Epigenome-wide DNA methylation and transcriptome profiling of localized and locally advanced prostate cancer: uncovering new molecular markers

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Background: Prostate Cancer (PC) is one of the most common neoplasms and a leading cause of cancer-related deaths among men. PC can be further distinguished as localized PC (LPC), being confined to the prostate gland, and locally advanced PC (LAPC), having metastasized past the primary site, but not to distant sites. Reliable markers are needed to distinguish LAPC from LPC for a better estimation of patients’ prognosis and further treatment plan.

Hypothesize: We hypothesize that a gene signature can be built to distinguish LAPC from LPC for a better estimation of patients’ prognosis and further treatment plan.

Methods

• The number of mutations for each gene of interest across 4 studies were counted in LAPC and LPC group, respectively.
• Fisher’s exact test was used to compare the number of mutations between the LPC and LAPC samples for each gene to select a list of significant genes after multiple testing.
• Oncoprint was used to visualize the genomic alterations in the genes of interest.

Results

Most significantly affected genes from the potential gene signature list.

Conclusion: 30 downregulated, hypermethylated genes were identified as gene signatures for LAPC. From these 30 genes we further determined that 6 are the most statistically significant in distinguishing LAPC from LPC at DNA level. Further experimental validation can be used to refine the gene list.

References: