RTEL1

Previous studies have identified multiple loci for inherited susceptibility to glioma development, including the regulator of telomere elongation helicase 1 (RTEL1). However, the association between RTEL1 variants and risk of glioma has not been well understood. Therefore, we sought to comprehensively examine the genetic interaction between RTEL1 variants and risk of glioma with respect to defined histological and molecular subtypes.

Namgoong et al. employed a case-control study involving 250 adult glioma patients with previous molecular alterations and 375 population-based controls within Korean populations. Statistical analyses on the association between RTEL1 single nucleotide polymorphisms (SNPs) and glioma risk were conducted using unconditional logistic regression. Additional conditional and stepwise analyses were performed on significant RTEL1 SNPs. We detected significant associations (Bonferroni P < .05) between six SNPs (rs6089953, rs3848669, rs6010620, rs3787089, rs6062302, and rs115303435) and risk of glioma in the Korean subjects. The two coding variants, rs6062302 (D664D) and rs115303435 (A1059T), were plausibly causal variants and were independent among the significantly associated RTEL1 variants. The glioma subgroup analyses showed that the causal variants (rs6062302 and rs115303435) may be associated with increased risk of glioma regardless of histological grades and molecular alterations. This study provides a deeper understanding of relationships between RTEL1 variants and risk of glioma. Further studies are required to ascertain the impact of those variants on glioma susceptibility [1].

[1]

Namgoong S, Cheong HS, Kim JH, Kim LH, Seo JY, Kang SG, Yoon SJ, Kim SH, Chang JH, Shin HD. Association analysis of RTEL1 variants with risk of adult gliomas in a Korean population. PLoS One. 2018 Nov 21;13(11):e0207660. doi: 10.1371/journal.pone.0207660. eCollection 2018. PubMed PMID: 30462709.

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