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Relationship of the *APOA5*/*A4*/*C3*/*A1* gene cluster and *APOB* gene polymorphisms with dyslipidemia

H.J. Ou[1], G. Huang[2], W. Liu[3], X.L. Ma[2], Y. Wei[4], T. Zhou[5] and Z.M. Pan[3]

[1]Department of Neurology, The First Affiliated Hospital, Medicine College, Shihezi University, Shihezi City, Xinjiang, China
[2]Department of Gerontology, The First Affiliated Hospital, Medicine College, Shihezi University, Shihezi City, Xinjiang, China
[3]Department of Biochemical Teaching and Research, Medicine College, Shihezi University, Shihezi City, Xinjiang, China
[4]Department of Clinical Laboratory, The First Affiliated Hospital, Medicine College, Shihezi University, Xinjiang, Shihezi City, Xinjiang, China
[5]Department of Medical Laboratory, The First Affiliated Hospital, Medicine College, Shihezi University, Shihezi City, Xinjiang, China

Corresponding author: G. Huang
E-mail: huanggang472601@aliyun.com

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ABSTRACT. We determined the alleles of ten single nucleotide polymorphisms (SNPs) in the *APOA5*/*A4*/*C3*/*A1* gene cluster and in *APOB* in Han Chinese from Xinjiang Shihezi, China using MALDI-TOF mass spectrometry, and explored the correlation between these SNPs and dyslipidemia through a case-control study design with 250 patients and 250 normal controls. All SNPs except for *APOA5* rs2072560 conformed to Hardy-Weinberg equilibrium (all $P > 0.05$). *APOA5* rs651821, *APOA4* rs5104, *APOC3* rs734104, and *APOC3* rs5128 genotype and allele frequencies were significantly different between groups (all $P < 0.01$). For rs651821, the risks of dyslipidemia for the CC or

CC+CT genotypes were 9.917 or 1.859 times that of TT, and the risk of the C *vs* T allele was 2.027. For rs5104, the AG, GG, or AG+GG risks were 1.797, 1.861, and 1.809 times AA, and the G *vs* A risk was 1.427. For rs734104, the CT, CC, or CC+CT risks were 1.851, 2.570, and 1.958 times TT, and the C *vs* T risk was 1.610. For rs5128, the GC or CC+GC risks were 1.738 or 1.749 times GG, and the C *vs* G risk was 1.477. Compared with the wild-type haplotype TATG, the risks of dyslipidemia with CGCC, TGCC, or CATG haplotypes (odds ratios = 2.434, 1.503, and 2.740, respectively) were significantly higher. Our results suggested that these four SNPs were significantly associated with dyslipidemia in Xinjiang Shihezi Han Chinese, and might serve as risk factors for dyslipidemia. Individuals carrying the CGCC, TGCC, or CATG haplotypes were prone to dyslipidemia.

Key words: *APOA5*/*A4*/*C3*/*A1* gene cluster; Apolipoprotein B; Dyslipidemia; Gene polymorphism