Association between FTO, MC4R, SLC30A8, and KCNQ1 gene variants and type 2 diabetes in Saudi population

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Received January 6, 2014
Accepted July 17, 2014
Published December 4, 2014
DOI http://dx.doi.org/10.4238/2014.December.4.14

ABSTRACT. Recent genome wide association studies identified many loci in several genes that have been consistently associated with type 2 diabetes mellitus in various ethnic populations. Among the genes that were most strongly associated with diabetes were fat mass- and obesity-associated, melanocortin 4 receptor, solute carrier family 30 member 8 (SLC30A8), and a member of the potassium voltage-gated channels. In the present study, we examined the association between variants in fat mass- and obesity-associated [rs9939609 (A/T)], melanocortin 4 receptor [rs17782313 (C/T), and rs12970134 (A/G)], SLC30A8 [rs13266634 (C/T)], and a member of the potassium voltage-gated channels [rs2237892(C/T)] genes in diabetes patients from Saudi Arabia. Genotypes were determined using the TaqMan single-nucleotide polymorphism genotype analysis technique. Minor allele frequency of the 4 variants tested was comparable between type
2 diabetes cases and controls. We observed an association between allele variants of SLC30A8 [rs13266634 (C/T)] and type 2-diabetes (P = 0.04). The other single-nucleotide polymorphisms examined in this study showed moderate or no correlation with diabetes in Saudis. Our data indicate that the SLC30A8 polymorphisms are associated with type 2 diabetes in the Saudi population. There is no evidence supporting an association between variants in the fat mass- and obesity-associated and melanocortin 4 receptor, and a member of the potassium voltage-gated channels genes and type 2 diabetes in the Saudi population.

**Key words:** Ethnicity; Fat mass- and obesity-associated; Polymorphisms; Solute carrier family 30 member 8; Type 2 diabetes mellitus