DEVELOPMENT OF NOVEL GENETIC SIGNATURE FOR PREDICTING SURVIVAL IN PATIENTS WITH LARYNGEAL SQUAMOUS CELL CARCINOMA

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Introduction. Results of laryngeal squamous cell carcinoma (LSCC) treatment and five-year survival rate of these patients remain poor. To purifytherapeutic targets, investigation of new specific and prognostic specific blood- or tissue-based biomarkers of LSCCis required.

Research objectives. This study aimed toevaluate the impact on selected single nucleotide polymorphisms (SNPs) (*IL-6* rs1800795, *IL-9*: rs2069884, rs2069885, rs1859430, rs2069870, rs11741137, *IL-10*: rs1800872, rs1800871, rs1800896, *BLK* rs13277113, *TIMP3* rs9621532, *IL1RL1* rs1041973, ant *IL1RAP* rs4624606) on LSCC development and to analyse associations of selected SNPs with patients' five-year survival rate.

Material and methods. 300 *LSCC* patients and 533 controls were included in the study. Genotyping of selected SNPs was carried out using the RT-PCR.

Results. Significant associations were identified between *IL-10* rs1800871 variants and advanced stage of LSCC patients'group in the codominant, recessive and additive models (p=0.027, p=0.040 and p=0.037). Significant variants of *IL-10* rs1800872 were determined in the codominant, recessive and additive models (p=0.027, p=0.040 and$p$=0.037). Significant genotype distribution was identified between *TIMP3* rs96215332 variants and LSCC in the codominant, overdominant and additive models (p=0.020, p=0.020 and p=0.045).Also, significant variants of *IL1RAP* rs4624606 were determined in the codominant, overdominant and additive models (p=0.030, p=0.037 and p=0.025). Multivariable Cox regression analysis revealed a significant association between the patients' survival rate and distribution of *IL-9* rs1859430 and *IL1RAP* rs4624606 variants: patients carrying AA genotype at *IL-9* rs1859430 and AA or TT at *IL1RAP* rs4624606 had a higher risk of dying (p=0.005; p=0.044).

Conclusions. *IL-10:*rs1800871, rs1800872 SNPs are associated with the development of advanced stages of LSCC. TIMP3 rs96215332 and *IL1RAP* rs4624606 SNPs play a significant role in the development of LSCC. The genotypic distribution of *IL-9* rs1859430 and *IL1RAP* rs4624606 negatively influences the five-year survival rate of LSCC patients, suggesting that they could contribute to developing blood-based biomarkers of LSCC.