

Drobková H.<sup>1</sup>, Jurečeková J.<sup>2</sup>, Mazuchová J.<sup>3</sup>, Kmeťová Sivoňová M.<sup>2</sup>, Šarlinová M.<sup>1</sup>, Kliment J.<sup>4</sup>, Halašová E.<sup>1</sup>

<sup>1</sup>Jessenius Faculty of Medicine in Martin, Comenius University in Bratislava, Biomedical Center Martin, Dept. of Molecular Medicine, Martin, Slovakia, <sup>2</sup>Jessenius Faculty of Medicine in Martin, Comenius University in Bratislava, Dept. of Medical Biochemistry, Martin, Slovakia, <sup>3</sup>Jessenius Faculty of Medicine in Martin, Comenius University in Bratislava, Dept. of Medical Biology, Martin, Slovakia, <sup>4</sup>Jessenius Faculty of Medicine and UNM in Martin, Comenius University in Bratislava, Dept. of Urology, Martin, Slovakia

**Introduction & Objectives:** Angiogenesis is a biological process that involves the division and migration of endothelial cells and leads to the formation of microvasculature. Vascular endothelial growth factor (VEGF) is a major proangiogenic factor contributing to the stimulation of angiogenesis. The main objective of the study was to evaluate the association between the selected polymorphisms in the *VEGF* gene (-2578 A/C - rs699947; 18 bp I/D - rs144854329; -460 C/T - rs833061; -634 G/C - rs2010963 and +936 C/T - rs3025039) and the risk of prostate cancer development and progression.

**Materials & Methods:** The present study included 446 prostate cancer patients and 241 healthy men. Selected polymorphisms were detected by PCR-RFLP. Comparison of genotype distribution and association with selected clinical data were performed with the Chi-square test and Fisher's exact test.

**Results:** We found no statistically significant association between the individual selected polymorphisms of *VEGF* gene and the risk of prostate cancer development and progression in overall group of patients. We observed only association between the GC genotype of the *VEGF* -634 G/C polymorphism and increased risk of prostate cancer development with low grade (Gleason score  $\leq$  7) after stratification of patients. On the contrary, the CC genotype of the *VEGF* -634 G/C polymorphism was associated with development of high-grade carcinomas (Gleason score  $\geq$  8). The CC genotype was also associated with increased risk of prostate cancer development in group of patients with PSA  $\geq$  10 ng/ml compared to the control group as well as compared to the group of patients with PSA  $\leq$  10 ng/ml ( $p = 0.036$ ). Based on the analysis of the combination of all observed polymorphisms, we found a statistically significant increased risk of prostate cancer development ( $p = 0.03$ ) as well as low-grade carcinomas (Gleason score  $\leq$  7,  $p = 0.015$ ) in a group of patients who had 9 or 10 risk allele.

**Conclusions:** The results of the study indicate that the *VEGF* -634 G/C polymorphism could affect the prognosis and aggressiveness of prostate cancer. We also found that the presence of 9 or 10 risk alleles of all combined polymorphisms may increase the risk of prostate cancer development as well as low-grade carcinomas (Gleason score  $\leq$  7).

This work was supported by the Agency of Ministry of Education, Science, Research and Sport of the Slovak Republic under grants no. 1/0172/18 and no. 1/0271/19. This work was also supported by the projects "Biomedical Center Martin" (ITMS: 26220220187) and "Competence Center for Research and Development in the Field of Diagnostics and Therapy of Oncological Diseases (ITMS: 26220220153).