Abstract

Prostate carcinoma is considered to be one of the main medical problem in male population. Prostate carcinoma is the most frequently diagnosed malignancy in men and the death rate has the second position within all diagnosed malignancies in Czech Republic (ÚZIS). There is only one reliable diagnostic tool: PSA (prostate specific antigen). Level of PSA is often elevated in men with prostate carcinoma.

This diploma thesis is focused on study of changes in gene expression in prostate carcinoma. Three candidate genes were analyzed: *VCL* (vinculin), *SHB* (Src homology 2 binding protein) and *OCT3* (organic cation transporter 3). According to recent publications, these genes are related to tumor progression and they could have prognostic significance.

In this thesis the following methodological approaches were used: 82 prostatic specimens were collected from patients and mRNA was isolated from these specimens; then RT-PCR was used to obtain cDNA, fragments were detected by electrophoresis. At the end statistical methods were used for evaluation. Relative expression of the genes in prostate carcinoma tissue was compared to relative expression of the genes in BPH (benign prostatic neoplasia) tissue.

Results showed higher expression of genes SHB and *OCT3* in prostate carcinoma tissue in compariscon to BPH tissue. No difference was found in *VCL* gene expression. By using next analyses, the difference in *SHB* gene expression was found, when Gleason scores of prostate carcinoma specimens were compared. The decrease of expression was detected in specimens with Gleason score 8 and 9. The correlation between age and *OCT3* gene expression was found, where the expression decreased with increasing age. No correlation with PSA levels was found in any of the analyzed gene expressions.

Gene SHB was evaluated to be potential diagnostic biomarker. However, it is necessary to confirm this theory in next clinical studies with a large pool of patients.