The relationship between Pembrolizumab for the treatment of PD-L1 positive advanced in cell lung cancer

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Abstract

Introduction: Pembrolizumab is a selective humanized IgG4 kappa monoclonal antibody that inhibits the programmed death-1 (PD-1) receptor, an integral component of immune checkpoint regulation in the tumor microenvironment. Despite the discovery of clinically-actionable driver mutations in genomic subsets of patients, lung cancer remains a leading cause of cancer-related death worldwide for both females and males.1,2 Platinum-based chemotherapy remains the preferred first-line treatment for most patients with advanced or metastatic non-small cell lung cancer (NSCLC) without targetable genomic alterations.

Materials and methods: Our statistical population included 94 male patients with esophageal cancer and 83 samples as control group. DNA was extracted using ethanol-chloroform precipitation method. The designed complementary sequence was amplified by PCR method, and specific fragments were excised using RFLP method. Finally, data were analyzed with SPSS Ver. 22 software

Results:Based on the results, there were no significant correlations between heterozygote genotypes and esophageal cancer in the patients group (OR = 1.17 95%Cl = 0.61-1.49). However, significant correlations were found between dominant homozygotes and the incidence of disease (P = 0.01 95%Cl = 0.31 – 0.92 OR = 0.019).

Conclusion: The results show that mutations in the Pembrolizumab for the treatment of PD-L1 positive advanced in cell lung cancercan only be used as a biomarker for detecting male esophageal cancer in dominant homozygous people with familial marriages.

Keywords: Pembrolizumab, lung cancer, PD-L1, PCR