Genetic Variation in Tumor Necrosis Factor Related Apoptosis-Inducing Ligand Receptor-1 (TRAIL-R1) Gene and the Susceptibility to B-Cell Non-Hodgkin Lymphoma in Egypt

Abstract:

Background: Dysregulated apoptosis is a hallmark of cancer development and progression. TRAIL and its receptors (R1 and R2) are key players in the extrinsic apoptotic pathway. Genetic alteration or blockade of TRAIL-R1 may alter its apoptotic function, and subsequently provide growth advantage to neoplastic cells. **Objective:** to investigate the possible association between -C626G, -A683C and -A1322G single nucleotide polymorphisms (SNPs) of TRAIL-R1 gene and the susceptibility to B-NHL in a cohort of Egyptians. **Methods:** Genotypic analysis was performed for 100 newly diagnosed B-NHL patients and 150 age and gender matched healthy controls. **Results:** The polymorphic alleles of -C626G and -A1322G conferred almost twofold increased risk of B-NHL (OR = 1.76; 95%CI = 1.01-3.22 and OR = 1.89; 95%CI = 1.01-3.75 respectively). There was no statistical difference in the distribution of TRAIL-R1-A683C alleles/genotypes between B-NHL patients and controls. B-NHL risk increased when -C626G and -A1322G polymorphic genotypes were co-inherited (OR = 3.57; 95%CI = 1.29-9.84). The risk conferred by -C626G SNP increased for DLBCL (OR = 3.39, 95% CI: 1.61-7.16). **Conclusion:** TRAIL-R1-C626G and -A1322G polymorphisms could be considered as molecular risk factors for B-NHL especially DLBCL. The data provided by the current study constitute an initial millstone towards developing a large-scale dataset for genetic variations that could contribute to lymphomagenesis in Egyptian population.

Cancer Biomarkers 2021;32(4):451-458, Erratum in: Cancer Biomarker. 2022;33(2):275. 15/1/2021
doi: 10.3233/CBM-201786, ISSN: 1574-0153