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115 Significance Estimation of EGFR and Their Polymorphisms -216G>T (rs712829), -191C>A (rs712830) and 181946C>T (D994D) (rs2293347) in Non-Small Cell Lung Cancer

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Hypothesis: Epidermal growth factor receptor (EGFR) was usually over expressed in many epithelial cancers including lung cancer. It is trigger molecule for many important processes in normal cells concerning growth, development, differentiation, but in tumor cells it conduct many abnormal messages through signaling network cascade leading to cancer genesis.

Objectives: Genetic and epigenetic changes in lung cancer, including single nucleotide polymorphisms (SNPs) are in the course of scientific interest with many reasons.

Methods: Here we described methods for standardization of PCR reaction including different additives, temperature and other conditions, for estimation of expression of promoter regulators of EGFR, including -216G>T, -191C>A and 181946 C>T (SNPs) in 47 NSCLC patients in comparison to 43 health persons in Serbia. These data were compared with results obtained in different ethnic populations.

Result: Significant differences in EGFR and SNPs distributions were noticed through great ethnic populations. These results showed that the most frequent haplotypes in both NSCLC patients and healthy subjects in Serbia were CG (54.96 %), CT (27.36 %), while AG (16.38 %) and AT where present at 1.30 %. Caucasians and Afro-Americans had more frequent -216G/T than Asians, but -191C/A was present only in Caucasians. SNPs -216G>T and -191C>A discussed here, were present with different frequency in great ethnic groups.

Conclusions: Still it is unclear relation between those polymorphisms and common mutations, but they were connected with enhanced EGFR promoter activity, with increased gene and protein expression, and some side effects of TKI used for NSCLC. According to those considerations, it could be noticed that investigation of SNPs could be potential pharmacogenetic biomarker for efficacy and safety of TKI treatment approach for NSCLC.

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116 Reactive Oxygen Species in Non-Hodgkin's Lymphoma patients

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Hypothesis: Non-Hodgkin's lymphoma (NHL) is a heterogeneous group of clonal, proliferative, abnormal diseases of B- or T-cells and is usually first diagnosed in lymph nodes or as extranodal lymphatic masses. The generation of free radicals and ROS contributes to a broad spectrum of normal physiological processes, while excess of ROS results in DNA and protein damage and consecutive participated in cancerogenesis.

Objectives: Identification of the effects of excess reactive oxygen species on DNA, protein damage, and consecutive cancerogenesis.

Methods: In this study, 32 patients with NHL and 13 healthy volunteers were studied. The diagnosis of NHL patients was based on histological

documentation of lymph node and/or bone marrow biopsies. Clinical staging was performed according to the Ann Arbor system based on combination of clinical routine examination, blood and ultrasound analyses, chest ray and computerized tomography (CT) scan. The pathohistological evaluations for 32 patients, aged from 27 to 57 years, with NHL was made according to the International Working Formulation, and IPI score index. Superoxide-anion radical and TBARS, and GSH (glutathione extraction) are determined by biochemical methods previously established.

Results: A statistically significant ($p < 0.05$) increase of levels of O₂ was measured in patients who were in advanced clinical stage IV. The levels of TBARS, as well as GSH, increased in plasma of NHL patients and correlated with increased clinical stage ($p < 0.05$, ANOVA). The generation of O₂ was significantly higher ($p < 0.05$) in plasma of NHL patients with high grade of malignancy as compared to the controls. There were no differences in the values in patients with low or intermediate grade of malignancy. The results showed significantly increased levels of TBARS ($p < 0.05$, ANOVA) in plasma of NHL patients in all three histological types as compared with controls. Plasma levels of GSH, were significantly increased ($p < 0.05$, ANOVA) in NHL patients as compared with controls in all histological types. There were no differences for these parameters between the histological types of NHL patients.

Conclusions: The abnormal production of cellular oxidants or the imbalance of the oxidant to the antioxidant control systems have been linked to mutation and by oxidant -induced DNA damage and many other changes in gene expression. Moreover, several signal transduction pathways, such as activator protein-1 and Nuclear Factor-Kb (NF-Kb), are known to be activated by ROS. This leads to the transcription of genes involved in cell growth regulatory pathways. Based on this estimation of these parameters in serum of patients with cancer can help in diseases monitoring.

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117 Are Circulating Growth Factors Suitable for Predicting Lymph Node Metastases and for Clinical Decision About Axillary Lymph Node Dissection in Early Breast Cancer Patients?

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Hypothesis: Growth factors actively participate in tumor-induced angiogenesis and lymphangiogenesis and their serum levels may reflect lymph node (LN) metastases formation in early breast cancer.

Objectives: Lymph node metastases are one of risk factor in early stage breast cancers and their presence determine the extent of surgical intervention. Axillary lymph node dissection (ALND) is a standard procedure, however a number of studies provided evidence that avoiding ALND does not worsen the general prognosis. The aims of our study were to evaluate the possibility of selected growth factors as biomarkers for lymph node status determination