for nephropathy provides useful information on the development of drugs with therapeutic benefits with reduced side effects. Mechanisms for drug-induced nephropathy include changes in glomerular hemodynamics, tubular cell toxicity, inflammation, crystal nephropathy, rhabdomyolysis, and thrombotic microangiopathy\(^2\). Biomarkers have been identified for the assessment of nephropathy. Although some of them fail to confer specificity and sensitivity, the discovery and development of novel biomarkers that can diagnose kidney damage earlier and more accurately are needed for effective prevention of drug-induced nephrotoxicity\(^3\). The main purpose of our study was to investigate the oxidative modifications of proteins in blood plasma of patients with drug-induced nephropathies.

**Materials and Methods.** There were 75 patients divided into 2 groups depending on the type of the drug. The first group was represented by patients with psychotropic drug-induced nephropathy (amitriptyline in 75% cases); the second one – by patients with nephropathy caused by nonsteroidal anti-inflammatory drugs (NSAIDs – painkillers in 55% cases). The control group consisted of 22 healthy subjects. In blood plasma were detected reactive protein carbonyl derivatives (Levine et al, 1990), advanced oxidation protein products (AOPP) in serum (Witko-Sarsat et al, 1996).

**Results.** The reactive protein carbonyl derivatives level in blood plasma of the 1st group was lower in comparison with control one (\(p<0.05\)). AOPP concentration was the highest in serum of the 2nd group (\(p<0.05\)). Our results demonstrated that in blood of patients the patterns of oxidized proteins to be varied depending on the type of the drug group.

Naturally, a lot of questions arise concerning the mechanisms of protein modification and the possible regulation of this process. Thus, it remains unclear how to regulate the processes of “directed”, or “targeted” carbonylation of certain proteins by using NSAIDs or psychotropic drugs. It proves the need for further studies of metabolic disorders in the formation of different types drug-induced nephropathy.

**References:**


Keywords: drug-induced nephropathy, modified proteins, AOPP, drug poisoning.

**OVEREXPRESSION OF STAT4 IS A POSSIBLE DIAGNOSTIC MARKER OF EARLY STAGES OF MYCOSIS FUNGOIDES**

Grekova Е.V., Olisova О.Yu., Alekseeva E.A., Zaletayev D.V.

1 V.A. Rakhmanov Department of Skin and Veneral Diseases, I.M. Sechenov First State Medical University, 119991, Russian Federation;

2 Laboratory of medical genetics, Institute of molecular medicine, I.M. Sechenov First Moscow State Medical University, Russian Federation

Cutaneous T-Cell Lymphomas (CTCLs) include a clinical-pathologically heterogeneous group of non-Hodgkin lymphomas primarily developing and affecting the skin. Mycosis fungoides (MF) is the most common disease among the cutaneous T-cell lymphomas (85-90%). The accuracy of the diagnosis of MF, which is confirmed only by clinical, histological and immunohistochemical signs, is 50-75%. The aim of the study was to investigate genetic markers (FOXP3, STAT4, IL12B) for early diagnosis of mycosis fungoides.

**Materials and Methods.** A study involving 42 patients with MF and plaque parapsoriasis (PP) treated at the Dermatology Department of I.M. Sechenov First Moscow State Medical University and National Medical Hematology Research Center, was performed. The analysis of gene expression FOXP3, STAT4, IL12B was carried out by TaqMan Real time-PCR. The objects of the study were lesional skin samples of patients. A group with MF consisted of 29 patients, a group with PP consisted of 13 patients, a control group included 10 healthy volunteers.

**Results.** The study revealed that the level of STAT4 gene expression showed a significant (9 times) increase in the mRNA expression of STAT4 transcripts in patients with MF (166) compared with patients with PP (17.9; \(p<0.05\)) and 553 times - with healthy volunteers (0.3; \(p < 0.05\)).

There was also a statistically significant predominance of the level of mRNA expression of STAT4 transcripts in patients with spotted and plaque stages of MF (180; 318) compared with patients with PP (17.9; \(p<0.05\)) and healthy volunteers (0.3; \(p < 0.05\)), as well as a sharp decrease in patients with erythrodermic form of MF (7.19).

**Summary.** For early diagnosis of MF the level of expression of mRNA transcripts STAT4 is of great importance. Inclusion of STAT4 in the list of diagnostic features increases the accuracy of differential diagnosis of MF and PP from 59.1% to 81.8%.

Key words: mycosis fungoides, early diagnosis, STAT4, FOXP3, molecular genetic method of diagnosis.