MGMT PROMOTER HYPERMETHYLATION AS A PROGNOSTIC FACTOR IN PATIENTS WITH LARYNGEAL SQUAMOUS CELL CARCINOMA

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Aim: Laryngeal squamous cell carcinomas (LSCC) are frequently occurring cancers with a high risk of local recurrences or second primary tumours developing within the first two years of diagnosis. A common feature of LSCC is the epigenetic inactivation of certain genes by promoter hypermethylation. In a previous study we found associations of promoter methylation with some clinical features of LSCC. The present study aimed at assessing promoter hypermethylation of CDKN2A, MGMT and MLH1 as prognostic factors in LSCC patients.

Methods: We examined the methylation status of the selected three genes in 61 laryngeal tumours by Methylation-specific High-Resolution Melting and analyzed its association with the overall survival of the patients.

Results: We observed promoter hypermethylation of MGMT, CDKN2A and MLH1 genes in 31 (50.8%), 25 (40.9%) and 24 (39.3%) patients, respectively. Kaplan-Meier survival analysis showed significant association of methylation status of MGMT gene with overall survival (p = 0.018). Patients with unmethylated MGMT had longer median survival (35.1 months) compared to those with methylation (25.7 months). Multivariate Cox regression confirmed that the association was independent of other clinical factors and/or smoking history of the patients.

Conclusions: Our results showed that MGMT promoter methylation is a promising prognostic factor for LSCC patients.

Disclosure: All authors have declared no conflicts of interest.