PTTG1 RS2910200 POLYMORPHISM AS A POTENTIAL MARKER OF LOCALLY ADVANCED LARYNGEAL SQUAMOUS CELL CARCINOMA

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Laryngeal squamous cell carcinoma (LSCC) is the most frequent malignant tumor of the larynx and represents an aggressive disease with increasing incidence worldwide [1]. LSCC development is multifactorial, with growing evidence indicating that genetic variability, particularly single nucleotide polymorphisms (SNPs), contributes to tumor progression and clinical outcomes [2, 3].

Tumor extent, as defined by the TNM classification system, reflects the size of the primary tumor and its invasion into surrounding tissues. Locally advanced primary tumors with extralaryngeal extension represent an aggressive disease phenotype associated with extensive local invasion and poor prognosis [4]. Invasion and metastasis are the main contributors to LSCC-related mortality. Therefore, improved understanding of the molecular mechanisms underlying advanced locally invasive LSCC is essential for improving risk assessment and treatment planning.

Pituitary tumor-transforming gene 1 (*PTTG1*) regulates cell proliferation, differentiation and apoptosis. *PTTG1* has been implicated in tumor growth and metastasis [5]. However, the role of *PTTG1* genetic variation in the development of locally advanced primary tumors with extralaryngeal extension in LSCC remains poorly understood. Clarifying this association may improve understanding of tumor aggressiveness and support the identification of potential molecular markers of advanced local disease.

The aim of this study was to investigate the association between the *PTTG1* rs2910200 genetic variation and the development of locally advanced primary tumors with extralaryngeal extension in LSCC patients.

The study involved 30 LSCC patients with locally advanced primary tumors with extralaryngeal extension and 200 healthy controls. DNA samples from peripheral blood leukocytes were purified by DNA salting-out method. *PTTG1* rs2910200 SNP analyses was determined using real-time polymerase chain reaction (RT-PCR). Statistical analysis ware conducted using ”IBM SPSS Statistics 31.0” program.

Binomial logistic regression analysis revealed a statistically significant association under the over-dominant genetic model. The CT genotype, compared to the combined TT and CC genotypes, was associated with 2.3-fold increased odds of presenting with locally advanced primary tumors with extralaryngeal extension (OR = 2.297 95% CI: 1.049–5.030, p = 0.037, AIC = 175.682). No statistically significant associations were observed under other genetic models, including codominant, dominant, recessive and additive models ($p > 0.05$).

Our results indicate that LSCC patients carrying the *PTTG1* rs2910200 CT genotype are more likely to develop locally advanced primary tumors with extralaryngeal extension. These findings suggest that *PTTG1* genetic variation may serve as a potential biomarker for tumor aggressiveness, providing valuable information for prognosis and guiding clinical management.

Keywords: PTTG1, RS2910200, laryngeal squamous cell carcinoma, oncology

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