Plasma Homocysteine and Gene Polymorphisms Associated with the Risk of Hyperlipidemia in Northern Chinese Subjects

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Objective To examine the relationship between occurrence of hyperlipidemia, plasma homocysteine and polymorphisms of methylenetetrahydrofolate reductase (MTHFR) gene and methionine synthase (MS) gene. Methods A total of 192 hyperlipidemia patients were selected and divided into hypercholesterolemia group, hypertriglyceridemia group, and combined hyperlipidemia group. Another 208 normal individuals were selected as control. Total plasma homocysteine (tHcy) concentration was measured by high-performance liquid chromatography (HPLC). Lipid profiles were measured for all subjects. The polymorphisms of MTHFR gene C677T and MS gene A2756G were analyzed by PCR-RFLP. Results The tHcy concentration in the combined hyperlipidemia patients was significantly higher than that in the control (15.95 μmol/L vs 13.43 μmol/L, P<0.05). The prevalence of hyperhomocysteinemia (HHcy) in the combined hyperlipidemia group was significantly higher than that in the control (42.2% vs 23.0%, P=0.015), with the odds ratio (OR) of 3.539 (95%CI: 1.600-8.849). The hyperlipidemia patients with HHcy had a higher concentration of total cholesterol (TC) than that in the normal tHcy patients (5.67±0.95 mmol/L vs 5.47±0.92 mmol/L, P=0.034). There was no significant difference in genotype or allele frequencies of MTHFR C677T between the hyperlipidemic and control groups. The hyperlipidemia patients with MTHFR CT/TT genotype had a higher concentration of triglyceride (TG) than those with CC genotype (2.24±1.75 mmol/L vs 1.87±0.95 mmol/L, P=0.05). Individuals with CT/TT genotype had a higher concentration of tHcy than those with 677CC genotype (14.04±1.48 μmol/L vs 12.61±1.24 μmol/L, P=0.05). The percentage of MS 2756 GG/AG genotype in the combined hyperlipidemia group was significantly higher than that in the control (26.7% vs 13.0%, P=0.012), with the OR of 3.121 (95%CI: 1.288-7.651). The hyperlipidemia patients with MS 2756AG/GG genotype had a higher concentration of TC (5.87±0.89 mmol/L vs 5.46±0.93 mmol/L, P<0.05) and LDL-C (3.29±0.81 mmol/L vs 2.94±0.85 mmol/L, P<0.05) than those with AA genotype. However, individuals with 2756AG/GG genotype showed no significant difference in tHcy among those with AA genotype. Conclusion HHcy and MS A2756G mutation may be the risk factors for combined hyperlipidemia. Further study is needed to confirm the role of HHcy and MS A2756G mutation in the development of hyperlipidemia.

Key words: Methylenetetrahydrofolate reductase; Methionine synthase; Gene polymorphism; Homocysteine; Hyperlipidemia

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