous (AT/CC) for obesity also had significantly higher BMIs. No significant association was found between the compound FTO/INSIG2 genotypes and any of the lipid parameters (P > .10).

An interesting pattern in mean BMI was found in the compound groups (Table 6). The mean BMI was about 4 kg/m² higher in the group homozygous for the obesity-risk genotypes (AA/CC) and was about 3 kg/m² higher in the homozygous/heterozygous (AA/GC) and the heterozygous/homozygous (AT/CC) groups compared with the other compound genotype groups. This is consistent with the contribution of an approximately 1 kg/m² increase in BMI for each copy of the FTO A and INSIG2 C obesity sequences in these groups. The association of at least 2 copies of 1 obesity SNP and at least 1 copy of the other with increased BMI also suggests some degree of interaction between FTO and INSIG2. However, biological factors appear to influence the observed data, because the group homozygous for normal weight/obesity (TT/CC, respectively) was approximately 2 kg/m² lower than the group homozygous for obesity/normal weight (AA/GG, respectively) and about 6 kg/m² lower than the group homozygous for obesity (AA/CC).

Obesity is a multifactorial condition, with substantial evidence supporting a strong genetic component. Such genetic factors may influence therapies, including bariatric surgery; thus, their identification may be important in guiding treatment. Mutations in several genes have been found to be responsible for rare familial monogenic forms of obesity, and a large number of genes have been analyzed in common sporadic multicentric obesity. However, many studies of genes in common obesity have not been replicated across different populations.

The 2 obesity gene variants studied here, rs9939609 (FTO) and rs7566605 (INSIG2), have previously been replicated in multiple, but not all, studies. For example, the INSIG2 variant was first replicated in 4 separate cohorts composed of individuals with Western European ancestry, African American individuals, and children, but later, it was found to have both negative and positive associations in genetic analyses of several thousand in-
obesity risk determined here. These results indicate that sporadic morbid obesity is likely to be influenced by other, unidentified genes, which were not addressed in the predominantly white female population studied here. The prevalence of morbid obesity is higher in women than in men and in individuals of African ancestry compared with white or Hispanic individuals, with the lowest prevalence in Asian persons. Two of the studies that found no association of BMI with the INSIG2 genotype were conducted in patients with primarily African ancestry. Data from the International HapMap Project indicate that the high-obesity risk INSIG2 CC genotype was present at a higher frequency in the Japanese and Han Chinese populations analyzed than in the European and African groups. In contrast, the high-obesity risk FTO AA genotype was present at a lower frequency in the 2 Asian populations compared with the European and African groups. These data suggest that the effects of the 2 obesity SNPs may not be similar in all racial groups and that further studies will be needed to address other populations.

A limitation of association studies is that potential causative mechanisms cannot be identified, thus the potential pathophysiological role(s) of the FTO and INSIG2 genes in morbid obesity are not known; INSIG2 codes for an endoplasmic reticulum protein that regulates the movement of sterol regulatory element, binding proteins to the Golgi apparatus and regulating the synthesis of fatty acid and cholesterol. Overexpression of INSIG2 in the liver of rats reduced plasma triglyceride levels. Despite this clear involvement in lipid metabolism, no association between common lipid parameters and the INSIG2 (or FTO) SNPs was found here. However, medication use was not accounted for in the analysis, thus the effects of lipid-lowering agents may have affected the phenotype of those genetically predisposed to dyslipidemia. The function of the protein product of FTO has not yet been elucidated. Mice with the Fto syntenic fused to mutation manifest developmental defects.

How the SNPs in INSIG2 and FTO alter the function of their respective RNAs and/or proteins, increasing the risk for higher BMI in the morbidly obese, is not yet known. The INSIG2 SNP is located about 10,000 base pairs upstream from the coding region, so it is likely involved in regulating the level of RNA and therefore the amount of protein produced. The FTO SNP is located in the first intron of the gene and also presumably affects levels of its RNA and protein. Future studies will be required to determine the molecular mechanism through which the specific DNA sequences, ie, A and T for FTO and G and C for INSIG2, affect the genes’ functions. Our results indicate that the 2 genes may interact, suggesting that the physiological pathways in which each is involved may be linked in some way.

The effect of these genetic variants on bariatric surgery and its expected outcomes has yet to be determined. Surgical treatment for morbidly obese patients results in greater weight loss than medical treatment does. Bariatric surgery has also been associated with increased life expectancy compared with the risk of surgical mortality and potential length of effectiveness. Recent data on the long-term effectiveness of bariatric surgery on BMI suggest that, for most patients, BMI will be maintained substantially below preoperative levels, though some patients regain weight and relapse toward morbid obesity. We hypothesize that this subgroup carries genetic susceptibility alleles that overcome the results of the Roux-en-Y gastric bypass surgery, as has been investigated for several candidate genes in laparoscopic adjustable-band therapy and laparoscopic mini-gastric bypass. The identification of such susceptibility genes may therefore be important in identifying patients at high risk for postoperative weight gain. These studies may also represent some of the first specific examples of "pharmacogenomics," paralleling the well-developed field of pharmacogenomics.

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