

Introduction: Prostate cancer is the second most diagnosed cancer, and the second most common cancer-cause of deaths in men worldwide. The apparent diffusion coefficient (ADC) derived from DWI has been shown to improve the detection of prostate cancer and is the primary imaging method for the differentiation between low to high grade cancers. ADC values show reduction with increasing Gleason's score.

Methods: Prospective study included 60 subjects. Male patients were divided into the groups with pathohistology verified benign and malignant lesions (aged, 46–81; average age, 67.7 years) with abnormal PSA values (>4 ng/ml), and into control group (aged, 44–81; average age 65.3) with normal PSA values (0–4 ng/ml). Prostates were first examined on MRI, determining the diffusion values on ADC map, by placing the region of interest (ROI), through the middle of lesions. Later, the TRUS-guided biopsies were performed. Three intersections of the prostate (apex, middle, and base) were observed, and at total of 12 places (4 places per section) the mentioned methods were indicated.

Results: Statistically significant difference ($p < 0.05$) between the groups of patients with malignant and benign lesions in relation to the ADC values of the apex, base and middle of prostate. ADC values of malignant lesions at apex were in range 952–1030, at base $859\text{--}977 \times 10^{-6} \text{ mm}^2/\text{s}$, while in benign lesion values at apex were in range 1234–1336, and at base $1096\text{--}1183 \times 10^{-6} \text{ mm}^2/\text{s}$.

Conclusion: Determination of the numerical value of ADC map represents a significant additional diagnostic parameter for prostate cancer. All values in the range of 1179–1229 for base, 1063–1139 for middle, and $1199\text{--}1379 \times 10^{-6} \text{ mm}^2/\text{s}$ for apex were considered normal. Values between the range of $857\text{--}1030 \times 10^{-6} \text{ mm}^2/\text{s}$ have been suspected for possible presence of the prostate cancer.

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PS101

Deoxycytidine kinase expression in AML blasts and its relationship to leukemia-free and overall survival

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Aim: Study the correlation of expression of genes involved in cytarabine metabolism to leukemia-free (LFS) and overall survival (OS) in AML.

Introduction: Cytarabine is the backbone of AML therapy. Understanding the roles and polymorphisms of genes involved in cytarabine metabolism and resistance in AML will facilitate development of novel therapeutics.

Methods: Adults less than 60 years with non M3 AML were included. Archived diagnostic marrow samples were studied for expression of 10 genes involved in cytarabine metabolism by RT-qPCR; gene expression normalized to GAPDH was compared

using the unpaired t-test with Welch correction. SNP rs4694362 in deoxycytidine kinase (DCK) gene was tested using Taqman assay. Median time to relapse and survival was calculated by Kaplan Meier method.

Results: 21 Han Chinese patients (median age: 50) were identified; 15 were male; 16 had intermediate risk cytogenetics; 5 had a blast count of over $100 \times 10^9/\text{L}$ at diagnosis. 17 patients achieved CR; 12 after first induction. No difference in gene expression was seen between CR ($n = 12$) versus non CR ($n = 9$) with first induction. 17 CR patients were followed for a median duration of 67.5 months; median time to relapse was 15 months. 1 patient who underwent allogeneic transplant in CR1 was excluded. Higher mean DCK expression was seen in patients with LFS longer than ($n = 7$) versus less than 2 years ($n = 9$) (1.91 ± 0.67 , $p = 0.01$) and in those with OS longer than ($n = 8$) versus less than 3 years ($n = 8$) (2.02 ± 0.69 , $p = 0.01$). DCK rs4694362 TT genotype was less prevalent than CT in patients with >2 year LFS; but not statistically significant. (49% vs 60%, $p = 0.6$).^{1,2}

Conclusion: DCK phosphorylates cytarabine to its active metabolite. Our work shows that higher DCK expression is correlated to LFS and OS in AML. The role of DCK SNP rs4694362 should be explored further in the Chinese.

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PS108

Analysis of MTHFR C677T polymorphism significance in patient preparation for the in vitro fertilization procedure



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Aim: The aim of this study is to determine if in relation to general population, there is a statistically significant difference in the frequency of alleles and genotypes of the C677T polymorphism of MTHFR gene, amongst women with unknown cause of infertility, who are undergoing in vitro fertilization preparation.

Introduction: Methylene tetrahydrofolate reductase (MTHFR) is an enzyme coded by MTHFR gene. Polymorphism of MTHFR gene C677T leads to decreased function of MTHFR enzyme, which is associated with high level of homocysteine and low concentration of folate, which can undermine female reproductive function and affect the outcome of in vitro fertilization.

Methods: The study included the experimental group consisted of 31 women and the control group consisted of 100 women. C677T polymorphism was detected via PCR/RFLPS method. The statistical difference in genotype and allele frequencies was conducted using the Chi-square test.

Results: The comparison of genotypes amongst the experimental and control group has not shown a statistically significant difference ($p > 0.05$). Frequency of the MTHFR677 TT genotype is 22.6% in the experimental group, and 12.0% in the control group, while the allele T frequency amongst the experimental group was

41.9%, and the frequency of the aforementioned allele amongst the control group was 34.5%.

Conclusion: The results of this study show that there is no statistically significant correlation between MTHFR C677T polymorphism in women with infertility of unknown cause, who are undergoing in vitro fertilization preparation, but also underline the need for further research.

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PS114

Assessing the oxidative modification of proteins in inflamed placenta combined with iron deficiency anemia in the pregnant through histochemical method with bromophenol blue based on Mikel Calvo



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Aim: To set features of OMB in the cytoplasm of decidua cells in basal plate of the placenta at chorioamnionitis with iron deficiency anemia in pregnant women by means of histochemical methods combined with computer microspectrophotometry.

Introduction: Decidua cells are important cells to the placenta, playing a significant role both in the physiology of pregnancy and during inflammation. The processes of oxidative modification of proteins (OMB) in inflammation are associated with increased levels of oxygen free radicals, which alter the properties of these macromolecules while oxidating amino groups of proteins. Anemic condition is accompanied by intensification of free radical processes in the blood and tissues, and iron deficiency additionally significantly modifies these processes.

Methods: 125 studied placentas, to compare the studied placental physiology of pregnancy and monitoring iron deficiency anemia without inflammation.

A histochemical reaction of bromophenol blue for “acidic” and “basic” proteins by Mikel Calvo was set in histological sections 5 µm thick.

Delta Optical Evolution 100 and Olympus SP-550UZ were used to obtain a digital copy of the image. Ratio R/B, which is the ratio between the amino and carboxyl groups in proteins, was determined by “ImageJ”.

Unpaired Student’s test calculated arithmetic mean and its error.

Results: When assessing visual histochemical preparations decidua cells are clearly stained, that is suitable for quantitative research, cell boundaries are defined through clear cell membrane coloring and contrasting color around decidua cells fibrinoid. Nuclei and nucleoli were visualized fairly well. “Basic” proteins prevailed in nucleoplasm, while “sour” in the nucleolus.

The decidua cells’ cytoplasm specific color has been mostly granular in nature, and spectral characteristics and optical density of color varied greatly.

Factor R/B at physiological pregnancy ($n = 20$) was -1.04 ± 0.008 and in iron deficiency anemia ($N = 21$) -1.06 ± 0.009 $P > 0.05$. In acute chorioamnionitis ($n = 23$) -1.08 ± 0.009 , and combined with iron deficiency anemia ($N = 21$) -1.09 ± 0.009 $P > 0.05$. Regarding chronic chorioamnionitis ($n = 20$) ratio -1.24 ± 0.011 , and combined with iron deficiency anemia ($N = 21$) -1.64 ± 0.016 $P < 0.001$.

Conclusion: Conclusion. The intensity of OMB increases only in chronic form of chorioamnionitis in the decidua cells cytoplasm,

and combined with iron deficiency anemia significant performance increase has been observed.

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PS121

Comparison of Ras/Raf/MAPK signaling pathway in primary tumour and lymph node metastases – A report on an experimental study of two colorectal cancer cell lines (SW480 and SW620) and tissue samples



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Aim: To compare the presence of mutations in essential genes of CRC pathogenesis pathway between tissues derived from the primary tumour site and lymph node metastases.

Introduction: Colorectal cancer (CRC) remains the third most commonly diagnosed malignancy worldwide and a leading cause of cancer - related death. One of the pivotal pathways leading to CRC development is Ras/Raf/MAPK which is regulated by the receptor for the EGF. Mutations in these genes predict lack of response to EGFR-targeting monoclonal antibodies. However it is a common practice to assess only the primary tumour site, while mutations in metastasis may also affect the response to treatment.

Methods: The study was conducted on 10 patient-derived tissue samples and two ATCC human CRC cell lines obtained from the same individual: SW480 (primary tumour) and SW620 (lymph node metastasis). Cell lines were cultured according to the protocol. Genomic DNA and RNA were isolated, and PCR and RT-PCR were conducted. Primers for PCR included the following fragments: KRAS (exons 2,3,4), NRAS (exons 2,3,4), BRAF (exon 15); and for RT-PCR: KRAS, NRAS, BRAF and EGFR. Restriction enzymes were used. Proteins were extracted, purified and Western-Blot (RAS, RAF, MAPK) was performed.

Results: For SW480 we detected a mutation in exon 3 of NRAS gene, whereas SW620 presented a wild type. The level of Ras protein remained the same. Raf protein expression was abundant in the primary tumour site as compared to the lymph node metastasis, whereas MAPK protein presented the opposite level of expression.

Conclusion: The analysis of Ras-Raf-MAPK pathway may suggest that along with the tumour progression, the dominating signal is located at deeper levels of signaling pathway. Due to existing differences in key molecular points between the primary tumour and its metastases, in the era of targeted therapy, pre-treatment assessment of both sites has a potential to become a standard of care.^{1,2}

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PS122

PI3K-Akt and Ras-Raf-MAPK signaling in colorectal cancer – Comparison of activity in primary tumor tissues and primary tumour – Derived human colorectal cancer cell lines

