Apolipoprotein A-V Genetic Variants in Obese Children

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Editorial

Apolipoprotein A-V (APOA5) gene located on human 11q23 is an important determinant of plasma triglyceride levels [1]. Obese children with hyperinsulinemia had higher triglyceride (TG) level and lower APOA5 level than those without hyperinsulinemia and serum APOA5 was correlated negatively with TG level [2]. Single nucleotide polymorphisms (SNPs) of APOA5 were found to be significantly associated with plasma/serum TG levels in children [3-7]. SNP3 (ss3199915, now merged into rs662799) of APOA5 gene was found to play an important role in the variation of serum TG levels. The serum TG levels of the subjects with C allele were significantly higher than those of the subjects with the T/T genotype. The TG levels of the subjects with the T/C and C/C genotype were 12.7% and 31.8% higher than those of the subjects with the T/T genotype, respectively [3]. Horvatovich et al [4] examined four SNPs including T-1131C (rs662799), IVS3+476A (rs2072560), T1259C (rs2266788) and C566G (rs3135506) of APOA5 and studied the frequencies of APOA5 haplotypes including APOA5*1 (TGTC), APOA5*2 (CACC), APOA5*3 (TGTG), APOA5*4 (CGTC) and APOA5*5 (TGCC) in obese children [4]. The results indicated that the prevalence of the APOA5*2 was about 2.59-fold increase while that of the APOA5*5 displayed 3.88-fold decrease in obese subjects compared with healthy children. Accordingly, carrying APOA5*2 and APOA5*4 haplotype variants resulted in a significant increase in serum TG levels, while the APOA5*5 haplotype had a serum TG level-decreasing. In Chinese child population, C carriers in rs662799 and rs651821 had 1.496-fold and 1.515-fold higher risk for developing obesity or overweight than those with T/T genotype. The TG levels of the subjects with the T/C and C/C genotype were 12.7% and 31.8% higher than those of the subjects with the T/T genotype.

In summary, APOA5 is a regulator of serum TG. SNPs of APOA5 gene appear to be genetic risk factors for hypertriglyceridemia, and therefore increase obesity risk in children. The associations between variants in APOA5 gene and obese children need further study to improve the understanding of biological functions of APOA5 gene variants. In above studies, genotyping of SNPs was carried out using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) analysis [3,4], PCR-direct sequencing method [5], PCR-high resolution melting analysis [6] and MassArray [7]. Here, I recommend a method named base-quenched probe [8] which is now available for detecting multi-mutations simultaneously in one tube [9].

References

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