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Association of *LPL* gene variants with dyslipidemia among the non-diabetic study subjects in the south Indian population

Kuppuswamy Ashok Ayyappa
Madras Diabetes Research Foundation, India

Aim: The aim of this study was to investigate the association of 12 common variants of the Lipoprotein lipase gene (LPL) with dyslipidemia among south Indian subjects with normal glucose tolerance (NGT).

Methods: A total of 1018 NGT subjects, were randomly selected from the Chennai Urban Rural Epidemiological Study (CURES). Genotyping of LPL gene variants were done by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method and 20% of samples were sequenced to validate the genotypes obtained. Haplotype analysis was also carried out.

Results: The TT genotype of the rs285 C/T (Pvu II) polymorphism was significantly associated with normal HDL-C subjects, with an adjusted odds ratio of 0.57, (95% Confidence Intervals (CI):0.38-0.84, p=0.005). The GG genotype of the rs327 T/G polymorphism located in the intron 8 was also associated with normal HDL-C subjects with an odds ratio of 0.45, p=0.03. The 'A' allele of the rs4922115 G/A variant was significantly associated with low HDL-C subjects, p=0.04. Haplotype analysis showed that the 'GTCGC' haplotype of the Block 1, 'GGA' in the Block 2 and 'TCGA' in the Block 3 were significantly associated with low HDL-C among the non- diabetic study subjects.

Conclusions: Among south Indian non-diabetic subjects, the rs285 C/T (Pvu II), rs327 T/G variants were significantly associated with normal HDL-C subjects, while the 'A' allele of the rs4922115 G/A variant of the LPL gene was associated with low HDL-C. The 'GTCGC', 'GGA' and 'TCGA' haplotypes were significantly associated with low HDL-C.

ashokayyappa@gmail.com