**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 859–977 × 10⁻⁶ mm²/s, while in benign lesion values at apex where in range 1234–1336, and at base 1096–1183 × 10⁻⁶ mm²/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 1199–1379 × 10⁻⁶ mm²/s for apex were considered normal. Values between the range of 857–1030 × 10⁻⁶ mm²/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:** 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:** Methylenetetrahydrofolate 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 MTHFR C677T TT genotype was 22.6% in the experimental group, and 12.0% in the control group, while the allele T frequency amongst the experimental group was

**References**


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