



Association of VDR polymorphisms with type 2 diabetes mellitus in Chinese Han and Hui populations

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Genet. Mol. Res. 13 (4): 9588-9598 (2014)
Received August 1, 2013
Accepted September 13, 2014
Published November 14, 2014
DOI <http://dx.doi.org/10.4238/2014.November.14.2>

ABSTRACT. We investigated the association between vitamin D receptor (VDR) and susceptibility to type 2 diabetes mellitus (T2DM). Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) analysis was conducted to examine single nucleotide polymorphisms (SNPs) of the rs1544410 (*BsmI*, G>A), rs757343 (*Tru9I*, G>A), rs731236 (*TaqI*, T>C), and rs739837 (*BglI*, G>T) loci of the VDR gene in 334 healthy individuals (Hui 115, Han 219) and 355 T2DM patients (Hui 154, Han 201) living in the Ningxia Hui Autonomous Region of China. The genotypic frequency and allelic frequency distributions in the VDR gene showed no significant difference between T2DM patients and controls in the Chinese Hui population. However, statistical differences in the genotypic frequency at rs739837 and in the genotypic and allelic frequencies

at rs1544410 were observed between T2DM patients and controls in the Chinese Han population ($P < 0.05$). Patient-control haplotype analyses using the SHEsis online haplotype analysis software showed that the G allele frequency of rs1544410 in the T2DM group was higher than that in the control group [odds ratio (OR) = 1.738, 95% confidence interval (CI) = 1.055-2.865], suggesting that the G allele is a risk factor of T2DM in the Chinese Han population. The frequency of haplotype GGCT between cases and controls was significantly different in both Chinese Hui [OR (95%CI) = 4.714 (1.04-21.36)] and Han populations [OR (95%CI) = 1.723 (1.03-2.883)] ($P < 0.05$), implying that the haplotype GGCT of the VDR gene is associated with susceptibility to T2DM in these ethnicities.

Key words: Vitamin D receptor; Polymorphism; Type 2 diabetes mellitus; Chinese Hui population; Chinese Han population