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Association of the methylenetetrahydrofolate reductase gene A1298C polymorphism with stroke risk based on a meta-analysis

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ABSTRACT. Several independent studies have reported the role of the methylenetetrahydrofolate reductase gene (*MTHFR*) A1298C polymorphism in strokes, but the results are inconclusive. To derive a more precise estimation of the relationship, a meta-analysis was performed in the present study. In this meta-analysis, a total of 13 studies, including 1974 cases and 2660 controls, were selected to evaluate the possible association. Crude odds ratios (ORs) with 95% confidence intervals (CI) were used to assess the strength of the association in additive, dominant, and recessive models. The overall analysis showed that

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MTHFR A1298C was associated with a significant increase in the risk of stroke in the heterozygote comparison (AC *vs* AA: OR = 1.17; 95%CI = 1.03-1.34) and in the dominant model (AC/CC *vs* AA: OR = 1.22; 95%CI = 1.01-1.49). Stratified analysis showed a significantly strong association between the *MTHFR* A1298C polymorphism and stroke risk in Asian populations (OR = 1.32 for AC *vs* AA; OR = 1.94 for CC *vs* AA; OR = 1.37 for AC/CC *vs* AA; OR = 1.33 for C *vs* A allele), but not in Caucasian populations. Additionally, the *MTHFR* 1298C allele was found to be a risk factor for developing ischemic strokes. However, no statistically significant increased risk of hemorrhagic stroke was found in any of the genetic models. In conclusion, this meta-analysis supported that the *MTHFR* A1298C polymorphism could be capable of increasing stroke susceptibility in Asian, but not in Caucasian, populations.

Key words: Stroke; Cerebrovascular disease; Meta-analysis; Methylenetetrahydrofolate reductase; Polymorphism

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