ID 68 Lung Cancer: a Study of Genetic Variants in the Romanian Population

Monica Dugaesescu[1], Ana-Maria Balan[1], Ioana Bejan[1], Simona-Elena Bonciu[1], Oana-Iulia Brinduse[1], Elena-Corina Ferdoschi[1], Elena Poenaru[1]

[1]Faculty of Medicine, „Carol Davila" University of Medicine and Pharmacy, Bucharest, Romania

Objectives: Lung cancer is one of most frequent types of cancer worldwide, while in Romania it ranks third. Genome-Wide Association Studies (GWASs) on lung cancer have been setting a milestone in understanding the individual's genetic risk and its impact on population.

The purpose of the study is to identify variants associated with lung cancer in Romanian population by performing a GWAS, finding previously unreported variants and searching information on the resulting Single Nucleotide Polymorphisms (SNP) in databases.

Methods: A GWAS was conducted on data obtained from patients admitted between 2014 and 2018 to 4 clinics in Bucharest, 1386 cases and 1437 controls, all of them self-reported European descent. DNA was extracted from whole blood at deCODE Genetics (Reykjavik, Iceland) and genotyped using Infinium OmniExpress-24 bead chips (Illumina). A total of 716.503 SNPs were genotyped and after data quality control, 91.897 variants entered data processing, performed in R Studio. PLINK tool was used for the association analysis. Information about the significant variants was searched in dbSNP, GWAS Catalog, PubMed, ClinVar and Tumor Portal.

Results: After applying statistical and genetic filters to the data, 69 SNPs with a p value smaller than 10-5 were identified. Four of them have a p value lower than 10-8 (rs10493170, rs17741574, rs16915833, rs4445762). After literature review, 16 of them were highlighted as possible clinically relevant SNPs for lung cancer pathology, as risk or protective factors. Some of the genes linked to the significant SNPs are: DRAM2, PROX1, RBM47, TIAM1, CXCL16, MAGI2. PLAG1.

Conclusions: The GWAS resulted in 69 SNP with a $p < 10\text{-}5$ and after a thorough literature review, multiple leads to lung cancer in Romanian population were found. Further research should be conducted in order to determine the complex involvement of these polymorphisms in lung cancer pathology.

ID 90 Alteration of Protein Glycosylation in Renal Cell Carcinoma

Corina-Daniela Ene[1,2], Ilinca Nicolae[3], Marilena Ciortea[1,4], Mircea Nicolae Penescu[1,2]

[1]„Carol Davila" University of Medicine and Pharmacy, Bucharest, Romania
[2]„Carol Davila" Clinical Hospital of Nephrology, Bucharest, Romania
[3]„Victor Babes" Hospital of Tropical and Infectious Diseases, Bucharest, Romania
[4]Gral Medical, Bucharest, Romania

Aim: Genetic and epigenetic alterations are considered primary causes in cancer development, while phenotipic characteristics define cancer progression and invasion due to postrtanslational changes.

The aim of the study was the evaluation of some soluble biomarkers protein glicosylation associated in renal cell carcinoma (RCC).

Material and method: We developed a prospective study that included 55 patients with primary renal cell carcinoma (age 58,6±11.3 years old, women: men ratio 1:1.25) and 33 healthy subject in the control group (age 57.8±9.5 years old, women: men ratio 1:1). Glycosylation was evaluated by assessment of serum levels of orosomucoids (g/L serum) and sialic acid (mg/dL serum).

Results: In RCC group, orosomucoids (50.13±3.66 vs 114.50±22.05, $p<0.001$) and sialic acid (0,86±0,14 vs 5.72±0.47, $p<0.001$) had significantly increased levels, compared with control group. Using Kolmogorov Smirnov test, we determined a normal distribution of orosomucoid and sialic acid levels in the RCC and control group. Using Anova test, we observed statistical significant differences between the two groups regarding orosomucoids and sialic acid.

The regression analysis showed statistically significant correlations between orosomucoids, sialic acid and inflammatory status (C reactive protein, fibrinogen, albumin, interlukin 6 and 8), respectively renal function (eGFR, albumin/creatinine ratio).

Conclusions: Serum variation of orosomucoids and sialic acid in the studied groups sustain the idea that renal oncogenesis is associated with aberrant glycosylation of proteins. Protein glycosylation status in patients with RCC compared with control group is an early alteration in renal cancer, a glycosignature of RCC. The model of proteic glycoforms could be used in diagnosis and management of nephro-oncologic patients.