Identification of Intronic Marker Candidates for Prostate Cancer Prognosis Using Oligonucleotide Microarrays

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Prostate cancer is the third leading cause of cancer death in men worldwide. It displays a broad range of clinical behavior, from relative indolent to aggressive metastatic disease, which is difficult to predict with current prognostic methods. This variation is likely to reflect a molecular heterogeneity, including a diverse pattern of transcription of genes and of intronic regions. To identify prostate cancer marker candidates for prognosis within this latter, novel category of transcripts, we profiled gene expression in tumor samples from patients with different clinical stages and known outcome (5 years). We used a custom-designed combined Intron-Exon Expression Oligoarray containing sense and antisense probes for each of 7,135 randomly-selected totally intronic non-coding transcripts plus the corresponding protein-coding genes. Using Significant Analysis of Microarray (SAM) and Signal-to-Noise-Ratio (SNR) plus bootstrap methods, and a total of 35 samples from patients with and without tumor recurrence, we found 53 differentially expressed transcripts (p-value<0.005), being 42 intronic and 11 exonic. An additional 25 patient samples will be studied as a validation outer group. Further analyses will be used to identify possible new transcripts associated with recurrence, as well as with different Gleason Scores and other clinically relevant parameters.

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