local inflammation was achieved (redness, swelling, infiltration of tissues, pain). After 6 days of treatment wound stitches were removed. Wound healing occurred by primary intention.

Bacteriological analysis after 24 hours after triple injection of a reference drug in the study group was negative. In the control group, even on the seventh day bacteriological analysis showed the presence of St / aureus 1*103.

Cytological analysis of the control group showed long exudative phase of inflammation was remained, later granulation tissue and epithelialization were appeared. The duration of complete epithelialization of the wound was not less than 15 days.

Cytological analysis of the study group showed acceleration of regenerative processes with early maturation of granulation tissue on the fourth day.

Fibroblasts with a higher degree of differentiation are arranged in groups in order of their direction. This indicates the primary wound healing.

Conclusions. We have experimentally proved the effectiveness of local application of autologous erythrocyte ghosts with ceftriaxone and cytokines (Betaleukine and Ronkoleukine) in the treatment of purulent wounds.

We assume that in the tissues of the wound, the conditions of maximum stimulation of immunogenic reparative processes due to the maintenance of high concentrations of anti-inflammatory cytokine and provide maximum antibacterial effects due to antibiotic administration in the form erythrocytes ghosts.

The proposed technology may allow to significantly improve the treatment of patients with purulent surgical diseases, by targeted delivery of cytokines and antibiotics to the purulent wounds.

ASSOCIATION OF DNA REPAIR GENE XRCC1 (ARG194TRP, ARG399GLN) POLYMORPHISM WITH THE RISK OF LUNG CANCER

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Kew word: lung cancer, XRCC1, gene polymorphism

Introduction. XRCC1 enzyme plays a key role in the excision repairtion of DNA. Actually described three encoding polymorphisms of gene XRCC1 in the codons 194 (Arg/Trp), 280 (Arg/His), and 399 (Arg/Gln). All three polymorphisms are associated with lung cancer risk, but an analysis of published data showed quite contradictory results. There is no evidence about the associations XRCC1 polymorphisms with lung cancer susceptibility in a Kazakh population.

Methods. Research material was collected in the city of Ust- Kamenogorsk (East Kazakhstan) in 2012 -2014 at the Regional Oncology Center. The analysis included 70 lung cancer cases and 70 controls from a Kazakh population. Genomic DNA was isolated from whole venous blood, followed by phenol- chloroform extraction. XRCC1 codons 194 and 399 were determined using PCR-RFLP. The amplified products have been analyzed within 1% agarose gel in front of ethydium bromide and imaging of fragments within UV-light. PCR amplified products were digested with PVU II (for XRCC1 (Arg194Trp)) and NciI (for XRCC1(Arg399Gln)) restriction enzyme (NEB, USA) and electrophoresed on an agarose gel, and then visualized under UV-light.

Results.. Our study showed that the frequency of alleles XRCC1Arg194Arg in patients with

lung cancer was 1.5 times lower than in the control group (p=0.004). By contrast, among the patients with lung cancer there is a higher incidence of genotypes Arg194Trp and Trp194Trp Arg194Trp XRCC1, than in the control. OR values indicate that the both genotypes are associated with risk of lung cancer (OR = 2,3; CI 95% =1,01 – 5,23 and CI 95% =0,91 – 5,78 respectively). According to the study the association between histological type and Arg194Trp XRCC1 gene polymorphism has not been identified. Genotype frequencies of gene XRCC1 Arg399Gln in the Kazakh population was as follows: homozygous for the normal allele Arg / Arg accounted for 37% of the total number (26/70), heterozygous Arg / Gln 26% (18/70) and homozygous for the mutant allele Gln / Gln 37% (26/70) respectively. The result revealed that XRCC1 Arg399Gln polymorphism was not associated with lung cancer risk.

Conclusions. XRCC1 Arg194Trp polymorphism is associated with an increased risk of lung cancer in Kazakh population.

EVALUATION OF AMINO ACID LEVEL IN THE BLOOD OF FETUSES AND NEWBORNS WITH INTRAUTERINE GROWTH RESTRICTION

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Keywords: intrauterine growth restriction, amino acids, newborn

Introduction. The processes of growth of the fetus are provided by a constant supply of amino acids from mother, which provides the production of proteins and muscle tissue of the fetus. The purpose of this research was to study the amino acid level in blood of fetuses and newborns with intrauterine growth restriction.

Methods. The umbilical blood of 36 fetuses and newborns (basic group) with intrauterine growth restriction (IUGR) and 32 fetuses and newborns with normal development (control group) have been examined. Amino acid levels were determined by enzyme immunoassay.

Results. The levels of 18 amino acids in both groups were normal, except essential amino acids such as glutamine, glutamic acid and lysine. The glutamine level in fetuses of control group was about low-level standards (262.0 ± 45.34 nmol/l), and the level of glutamic acid was significantly higher (372.33 ± 44.31 nmol/l) compare to standards (20-110 nmol/l).

Elevated levels of glutamic acid is caused by the fact that it belongs to glyukoplastic acids which are used as distributors for pyruvic, oxaloacetic and α-ketoglutaric ones, which are transformed to glucose and glycogen .

In fetuses with IUGR the histamine levels (36.33 ± 2.44 nmol/l) were almost 8 times lower, while the glutamic acid was 4 times higher (420.66 ± 63.81Nmol / l) than in control group.

Revealed imbalance in amino acid content in the umbilical cord blood of newborns with IUGR is apparently due to declining revenues of glutamine from the mother's blood to the fetus and disturbance of glutamine glutamate metabolism in fetal tissues.

Conclusions. The decrease in the concentration of glutamine and glutamate, accompanied by disturbance of the biosynthesis of progesterone may play a role in triggering preterm birth of a fetus with IUGR.