LITHUANIAN UNIVERSITY OF HEALTH SCIENCES

International Summer School Practice

Associations Between RYR2 Gene Single Nucleotide Variants and Laryngeal Squamous Cell Carcinoma Progression

Laryngeal squamous cell carcinoma (LSCC) is one of the most common malignancies of the head and neck region and remains a significant clinical challenge due to its potential for local invasion, regional metastasis, and high mortality rates, particularly in patients diagnosed at advanced stages. One of the major challenges in LSCC management is the difficulty of early detection, as initial symptoms may be nonspecific and the disease is frequently diagnosed at more advanced stages. Delayed diagnosis can limit treatment options and negatively affect patient survival. Therefore, the identification of reliable molecular biomarkers that could facilitate earlier diagnosis, improve risk stratification, and predict disease progression is of considerable clinical importance.

Genetic biomarkers have emerged as promising tools for improving cancer detection and prognosis. The identification of genetic variants associated with tumor development and progression may contribute to a better understanding of disease pathogenesis and potentially support more personalized approaches to cancer management. However, the molecular mechanisms underlying LSCC progression remain incompletely understood, highlighting the need for further investigation of genetic factors potentially associated with tumor aggressiveness.

The RYR2 gene encodes ryanodine receptor 2, an intracellular calcium release channel primarily involved in the regulation of calcium signaling. Calcium signaling plays an essential role in various cellular processes, including proliferation, differentiation, migration, and apoptosis. Dysregulation of intracellular calcium homeostasis has been implicated in cancer-related processes, suggesting that genetic variations in calcium-regulating genes may influence tumor biology. Nevertheless, the potential associations between RYR2 gene single nucleotide variants (SNVs) and LSCC progression remain insufficiently investigated.

The aim of this scientific internship project is to investigate the associations between selected RYR2 gene single nucleotide variants and the progression of laryngeal squamous cell carcinoma.

Objectives:

1. To determine the genotype and allele frequencies of selected RYR2 gene single nucleotide variants in patients with laryngeal squamous cell carcinoma.
2. To evaluate the associations between selected RYR2 gene variants and tumor stage and lymph node involvement in patients with LSCC.
3. To investigate the associations between selected RYR2 gene variants and histological differentiation grade of LSCC.

During the internship, selected RYR2 gene variants will be analyzed in patients diagnosed with LSCC. The study will focus on evaluating genotype and allele frequencies and investigating their potential associations with available clinicopathological characteristics, including tumor stage, lymph node involvement, histological differentiation grade, and other indicators related to disease progression. Appropriate statistical methods will be applied to assess potential associations between the investigated genetic variants and clinical parameters.

The expected results may provide preliminary insights into the potential role of RYR2 genetic variability in LSCC progression. Identifying genetic variants associated with more aggressive disease characteristics could contribute to the discovery of potential prognostic biomarkers and support future research aimed at improving patient risk stratification and clinical decision-making. Although further validation would be required before clinical application, these findings may contribute to broader efforts to improve the molecular characterization, early detection, and management of LSCC. This scientific internship will provide practical experience in molecular genetics research, genetic data analysis, statistical evaluation, and interpretation of genotype–phenotype associations in oncology.