

Quantitative analysis of kallikrein 15 gene expression in prostate tissue

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Abstract:

The newly discovered human kallikrein 15 gene KLK15 has been shown in preliminary analysis to be associated with more aggressive types of prostate cancer. We quantitatively measured and compared gene expression of KLK15 in malignant and benign prostate tissues. MATERIALS AND METHODS: Matched prostate tissue samples from the cancerous and noncancerous parts of the same prostates were obtained from 90 patients who underwent radical prostatectomy. Quantitative reverse transcriptase-polymerase chain reaction using SYBR Green I and the LightCycler system (Roche Applied Science, Mannheim, Germany) was performed. Associations of KLK15 expression with clinicopathological parameters were analyzed. RESULTS: KLK15 over expression in cancerous versus noncancerous tissue was found in 76 of the 90 patient samples (84.4%, $p < 0.001$). The ratio of cancerous-to-noncancerous KLK15 expression tended to be higher in patients with stage pT3/4 versus pT2 tumors ($p = 0.1$). KLK15 expression tended to be higher in grade 3 than in grade 2 tumors and in Gleason score 7 or greater than in Gleason score less than 7 tumors ($p = 0.18$ and 0.23 , respectively). A 1.7 cutoff at the 40th percentile provided a significant difference in stages pT2 and pT3/4 tumors ($p = 0.029$). CONCLUSIONS: On quantitative real-time polymerase chain reaction KLK15 expression was significantly higher in cancerous than in noncancerous tissue. Up-regulation of the KLK15 gene in advanced and more aggressive tumors may indicate a possible role for KLK15 protein as future serum marker for prostate cancer and for distinguishing tumor aggressiveness