Aggressive and non-aggressive prostate cancer: two sides of the same coin or two different coins?

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Objective: To improve the current molecular diagnosis of prostate cancer (PCa), and prognosis to aggressive PCa, the present clinical screening methods need to be improved.

Methods: Our research analyses the link between several genetic and external factors and risk of aggressive and non-aggressive PCa using various analytical platforms, including machine learning. A total of 138 single nucleotide polymorphisms (SNPs), located in 60 genes and 10 chromosomal locations that had been associated with risk and progression of PCa were identified through an extensive literature search. 197 men identified to have aggressive and 57 non-aggressive PCa, and 369 men with no known diseases of the prostate (between the ages of 40-81 years and self-reported European ancestry) were recruited for this study between the years 2006 to 2014. Past and/or present smoking status and alcohol intake, BMI and details about Gleason score, staging data, and prostate-specific antigen (PSA) level were also collected from these cohorts. Genotyping for the SNPs was carried by using SEQUENOM MassARRAY iPLEX assay or TaqMan® Assay.
PLINK- a reliable data analysis approach employed for such dataset, and artificial neural network using WEKA were used to parallel the clinical findings and the story derived from SNP genotyping of the samples.

Results: Common SNPs as risk for aggressive PCa and non-aggressive PCa were not identified even after extensive analyses.

Conclusions: We believe that the way we have been looking at the disease needs to be changed. We feel that not only do the environmental factors play a crucial role, but also cause certain triggers to alter the expression of the disease to non-aggressive or aggressive PCa rather than non-aggressive and aggressive PCa.

References

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