"Determining Germline Risk Factors for Lethal Prostate Cancer: the Role of Copy Number Variations in Prostate Cancer Progression"

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Abstract: The early detection of clinically significant prostate cancer (PCA) is based largely on the prostate specific antigen (PSA) blood test. This screening test identifies cancer but also has many false positive results due to a myriad of benign conditions such as inflammation of the prostate gland. PSA screening currently requires performing biopsies on 100 men to detect 30 cancers. In additional to unnecessary clinical procedures, many of these cancers are not clinically significant. Therefore the goal of our research proposal is to detect clinically significant PCAs by exploiting new understanding of the human genome. Recently, variations in the number of segments of DNA, called copy number variations (CNVs) polymorphisms, have been reported as associated with common diseases such as Alzheimer's disease and susceptibility to HIV infection. The current study will explore for CNVs associated with PCA risk with the hope of developing tests that can be used clinically to improve on specificity in diagnosing clinically significant PCA. We will use DNA from a well-defined PSA screening population. We will interrogate these samples using the latest high-throughput genome scanning technology that will allow us to query all the appropriate known CNVs for associations with PCA risk. We expect to credential our findings in a confirmation stage on independent samples using a custom designed CNV array (BioTrove technology) that will allow for more efficient future validation. Successful completion of this project will impact the early detection of PCA and our insight of why some individuals are at higher risk of developing aggressive disease.