Associations of the FTO rs9939609 variant with discrete body fat depots and dietary intake in a multi-ethnic cohort

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Summary

The fat mass and obesity associated (FTO) gene has been implicated with obesity and dietary intake predominantly in European populations. We assessed the association between the FTO rs9939609 variant with body fat distribution and dietary intake in a multi-ethnic population. Aboriginal, Chinese, European and South Asian participants living in Canada (n = 706) were assessed for body fat and inner-abdominal fat using imaging techniques, dietary intake and genotyped for the FTO rs9939609 variant. Linear regression was used to study the associations between the minor allele of the variant and measures of adiposity and dietary intake. Minor allele frequencies were: Aboriginals (17%), Chinese (17%), Europeans (39%) and South Asians (31%). The rs9939609 variant was associated with intake of dietary macronutrients in Aboriginals and Europeans only. In the total population, there were positive associations between the rs9939609 minor allele and greater fat mass (0.94 ± 0.56 kg, P = 0.045), per cent body fat (0.7 ± 0.4%, P = 0.031), relative greater subcutaneous abdominal adipose tissue (4.9 ± 2.8%, P = 0.039) and percent daily calories from fat (0.4 ± 0.2%, P = 0.064). Our findings suggest that the FTO rs9939609 minor allele may be associated with dietary intake in adults and is positively associated with regional fat deposition.

1. Introduction

The fat mass and obesity associated (FTO) gene is associated with body mass index (BMI), waist circumference (WC) and obesity risk (Frayling et al., 2007; Willer et al., 2009), and has been implicated in food and total energy intakes (Cecil et al., 2008; Speakman et al., 2008). These studies have been mainly in people of European origin but in the coming years, the greatest increases in obesity rates will occur in Asian countries, therefore, investigation of genetic associations in these populations is warranted. Genome-wide association studies have identified at least 50 genetic loci that are associated with obesity-related traits. The locus that was first identified as an obesity-susceptibility locus is the fat mass and obesity associated (FTO) gene in which genetic variation (e.g. the rs993609 SNP) has been convincingly associated with BMI, WC and obesity risk (Frayling et al., 2007; Andreasen et al., 2008; Bauer et al., 2009; Willet et al., 2009). To date, only a handful of studies have investigated associations between the rs993609 variant with obesity in Asian populations. These studies reported the rs993609 variant to be associated with increased BMI and/or WC in Chinese (Chang et al., 2008; Li et al., 2010) and South Asian people (Al-Attar et al., 2008). Furthermore, this association has also been reported in North American Aboriginals (Al-Attar et al., 2008; Rong et al., 2009). However, not all of these studies are consistent as several others have found no associations in these populations, and none was conducted in multiple...
ethnic groups living in the same environment (Al-Attar et al., 2008; Li et al., 2008; Rong et al., 2009; Yajnik et al., 2009).

Many of the above studies have focused on anthropometric measures, but there is general agreement that BMI does not distinguish between individuals of increased weight due to excess body fat or greater muscle mass. The WC is limited in its ability to reflect total body fat and is unable to discriminate between the more metabolically active inner abdominal adipose tissue (visceral adipose tissue (VAT)) and subcutaneous abdominal adipose tissue (SAT). Our earlier research has indicated that Chinese and South Asians have a unique phenotype of increased VAT compared with Europeans of the same body size (Lear et al., 2007a,b). Therefore, the purpose of this investigation was to assess the association of the FTO rs9939609 variant with measures of body fat using precise imaging techniques in a multi-ethnic adult population and report on the effect sizes. We further assessed the association of the FTO variants with total and macronutrient energy intakes because studies have shown associations between homozygosity for the rs9939609 minor allele with food and total energy intakes in children (Cecil et al., 2008; Speakman et al., 2008; Wardle et al., 2008, 2009).

2. Materials and methods

Participants for this study were from the Multicultural Community Health Assessment Trial (M-CHAT) (Lear et al., 2006). Apparently healthy men and women between 30 and 65 years of age were recruited from the greater Vancouver area in Canada of either Aboriginal (reserve and non-reserve residents), Chinese (China, Hong Kong and Taiwan), European (continental Europe, Ireland and UK) or South Asian (Bangladesh, India, Nepal, Pakistan and Sri Lanka) origin. Based on self-report, participants must have indicated that all known ancestors were either of Aboriginal origin or descended from one of the three geographical areas. Due to the high prevalence of mixed ethnic origins in Aboriginal populations, Aboriginals with at least three grandparents of exclusive Aboriginal origin were recruited into the main M-CHAT study; however, only those who reported that all four grandparents were of exclusive Aboriginal origin were included in the present analyses. Of the 828 M-CHAT participants recruited, 742 provided consent for DNA collection, after excluding Aboriginal participants without four Aboriginal grandparents, the sample size available for analysis was 706 (131 Aboriginals, 202 Chinese, 184 Europeans and 189 South Asians). The study was approved by the Simon Fraser University and Children and Family Research Institute Research Ethics Boards.

(i) Participant assessment

Participants were assessed for diet, anthropometry, intra-abdominal fat, total body fat and provided a blood sample for DNA extraction. All data were collected on the same day, except for the blood sample that was collected within 3 weeks of the main assessment.

(ii) Body composition assessment

Weight was assessed using a balance-beam scale with participants in light street clothing, footwear removed and pockets emptied. Height was assessed by stadiometer and BMI was calculated as weight in kilograms divided by height in metres squared. Waist circumference was recorded in centimetres as the average of two measures taken against the skin at maximal narrowing of the waist following a normal expiration. Hip circumference was recorded in centimetres as the average of two measures taken at the point of maximal gluteal protuberance from the lateral view over undergarments.

Inner abdominal fat was assessed by computer tomography (CT) scan using a CTi Advantage scanner (General Electric, Milwaukee, WI). A cross-sectional 10 mm slice at the L4/L5 intervertebral disc was obtained and the attenuation range of −190 to −30 Hounsfield units was used to identify adipose tissue. Computation of surface areas from the CT scans was conducted using SliceOmatic 4.2 medical imaging software (SliceOmatic v.4.2, Tomovision, Montreal). Total abdominal fat was calculated as all pixels within the attenuation range and VAT was defined as adipose tissue within the inside edge of the abdominal wall. SAT was the difference between total abdominal adipose tissue and VAT.

Total body fat was assessed by dual energy X-ray absorptiometry with a Norland XR-36 scanner (Norland Medical Systems, White Plains, NY) using Host Software Version 3.9.4 and Scanner Software 2.1.0. Where possible, participants removed all jewellery and metallic objects that could potentially affect the scan results. In some instances, participants could not remove rings from fingers or bracelets from their wrist. Per cent total body fat was calculated as total body fat divided by total body mass. Peripheral fat mass was the sum of fat mass in the arms and legs. Per cent peripheral fat mass was calculated as peripheral fat mass divided by total body mass.

(iii) DNA extraction and genotyping

DNA was extracted from whole blood samples using the QIAamp DNA Blood kit (Qiagen) following the manufacturer’s suggested protocol. Genotyping of the FTO rs9939609 variant was performed by
real-time PCR using TaqMan pre-designed SNP genotyping assays (Applied Biosystems) and a 7500 Real-Time PCR System (Applied Biosystems with a call rate of 100%). Table 1 presents data on the minor allele and genotype frequencies. The rs9939609 variant was in Hardy–Weinberg equilibrium in each ethnic group (P >0.05).

(iv) Statistical analyses
Continuous variables are presented as means ± SD, and categorical variables as percentages and counts. Visceral adipose tissue and SAT had non-normal distributions and were log transformed prior to analyses. Within each ethnic group additive linear regression was used to identify the association of the rs9939609 genotype with the anthropometric, body fat and dietary data adjusted for age and sex. As the associations between the FTO genotype and per cent daily calories from carbohydrates were in opposite directions for the Aboriginals and Europeans, we also tested for an inter-ethnic interaction for the dietary outcomes. There were 34 participants with incomplete dietary records, resulting in 672 participants included in the regression models with the dietary outcomes. To ensure that insignificant P values were not due to the low sample sizes within each ethnic group, we conducted an analysis combining all ethnic groups using the same linear models previously described and adding three indicator variables to account for inter-ethnic differences. Based on an effect size for the rs9939609 minor allele of 0.34% of the variance in BMI (Willer et al., 2009) and an alpha of 0.1 (one-sided), our power to detect an association is 46.3% power (for a power of 80%, a sample of 1813 participants is needed). All analyses were conducted using R and the α-level was set at <0.05 (one-sided) for significance.

3. Results
Table 1 outlines the minor allele and genotype frequencies, and the outcome variables. The minor allele and genotype frequencies differed among the ethnic groups (P <0.001). Europeans and South Asians had greater minor allele frequencies compared with the Aboriginals and Chinese (P <0.001 for all comparisons). There were no differences between the Europeans and South Asians, or the Aboriginals and Chinese. Dietary and anthropometric measures were significantly different across the four ethnic groups (P <0.001 for all).

In Aboriginals, the rs9939609 minor allele was associated with a −2.2 ± 1.3 and 1.1 ± 0.6% absolute change in per cent daily calories from carbohydrate (P =0.049) and proteins (P =0.029), respectively (Table 2). In Europeans, the rs9939609 minor allele was associated with a 9.7 ± 5.7% relative increase in VAT (P =0.047) and a 2.3 ± 0.9% absolute increase in percent daily calories from carbohydrates (P =0.007). There was a significant inter-ethnic interaction between ethnicity (Aboriginal versus European) and the FTO genotype for per cent daily calories from carbohydrates (P =0.004), there were no other significant interactions for dietary outcomes (data not shown). There were no other significant associations within the ethnic groups. When the four ethnic groups were analysed together (Table 2), there were significant associations between the rs9939609 minor allele with greater fat mass (0.94 ± 0.56 kg, P =0.045), per cent body fat (0.7 ± 0.4%, P =0.031) and relative greater SAT body fat (4.9 ± 2.8%, P =0.039).

4. Discussion
The purpose of this study was to assess the association and report effect sizes between the rs9939609 SNP in the FTO gene with direct measures of body fat using imaging techniques in a multi-ethnic cohort. We found differences in minor allele frequency among the four groups such that the frequency of the minor allele was highest in the European and South Asian groups, and lowest in Aboriginal and Chinese groups. In Aboriginals and Europeans, the minor allele was associated with dietary intake and VAT (Europeans only). When the four ethnic groups were analysed together, the FTO rs9939609 minor allele was also associated with body fat measures and SAT.

The minor allele frequencies reported in the present study are similar to that found in a number of studies investigating similar ethnic groups (Al-Attar et al., 2008; Li et al., 2008; Sanghera et al., 2008; Rong et al., 2009; Yajnik et al., 2009). Our investigation adds to this by providing direct comparisons of allele frequency in these ethnic groups recruited under the same criteria and indicates that the minor allele frequency is no different in Europeans and South Asians, and higher in Aboriginals and Chinese, with no difference between these two latter groups.

Although not significant, our per minor allele effect size on BMI was highest in Aboriginals (0.75 kg/m²) and similar to that reported by Rong et al. (0.8 kg/m²) (Rong et al., 2009). Studies in Chinese populations have reported the FTO rs9939609 variant to be associated with increased obesity (Li et al., 2010) with the effect sizes of the minor allele for BMI ranging from 0.37 to 0.68 kg/m² (Chang et al., 2008; Tan et al., 2008), which is somewhat higher than what we reported. However, not all studies are consistent as Li et al. did not report an association between the minor allele and BMI in 3210 Chinese men and women (Li et al., 2008). For Europeans, our per minor allele effect size for BMI was 0.22 kg/m² and similar to that
Table 1. Participant demographics, allele and genotype frequencies, dietary and anthropometric data

|                        | Aboriginal (n = 131) | Chinese (n = 202) | European (n = 184) | South Asian (n = 189) | P values for inter-ethnic comparisons |
|------------------------|----------------------|-------------------|--------------------|-----------------------|--------------------------------------|
| Age (years)            | 45.4 ± 8.1           | 48.0 ± 8.1        | 50.8 ± 9.1         | 45.0 ± 8.4            | <0.001                               |
| Male gender (%)        | 66 (50%)             | 92 (46%)          | 93 (51%)           | 100 (53%)             | 0.527                                |
| FTO rs9939609 genotype |                      |                   |                    |                       | <0.001                               |
| TT                     | 91 (70%)             | 140 (70%)         | 66 (36%)           | 89 (47%)              | <0.001                               |
| TA                     | 33 (25%)             | 53 (27%)          | 92 (50%)           | 82 (44%)              | <0.001                               |
| AA                     | 6 (5%)               | 7 (4%)            | 26 (14%)           | 17 (9%)               | <0.001                               |
| FTO rs9939609 minor allele frequency | 0.173               | 0.168             | 0.391              | 0.309                 | <0.001                               |
| Diet                   |                      |                   |                    |                       |                                      |
| Total kilocalories     | 1784 ± 517           | 2012 ± 531        | 2045 ± 654         | 1748 ± 594            | <0.001                               |
| Carbohydrate (% daily kilocalories) | 50.7 ± 8.1          | 47.8 ± 8.1        | 46.8 ± 8.5         | 55.7 ± 8.5            | <0.001                               |
| Protein (% daily kilocalories) | 15.5 ± 3.7           | 19.3 ± 4.3        | 17.3 ± 4.3         | 16.4 ± 3.7            | <0.001                               |
| Fat (% daily kilocalories) | 33.1 ± 6.9           | 32.4 ± 6.7        | 33.9 ± 7.6         | 27.2 ± 7.5            | <0.001                               |
| Body mass index (kg/m²) | 29.6 ± 5.3           | 25.7 ± 3.5        | 27.8 ± 5.1         | 27.9 ± 5.0            | <0.001                               |
| Waist circumference (cm) | 96.2 ± 12.0          | 83.1 ± 9.2        | 89.7 ± 12.7        | 88.8 ± 12.2           | <0.001                               |
| Total fat mass (kg)    | 29.7 ± 10.5          | 21.3 ± 6.8        | 27.0 ± 10.6        | 28.2 ± 10.0           | <0.001                               |
| Body fat (%)           | 35.3 ± 9.3           | 31.1 ± 8.5        | 32.5 ± 10.0        | 35.9 ± 9.3            | <0.001                               |
| Peripheral fat mass (kg) | 11.5 ± 3.9          | 9.2 ± 3.0         | 11.9 ± 4.8         | 12.5 ± 4.9            | <0.001                               |
| Per cent peripheral fat (%) | 13.9 ± 4.1           | 13.5 ± 4.1        | 14.6 ± 5.1         | 16.0 ± 5.3            | <0.001                               |
| Total adipose tissue (cm²) | 470.2 ± 155.4        | 330.8 ± 117.1     | 411.8 ± 176.7      | 448.9 ± 164.7         | <0.001                               |
| Subcutaneous abdominal adipose tissue (cm²) | 335.3 (252.3, 427.0) | 222.0 (162.6, 281.4) | 266.7 (198.9, 385.3) | 309.4 (224.4, 391.5) | <0.001                               |
| Visceral adipose tissue (cm²) | 123.0 (90.4, 162.6) | 99.4 (72.6, 123-6) | 102.6 (79.1, 145-6) | 118.9 (88.3, 162-4) | <0.001                               |

*a Medians and 25th and 75th percentile values presented.

Data are expressed as means and so unless otherwise indicated.
### Table 2. Beta coefficients of the FTO rs9939609 minor allele for the dependent body composition and food intake variables

|                        | Aboriginal (n = 131) | Chinese (n = 202) | European (n = 184) | South Asian (n = 189) | Total Cohort (n = 706) |
|------------------------|---------------------|------------------|--------------------|----------------------|------------------------|
| Body mass index (kg/m²) | 0.75 ± 0.82 (P = 0.182) | 0.24 ± 0.45 (P = 0.297) | 0.22 ± 0.56 (P = 0.0346) | 0.62 ± 0.57 (P = 0.139) | 0.43 ± 0.29 (P = 0.071) |
| Waist circumference (cm) | 1.1 ± 1.9 (P = 0.620) | 1.1 ± 1.1 (P = 0.160) | 1.0 ± 1.3 (P = 0.216) | 0.0 ± 1.3 (P = 0.236) | 0.7 ± 0.7 (P = 0.0247) |
| Total fat mass (kg)     | 1.56 ± 1.91 (P = 0.153) | 0.71 ± 0.81 (P = 0.192) | 1.17 ± 1.01 (P = 0.145) | 0.66 ± 1.12 (P = 0.278) | 0.94 ± 0.56 (P = 0.045) |
| Body fat (%)            | 0.5 ± 1.0 (P = 0.295) | 1.0 ± 0.7 (P = 0.094) | 1.0 ± 0.8 (P = 0.103) | 0.5 ± 0.8 (P = 0.263) | 0.7 ± 0.4 (P = 0.031) |
| Peripheral fat mass (kg) | 0.69 ± 0.54 (P = 0.101) | 0.18 ± 0.33 (P = 0.290) | 0.53 ± 0.46 (P = 0.127) | 0.16 ± 0.51 (P = 0.375) | 0.38 ± 0.23 (P = 0.053) |
| Per cent peripheral fat (%) | 0.3 ± 0.4 (P = 0.205) | 0.2 ± 0.3 (P = 0.233) | 0.4 ± 0.3 (P = 0.127) | 0.5 ± 0.4 (P = 0.443) | 0.3 ± 0.2 (P = 0.009) |
| Total adipose tissue (cm²) | 28.1 ± 23.9 (P = 0.120) | 16.4 ± 14.7 (P = 0.132) | 22.7 ± 19.3 (P = 0.120) | 3.9 ± 19.2 (P = 0.460) | 13.8 ± 9.5 (P = 0.074) |
| Subcutaneous abdominal adipose tissue (%) increase | 5.9 ± 5.9 (P = 0.158) | 9.5 ± 5.7 (P = 0.051) | 5.9 ± 5.6 (P = 0.146) | 1.0 ± 5.2 (P = 0.427) | 4.9 ± 2.8 (P = 0.039) |
| Visceral adipose tissue (%) increase | 1.5 ± 7.2 (P = 0.415) | 7.1 ± 6.0 (P = 0.119) | 9.7 ± 5.7 (P = 0.047) | 0.1 ± 5.2 (0.465) | 4.3 ± 2.9 (P = 0.069) |
| Total kilocalories       | −54.0 ± 80.9 (P = 0.312) | −7.3 ± 6.8 (P = 0.457) | 18.9 ± 65.3 (P = 0.387) | 10.7 ± 68.6 (P = 0.438) | 4.2 ± 35.1 (P = 0.0452) |
| Carbohydrate (% daily kilocalories) | −2.2 ± 1.3 (P = 0.049) | 0.2 ± 1.1 (P = 0.440) | 2.3 ± 0.9 (P = 0.007) | −0.9 ± 1.0 (P = 0.188) | −0.2 ± 0.5 (P = 0.345) |
| Protein (% daily kilocalories) | 1.1 ± 0.6 (P = 0.029) | −0.4 ± 0.6 (0.246) | −0.4 ± 0.5 (P = 0.223) | 0.3 ± 0.4 (P = 0.264) | 0.0 ± 0.3 (P = 0.496) |
| Fat (% daily kilocalories) | 1.1 ± 1.1 (P = 0.150) | 0.4 ± 0.9 (P = 0.322) | 0.4 ± 0.8 (P = 0.084) | 0.8 ± 0.9 (P = 0.187) | 0.1 ± 0.5 (P = 0.380) |

Adjusted for age and sex. Data are reported as per the allele change and so with P values in parentheses.
nutrient intake in women (Bauer et al., 2009). At present, it is unclear why our findings are not consistent with the other study in adults, but it may be due to differences in the variants, our assessment of both men and women, and/or the assessment of dietary intake (food frequency questionnaire compared with our three-day food record). As a result, it remains unknown whether the associations reported in children do indeed extend to adults. However, studies in mice indicate that \textit{FTO} mRNA is highly expressed in hypothalamus and regulated by fasting and refeeding (Gerken et al., 2007) and while the biological function of \textit{FTO} has not been fully characterized, mice overexpressing one or two additional copies of \textit{FTO} have a dose-dependent increase in body and fat mass and increased food intake (Church et al., 2010) supporting a role for \textit{FTO} in food intake and energy homoeostasis.

(i) Limitations

The small sample size of our study may have limited the ability to detect certain associations, particularly within ethnic groups. However, our effect sizes for BMI are similar to that reported in previous studies giving us confidence that our analyses of associations with discrete areas of body composition using accurate imaging techniques provide novel information on effect sizes for these outcomes. We must also acknowledge the limitation of multiple comparisons; however, the majority of literature to date would indicate that the \textit{FTO} variant is associated with measures of body fat and food intake. As our findings are consistent with the previous literature, we believe the likelihood of spurious findings is low. Lastly, as our study is cross-sectional, we are limited to identifying associations only and longitudinal studies investigating changes in body fat over time are needed to identify and understand more clearly the role of \textit{FTO}.

(ii) Conclusions

A unique contribution of our investigation is the comparison of precise body fat imaging and dietary measures in a cohort of different ethnic groups recruited from the same environment. Our results confirm that the frequency of the minor allele of the \textit{FTO} rs9939609 variant differs across ethnic groups and the presence of minor allele may be associated with increased body fat and SAT independent of ethnicity. In addition, our finding that the \textit{FTO} rs9939609 variant is associated with energy intake supports a possible role for \textit{FTO} in relation to obesity that has been observed in studies of children. Although our study is limited by a small sample size, our reported per allele effect sizes for BMI are consistent with previous studies. These results suggest that carriers of the minor rs9939609 allele may be at increased risk for excess body fat, and therefore at greater risk for cardiometabolic diseases.

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5. Declaration of Interest

None.

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