TORAKS 2020
10. kongres Hrvatskog torakalnog društva
10th Congress of the Croatian Thoracic Society
16.–19. rujan | September
Hotel Hilton Garden Inn, Zagreb

htd hrvatsko torakalno društvo

IDENTIFICATION OF NOVEL SINGLE-NUCLEOTIDE POLYMORPHISMS IN CHRONIC OBSTRUCTIVE PULMONARY DISEASE (COPD) AND LUNG CANCER USING GENOME-WIDE ASSOCIATION ANALYSIS

BARANAŠIĆ J.[1], Niazi Y.[2,3], Chattopadhyay S.[2], Försti A.[2,3], Knežević J.[1]

[1] Institut Ruđer Bošković, Zagreb, Croatia
Laboratorij za naprednu genomiku

[2] German Cancer Research Center (DKFZ), Heidelberg, Germany
Department of Molecular Genetic Epidemiology

[3] German Cancer Research Center (DKFZ), Heidelberg, Germany
Division of Pediatric Neurooncology

Objective:

Chronic obstructive pulmonary disease (COPD) is a major public health problem associated with long-term exposure to toxic gases and particles. Patients with COPD have higher risk of developing lung cancer (LC). Lung cancer is the leading cause of cancer-related deaths worldwide. Even though LC is associated with tobacco smoking, genetic susceptibility plays an important role in disease etiology. Candidate susceptibility genes coding for enzymes involved in the activation, detoxification, and repair of damages caused by tobacco smoke as well as genes in inflammatory and cell-cycle pathways have been extensively studied. Immune system has been shown to be a determining factor during

cancer initiation and progression. In recent years there is more and more focus on immune therapy, but still, genes that are involved in the regulation of the immune response haven't been fully identified/studied.

Genome-wide association studies (GWAS) have a great capability of detecting genetic variants for complex diseases like COPD and LC. In GWAS a cohort is genotyped and the resulting data is then analyzed in relation to disease or to quantitative trait phenotype. The results of the study are genetic variants, single nucleotide polymorphisms (SNPs). Each SNP is then analyzed according to minor allele frequency, P-value, biological significance and other factors.

The aim of this study is to find new SNPs that are associated with COPD and LC risk, with focus on immune genes. Using statistical analysis of GWAS data, two case-control studies (early and late COPD-control and lung cancer-control), we identified several SNPs related to immune response that could be important in developing COPD and LC. The results of the analysis shows 96 SNPs in vicinity of immune-related genes that are associated with development of COPD and 13 SNPs in vicinity of immune-related genes that are associated with development of LC._Even thou the results don't show a common SNP associated with these two diseases, there are two different SNPs rs11569805, associated with COPD, and rs1148471, associated with LC, in intronic regions of TNFRSF8 gene. Therefore TNFRSF8 gene is an interesting target for future functional studies to see it's implication in development of COPD and LC.