age at first delivery etc.) and symptoms for breast cancer. The model was based on data of two main groups (group of women with breast cancer and the control - healthy group). The verification of the model performed on set of 100 test patterns. Accuracy of identification of high-risk group was 98%.

**Conclusion:** Advantage of this model is quick and easy identification of women with high risk for breast cancer enabling individually tailored prevention of the disease.

## P16

### A case-control study on the role of blood group and family history in developing gastric cancer before the age of 50

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**Introduction:** Development of gastric cancer (GC) before 50 is likely to have a genetic basis. Blood group A has been shown as a risk factor for GC. Some parts of Iran are endemic regions for GC.

**Aims & methods:** In this prospective case-control study, we enrolled Iranian gastric cancer patients under the age of 50 and sex-matched controls over 50. All the patients and (if alive)/or their family members were interviewed and their pedigrees were drawn. The blood group of the patients were also tested or obtained from the in-patients records.

**Results:** 54 cases (mean age: 37.1, 18-49; m/f=1) under 50 years old and 54 sex-matched controls (mean age: 68.2, 50-88) were enrolled in the study. 40.7% of the study group were dead and 59.3% were alive at time of study. Distribution of blood groups is as follow: 68.6% O, 13% A, 13% B and 5.4% AB in cases and 27.7%, 63%, 6.5% and 2.7% in controls, respectively. 50% of the cases and 9% of controls had some first or second-degree relatives with gastric or other types of cancers ($p<0.01$). Breast, lung, gynecological and hematological malignancies constituted other type of cancer in their families.

**Conclusion:** It seems that gastric cancer before 50 is accompanied with a familial aggregation. Interestingly, our study shows the significant correlation between blood group O and the development of gastric cancer under 50. This arises the need for more linkage analysis study on the role of blood group genetic area in familial aggregation of gastric cancer.

## P17

### The role of clinico-genetic monitoring of risk groups for early diagnostics of female reproductive system tumors

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The oncoepidemiologic situation in Ukraine is marked by the continuous increase of female reproductive system tumors. More than 50% of the new diagnosed cases depend on the influence of external and internal factors. The risk of developing the similar disease in healthy relatives (mother, sister, daughter) of the patients with cancer is about 50%. We performed clinical and genealogical analysis of 513 healthy women, 44% of them had relatives with benign and malignant tumors. Clinical and genealogical analysis, performed in 520 probands with ovarian cancer revealed 34 families with 2 or more relatives suffering from cancer (6.54%). 81 patients with ovarian cancer had 1 close relative with tumors (15.57%). The similar analysis was conducted in genealogies of 482 probands with endometrial cancer. It revealed 13 families with 2 or more relatives suffering from cancer (2.69%). 49 patients with endometrial cancer had 1 close relative with tumors (10.2%). Frequently the relatives of patients with ovarian and endometrial cancers suffered from tumors of female reproductive sphere combined with gut tumors. We examined 110 close relatives of patients with ovarian and endometrial cancer who had an increased risk of developing tumors. Only 19 women manifested with the female reproductive system disorders at the time of their first consultation. The other 91 women were practically healthy. It should be stressed that the risk of developing cancer was 52-54% in the examined women. During a 3-year follow-up of these patients we diagnosed benign tumors, precancrous diseases of female reproductive system and the disorders that were unfavorable for tumor development: myoma of the uterus – 8, ovarian cysts and cystomas – 7, nodular and diffuse mastopathies – 29, tuboovarian tumors – 5, endometrial hyperplasia – 9, chronic adnexitis – 11. This approach is effective because it became possible to diagnose ovarian and endometrial cancers 4 women of the group with the increased genetic risk quite early (sisters of the probands with ovarian cancer – highly differentiated endometrial adenocarcinoma IIa; daughter of the proband with ovarian cancer – serose ovarian cystadenocarcinoma Ib; sister of the proband with endometrial cancer – ovarian cystadenocarcinoma I). The suggested approach to the prevention and early diagnostic of female reproductive system tumors has clinical and social benefits. It could be recommended as a model to the creation of the system of the oncogenetic help to the population.

## P18

### The dependence of VEGF level from characteristics of Lewis lung carcinoma development in C57BL6 mice

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Targeting angiogenesis represents a new strategy for the development of cancer prevention. Angiogenesis,or new blood vessel growth from an existing vasculature,expression of vascular endothelial cell growth factor (VEGF), has become a veri promising target for experimental therapies in cancer. The aim of the study was to investigate dependence of VEGF level from characteristics of Lewis lung carcinoma (LLC) development in C57BL6 mice for the use in perspective as experimental model for the screening new antiangiogenic agents. LLC transplantation was performed by injection i.m. of 0.02 ml of the tumor cell suspension of $2 \times 10^5$ cells. For monitoring of the primary tumor, the levels of tumor dissemination, the tumor volumes (VT, $mm^3$), the number and volumes of the lung metastasis (VLM, $mm^3$), and VEGF levels in serum were estimated.

Blood serum levels of VEGF (ng/ml) were measured by an enzyme immunoassay. All experimental parameters estimated with the use of models of the regression analysis. On the 24th and 33rd day after tumor cells inoculation the dependence of VEGF level from the volume of tumor and metastases has significant correlation and linear character. On the terminal stage of tumor development (41st day) correlation in these parameters was lost, bat significant correlation between VLM and VEGF levels was present. These results indicate that major factor which determine the VEGF level is the size of tumor but not metastatic injuries. We suggest that the LLC in C57BL6 mice has become a veri promising preclinical model for the screening new antiangiogenic agents in prevention of tumor growth and metastasis.

## P19

### Estrogen receptor negative breast cancers express estrogen receptor mRNA

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**Introduction:** Approximately one third of primary human breast cancers do not express the estrogen receptor alpha and are termed ER-negative. Compared to ER-positive breast cancers, these cancers have a worse prognosis and limited treatment options. The ER-negative status of breast cancers is ascertained by ER alpha protein assays and very few studies have assayed ER alpha gene expression in this aggressive form of breast cancer. In this study, we have assayed ER alpha mRNA levels in a large cohort of archival primary human breast carcinomas to further elucidate the mechanisms leading to the ER-negative phenotype.

**Methods:** We examined the relationship between ER alpha mRNA expression using quantitative real time PCR and ER a protein status obtained by cytosolic assays in 250 archival primary human breast tumors. High quality RNA was extracted from 250 primary tumors that had been cryopreserved for up to nine years. RNA quality was verified by gel electrophoresis and visualization of ribosomal bands, by OD260/280 ratios and by amplification of house keeping genes. Quantitative real time PCR using the Light Cycler system was used to determine ER mRNA concentrations for all tumors.

**Results:** All of 200 ER-negative tumors expressed ER alpha mRNA at levels that significantly overlapped those in 50 ER-positive tumors. The mean ER alpha mRNA concentrations for the ER-positive and ER-negative tumors were 1.14 × 10exp3 fmol/ug RNA and 1.27 × 10exp3 fmol/ug RNA respectively. The lowest and highest ER mRNA concentrations were similar and the mean ER mRNA values did not differ significantly between the two breast cancer groups ($p>0.50$). Quantitative PCR of housekeeping gene h-PBGD in the ER-positive and ER-negative tumors showed similar starting RNA quantities and qualities in the two groups. This was further demonstrated on agarose gel electrophoresis.

**Conclusions:** Thus, the lack of ER alpha protein in ER-negative breast cancers is not due to a lack of ER alpha gene expression but is due to post-transcriptional mechanisms. Increasing evidence links ligand-activated ER-dependent gene transcription with ER proteolysis. The presence of ER alpha gene expression in ER-negative breast cancers may explain why some of these cancers respond to tamoxifen. Our data raise the possibility that ER-negative breast cancers are not estrogen-independent for growth.

## P20

### A new look at the prognostic value of the presence of estrogen, progesterone and epidermal growth factor receptors in breast cancer tissue of women patients

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The aim of the study was to evaluate the influence of the presence or absence in tumours of estrogen (ER), progesterone (PR) and epithelial growth factor receptors (EGFR) on the survival of women with breast cancer. The receptors were determined by biochemical radiocompetitive methods. In order to analyse disease-free survival (DFS) and overall survival (OS) we applied Cox's proportional hazard model, in which we analysed both the presence of receptors and clinical and morphological parameters of survival. The tumour size, metastatic lymph nodes and the presence of cancer infiltrations outside lymph nodes were negative prognostic factors. The mean relative risk (RR) were between 1.50 and 3.91. Our results suggest, that both disease free survival and overall survival is directly related to the concomitant presence or absence of ER, PR and EGFR in breast cancer. It was found that patients with receptor status ER+PR+EGFR+, ER-PR+EGFR-; ER+PR+EGFR-; and ER-PR-EGFR- had better parameters of DFS and OS (RR for DFS or OS were between 0.22-1.16). The patients with receptor status: ER-PR+EGFR+; ER+PR-EGFR-, ER-PR-EGFR+ and ER+PR-EGFR+ presented a more aggressive disease course (RR for DFS and OS were between 1.46-3.95). The presence of EGFR in breast cancer tissue is not always a negative prognostic factor for survival. It's coexistence with ER and PR is related to the best survival parameters (the group ER+PR+EGFR+, RR for DFS - 0.45 and for OS - 0.22). The survival of patients with only PR receptors or no receptors (ER-PR-EGFR-) within breast cancer tissue do not differ significantly from the parameters found in the reference variable ER+ PR+EGFR-, RR for DFS and OS are, respectively, less than 1 (0.63 and 0.26) or only slightly greater than 1 (1.07 and 1.16).