CCDC26 rs4295627 polymorphism (8q24.21) and glioma risk: a meta-analysis


National Key Clinic Specialty, Neurosurgery Institute of Guangdong Province, Guangdong Provincial Key Laboratory on Brain Function Repair and Regeneration, Department of Neurosurgery, Zhujiang Hospital, Southern Medical University, Guangzhou, China

Corresponding author: Y.Q. Ke
E-mail: luhongwei11@foxmail.com

Received February 3, 2015
Accepted May 15, 2015
Published October 5, 2015
DOI http://dx.doi.org/10.4238/2015.October.5.20

ABSTRACT. The association between the CCDC26 rs4295627 single nucleotide polymorphism (SNP) and the glioma risk has been studied previously, but these studies have yielded conflicting results. The aim of the present study is to analyze this association more vigorously, by means of a meta-analysis. A comprehensive literature search was performed in databases PubMed and EMBASE. Six articles including 12 case-control studies in English with 11,368 controls and 5891 cases were eligible for the meta-analysis. We conducted subgroup analyses by the source of controls, ethnicity, and country. Our meta-analysis revealed that the rs4295627 SNP was associated with the glioma risk in a heterozygote model (TG versus TT: odds ratio = 1.35, 95% confidence interval = 1.26-1.45, P = 0.066). Moreover, our results suggested that the rs4295627 SNP was associated with a notably increased risk of glioma among Caucasians except for Swedes in 4 models (the homozygote model, recessive model, dominant model, and additive model). Nonetheless, in Sweden and China, the results showed no associations. No evidence of the publication bias was uncovered. Thus,
our meta-analysis suggests that the rs4295627 SNP is associated with an increased risk of glioma. Additional studies are needed to derive more precise conclusion.

**Key words:** Glioma; *CCDC26*; rs4295627; Polymorphism; Meta-analysis