<table>
<thead>
<tr>
<th><strong>Title</strong></th>
<th>Polymorphisms in FTO, TMEM18 and PCSK1 are associated with BMI in southern Chinese population</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Author(s)</strong></td>
<td>Chen, J; Yang, M; Zhao, K; Xu, A; Huang, Q</td>
</tr>
<tr>
<td><strong>Citation</strong></td>
<td>Journal of Genetics, 2014, v. 93 n. 2, p. 509-512</td>
</tr>
<tr>
<td><strong>Issued Date</strong></td>
<td>2014</td>
</tr>
<tr>
<td><strong>URL</strong></td>
<td><a href="http://hdl.handle.net/10722/214316">http://hdl.handle.net/10722/214316</a></td>
</tr>
<tr>
<td><strong>Rights</strong></td>
<td>Creative Commons: Attribution 3.0 Hong Kong License</td>
</tr>
</tbody>
</table>
RESEARCH NOTE

Polymorphisms in FTO, TMEM18 and PCSK1 are associated with BMI in southern Chinese population

JIE CHEN1, MEI YANG1, KEHUI ZHAO1, AIMIN Xu2 and QINGYANG HUANG1∗

1College of Life Sciences, Central China Normal University, Wuhan 430079, People’s Republic of China
2Li Ka Shing Faculty of Medicine, The University of Hong Kong, Pokfulam, Hong Kong

[Chen J., Yang M., Zhao K., Xu A. and Huang Q. 2014 Polymorphisms in FTO, TMEM18 and PCSK1 are associated with BMI in southern Chinese population. J. Genet. 93, 509–512]

Introduction

Obesity is a major health problem in the world, and is defined as excessive fat accumulation and quantified by body mass index (BMI). Genetic factors play a key role in obesity. In the last few years, genomewide association studies (GWAS) have produced a number of novel genes and polygenic variants associated putatively with obesity. Common variants at FTO, INSIG2 and MC4R loci were previously reported to be associated with fat mass, weight and obesity in several populations (Sandholt et al. 2010). Yanagiya et al. (2007) revealed that genetic variations in MTMR9 may confer a predisposition towards obesity. PCSK1 was also firmly placed on the short list of genes reproducibly associated with common obesity (Benzinou et al. 2008). A meta-analysis of 15 GWAS performed by the GIANT consortium on total 32,387 individuals of European ancestry discovered that six previously unreported loci in or near KCTD15, SH2B1, GNPDA2, TMEM18, NEGR1 and MTCH2 are associated with BMI (Willer et al. 2009).

In this study, we attempt to examine the association between BMI and the genes mentioned here by genotyping the previously reported 11 single-nucleotide polymorphism (SNP) in southern Chinese.

Materials and methods

Subjects

This study included 1560 southern Chinese individuals (288 men and 1272 women) with mean age of 49.8 ± 15.9 years (women, 49.5 ± 15.9, men, 50.9 ± 15.9), mean height of 1.57 ± 0.08 m (women, 1.55 ± 0.07, men, 1.67 ± 0.07), and mean weight of 55.7 ± 10.8 kg (women, 53.4 ± 9.3, men, 53.4 ± 9.3). A detailed description of subject ascertainment, inclusion and exclusion criteria has been described previously (Ng et al. 2006). BMI was calculated as weight (kg)/height2 (m2).

SNP selection and genotyping

Eleven SNPs from 10 candidate genes (FTO, KCTD15, INISG2, SH2B1, PCSK1, MTMR9, GNPDA2, TMEM18, MC4R and NEGR1), which have been reported to be associated with BMI, were selected for genotyping in 1560 subjects using the high-throughput mass array technology. Five percent of samples were duplicated for quality check in the genotyping process and the reproducibility rate exceeded 99.8%.

Statistical analysis

Since the raw data of BMI deviated from normal distribution, a square root transformation was conducted. Genotype–BMI association analyses were performed by linear regression, SNP being coded as 0, 1 and 2 according to genotypes. Analyses included linear regression of single SNP (adjusted with age) with BMI and multiple stepwise regressions of 11 SNPs, and age with BMI. Statistical analyses were performed using SPSS 11.5 for Windows software. A P value less than 0.05 was considered to be statistically significant.

Results and discussion

The BMI in our samples ranged from 14.97 to 37.95 kg/m2. Kolmogorov–Smirnov test suggested that the distribution of BMI deviated from normal distribution (P = 0.001), but square root of BMI (sqr BMI) followed normal distribution (P = 0.056) (figure 1).

Keywords. association; FTO; TMEM18; PCSK1; BMI.
Linear regression between single SNP and age, and square root of BMI was performed (Table 1). Significant partial regression coefficient were found for FTO rs9939609 (P = 0.004) and TMEM18 rs6548238 (P = 0.003). KCTD15 (rs11084753), PCSK1 (rs6234, rs6235), MTMR9 (rs2293855) and NEGR1 (rs2815752) showed a weak correlation with BMI. For FTO rs9939609, BMI of AA (23.25 kg/m^2) and AT (22.87 kg/m^2) genotypes were significantly higher than those of TT (22.35 kg/m^2) genotype (P = 0.010). It seems that the A allele increases BMI in dominant model. For rs6548238 (TMEM18), there is significant difference in BMI between CC (22.60 kg/m^2) and TC (21.98 kg/m^2) genotype (P = 0.015). TT genotype had the lowest BMI (20.84 kg/m^2). Multiple stepwise regression equation of BMI on 11 SNPs and age included FTO, TMEM18 and PCSK1 genes: sqrt BMI = 4.216 + 0.067x_1 + 0.058x_2 + 0.030x_3 + 0.071 (age), R^2 = 0.42.

Subgroup analyses were also performed to examine gender difference of obesity genetics. For women, apart from FTO rs9939609 (P = 0.006) and TMEM18 rs6548238 (P = 0.007), an association was found between GNPDA2 rs10938397 (P = 0.014) and BMI. For men, only MC4R rs17782313 was associated with BMI (P = 0.034). Causes for gender difference included sex-specific genetic control and small sample size of men’s subgroup.

FTO, located on chromosome 16q12.2, was earliest identified as a susceptible locus for obesity. rs9939609 in FTO was identified to be predisposed to diabetes through an effect on BMI in a genomewide search for type 2 diabetes, and then first reported as obesity susceptibility gene (Sandholt et al. 2012). In two ongoing longitudinal studies, Liu et al. (2011) assessed the influence of rs9939609 on development of adiposity in European-American and African-American youth, and found that rs9939609 was associated with logBMI. So far, six studies have been published on rs9939609 locus of FTO in Chinese populations. Although two studies found no association of rs9939609 variant with obesity (Li et al. 2008; Yan et al. 2009), rs9939609 is associated with BMI in ethnic Chinese in Singapore (Tan et al. 2008), Chinese children (Fang et al. 2010), Taiwan Chinese Han populations (Chang et al. 2008) and Hubei Han Chinese aged from 50–70 years (Huang et al. 2011). Our current study successfully replicated association between FTO rs9939609 and BMI in southern Chinese from Hong Kong. Four meta-analyses of associations between rs9939609 and obesity / BMI have been published in recent years and FTO rs9939609 was significantly associated with BMI (Xi and Mi 2009; Liu et al. 2010; Chauhan et al. 2011; Li et al. 2012).

TMEM18-associated SNPs were first found to be associated with obesity by two GWAS (Willer et al. 2009; Thorleifsson et al. 2009). From then on, the association with obesity was confirmed on Swedish children (Almén et al. 2010), Greek (Rouskas et al. 2012) and Japanese populations (Takeuchi et al. 2011) and children and adolescents from Denmark and Estonia (Den Hoed et al. 2010). Although two previous studies found no association of TMEM18 polymorphisms with BMI in Chinese populations (Ng et al. 2010; Huang et al. 2012), our study demonstrated that rs6548238 was associated with BMI in southern Chinese aged 18–85.
years. In addition, a study on Chinese children (10–20 years aged boys) from Shanghai also validated that rs6548238 in TMEM18 has an association with obesity-related indices during puberty (Wang et al. 2012). A recent research has shown that TMEM18 plays a regulatory role in human adipocyte differentiation (Bernhard et al. 2013).

PCSK1 encodes prohormone convertase 1/3 which can convert inactive prohormones into biologically active peptide hormones. Loss-of-function mutations in PCSK1 give rise to monogenic obesity (Jackson et al. 1997). Benzinou et al. (2008) initially uncovered rs6232 and rs6234–rs6235 in PCSK1 strongly associated with obesity risk among adults and children in European populations. Association of rs6232 and rs6235 with obesity, and BMI were also replicated in European (Kilpeläinen et al. 2009; Sandholt et al. 2010; Rouskas et al. 2012) and Mexican populations (Villalobos et al. 2012). Here, our study demonstrated that rs6234 was associated with BMI in Chinese.

Our present study demonstrated that FTO-rs9939609, TMEM18-rs6548238 and PCSK1-rs6234 polymorphisms are significantly associated with BMI in southern Chinese population. However, we are unable to replicate the associations for other loci; due to small sample size and limited statistical power.

Acknowledgements

This work was supported by National Basic Research Program of China (973 programme, no. 2011CB504004) and selfdetermined research funds of CCNU from the colleges’ basic research and operation of MOE.

References


Jie Chen et al.


