Diabetes-2013
OMICS Group Conferences
Accelerating Scientific Discovery
4th World Congress on
Diabetes & Metabolism
August 14-16, 2013 Holiday Inn Chicago-North Shore, USA

Common variation in the fat mass and obesity-associated (fto) gene confers risk of obesity and metabolic traits in the Chinese children

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Abstract

Background: The fat mass and obesity associated gene (FTO) expressions have been implicated in the development of obesity. We investigated whether SNP polymorphisms of FTO gene might be associated additionally with metabolic traits in Chinese children.
Methods: Targeted genotyping of five common single nucleotide polymorphisms (SNPs: rs1421085, rs17817449, rs8050136, rs3751812 and rs9939609) was performed using an automated platform MassARRAY for 405 obese or overweight and 194 normal children.
Results: When all obese or overweight cases were compared with all normal cases, significant differences were found in the allele frequency and in the genotype distribution. Compared with the wide-type genotype, minor allele carriers of the five SNPs were associated with increased risks of childhood obesity or overweight (rs1421085, OR = 1.980; rs17817449, OR = 2.011; rs8050136, OR = 1.925; rs3751812, OR = 1.911; rs9939609, OR = 1.930). After adjustment of age, sex and BMI-z score, all of the five SNPs showed a trend towards higher SBP. In addition, rs3751812 and rs8050136 showed significant association with LDL-C and HOMA-IR levels. Strong evidence of total association was found for BMI in relation to haplotype TTCGT and haplotype CGATA (after 10000 permutations, P=0.015 and 0.011, respectively)
Conclusions: In conclusion, genetic variation in the FTO locus contributed to the etiology of obesity, hypertension, insulin resistance, and increased plasma LDL levels.