expression of CD79b (in 94.2% of cells). The same phenotype was registered in one patient with del(6q23), comprising CD78b+ (in 97.8% of cells), CD22+ (in 62.6% of cells) and CD38+ (in 32.5% of cells). In 2 patients (6%) with del(11)(q23) expression of CD79b (in 47.3–44.8% of cells) and CD38 (in 35.3–64.4% of cells).

**Conclusion:** Expression of CD79b, CD22, CD38 is the main feature of cells with recurrent genetic injuries. Immunophenotype without expression of CD79b, CD22, CD38 in most cases differentiates CLL patients with del(13)(q14.3), del (13)(q34), (13q)(34) trisomy and with normal karyotype. Coexpression of the most of the cells of the three antigens CD79b, CD22, CD38 and more bright expression of CD20 proposes trisomy 12 or del(6q). Partial expression of CD79b and CD38 may correlate with del(11)(q23).

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A75

Modern concepts of cellular and molecular mechanisms of breast cancer and their prognostic significance

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Breast cancer is one of the most common cancers in women. The incidence of breast cancer in 2014 in the Republic of Mordovia was 69.9 per 100,000 female populations. Breast cancer occurs when excessive expression of oncoproteins switches in the case of transformation of proto-oncogene in PRADI. In primary breast tumors, mutations and the expression of the three oncogenes Her2/neu, C-mys, Int-2, as well as supression of the p53 and the retinoblastoma gene RB are the most common. Several studies found that oncogene – C-mys was expressed in 16.8% of primary breast cancer cases and in 35% cases with subsequent development of metastases. Proteins that stimulate the phosphorylation of mitogen-activated protein kinases are activators of the influence of growth factors. Development of breast cancer is regulated by a complex interaction of many hormones and growth factors. Currently, one of the leading theories of developing breast cancer is the increased hormonal stimulation of proliferative processes in the development of neoplasia. One of the manifestations of hormonal imbalance in tumor during a regular decrease in blood competitive inhibitor of the biological effects of estrogen – progesterone, which is in correlation with the stage of the spread of neoplasia. The role of the overproduction of estrogen in the pathogenesis of breast cancer is confirmed by the fact that in women who underwent oophorectomy before the age of 38 years, the risk of breast cancer development is 1.5 times less than in those who did not have such operation. Excessive accumulation of lipid peroxidation products in the area of neoplasia activates mechanisms violation of intercellular interaction that caused the destruction of the lipid components of membranes.

The study group included 112 patients treated at the State Institution of Health of the Republic of Mordovia "National Oncology Center". To identify the nature of tumors, all patients underwent immunohistochemical analysis. Androgen receptors were found in 48% of breast cancer cases, the expression level of androgen receptor in the tumor was much lower than the expression level of estrogen and progesterone receptors. Low levels of progesterone receptor expression in breast cancer cells were combined with high levels of expression of Ki-67 antigen, HER-2 oncoprotein in tumor cells. Patients with HER-2 (3+) and (2+) had more frequent multiple metastases in lymph nodes compared to patients with HER-2 (0) and (1+) phenotypes. Maximum expression of HER-2 oncoprotein in tumor cells indicated high metastatic potential and poor prognosis.

It may be concluded that the cellular and molecular mechanisms of breast cancer are complex. Therefore, carcinogenesis has a "multistep" nature and at least two or more mutations in the cells of the same clone – parent and child are required to generate malignant tumors. Thus, the development of oncogenic transformation does not necessarily mean the process of tumor formation.

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P156

Detection adducts DNA in human blood and lung cancer tissue by a hybrid quadrupole time-of-flight (Q-TOF) mass spectrometer

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**Background:** Identification of DNA-based biomarkers of cancer cells is highly promising and rapidly developing direction that can advance early detection and therapy of malignancies. DNA adducts are felicitous markers of cancer, because their chemical structure is significantly different from that of mutated or methylated DNA, that allows to determine them with high precision using mass spectrometry. The aim of this work is to develop the methodology of sample preparation and its mass spectrometric analysis. Samples were prepared from the blood plasma and from the tumor tissue from lung cancer patients and from blood of healthy individuals.

**Materials and methods:** DNA was isolated from the blood plasma and tissue by using column method (BioSilica, Russia). The final yield from 1 ml of blood was 100 ng. DNA samples were subjected to acid hydrolysis (1 M HCl) at 70°C. After 3 h, the hydrolysis was stopped by cooling on ice for 5 min and later on adding an equivalent amount of an alkali and a phosphate buffer solution (pH 7). To assess the extent of hydrolysis of the samples they were analysed by electrophoresis on a 1.2% agarose gel in Tris-acetate buffer. The samples were extracted at cartridge HF Bond Elut-C18 100 mg, 1 ml (Agilent Technologies, USA) and eluted in several fractions with a gradual increase of methanol in the eluent. Stream of nitrogen was applied to dry the extract.