

Full Project A: Multivariate Prediction of Prostate Cancer in Puerto Rican and African American Men
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The overall goal of the Multivariate Prediction of Prostate Cancer in Puerto Rican and African American Men study is to design multivariable models to potentially define key factors associated with the detection of PCA and its aggressive features in both high risk populations.

Inputs	Aims	Activities	Short-term	Outcomes -- Impact	
				Intermediate	Long-term
<ul style="list-style-type: none"> • UPR Comprehensive Cancer Center • MD Anderson Cancer Center • UPR Medical Sciences Campus • Puerto Rico Clinical and Translational Research Consortium • The Robotic Urology and Oncology Institute • University of Illinois at Chicago • Veterans Administration Caribbean Health System • Lyndon Baines Johnson Hospital • Michael E. DeBakey Veterans Administration Medical Center • Industry partners: Hologic-Gen Probe, Beckman Coulter • BEBiC • NCI Program Director • Internal Advisory Committee (IAC) • Program Steering Committee (PSC) members • Other funds 	<ol style="list-style-type: none"> 1. Establish & characterize a unique specimen/data repository among AA & PR men in 2 distinct studies (a) A prospective collection of tissue, blood, urine, along with well annotated clinical, epidemiologic data among both cohorts undergoing prostate biopsy & (b) Expansion of our current retrospective cohort database of PR and AA patients with PCA having undergone RP. 2. Prospectively assess genotypic, clinical, pathologic, and epidemiologic data collected in Aim 1a and correlate the variables with the presence (or absence) and aggressiveness of PCA subsequent to biopsy among AA and PR patients 3. Assess genotypic, clinical, pathologic, and epidemiologic data collected in Aim #1b and correlate the variables with adverse pathologic features and disease recurrence among AA and PR patients. 	<p>Aim 1a</p> <ol style="list-style-type: none"> 1. Recruitment of 400 AA & PR men each (i.e., 800 men total) will be recruited from Houston and Puerto Rico study sites over a two and half year time frame according to the inclusion criteria established in the study. 2. Take samples from this population: whole blood, prostate biopsy tissue and urine. 3. Administration of a structured questionnaire <p>Aim 1b</p> <ol style="list-style-type: none"> 4. Recruitment of additional prostatectomy paraffin blocks in PR=220.Houston= 388. Testing for genetic admixture and SNPs <p>Aim 2.</p> <ol style="list-style-type: none"> 5. Testing for total PSA, fPSA and p2PSA, urine PCA3 and TMPRSS2, genetic admixture and SNPsfor subjects in aim 1 <p>Aim 3</p> <ol style="list-style-type: none"> 6. Testing for genetic ancestry and SNPs in samples recruited in aim 1 b 7. Design a predictive model 	<p>Expected outcomes for Aim 1</p> <ol style="list-style-type: none"> A. Develop an unique data to understand the multifactorial nature of the disease in two understudied populations with increased prostate cancer mortality. B. Advance both genotyping and genetic analysis capabilities of the UPRCCC. <p>Expected outcomes Aim 2</p> <ol style="list-style-type: none"> C. Assess the performance of novel serum and urine markers, genetic polymorphisms, and epidemiologic data in an effort to both predict the presence of cancer and its features in two understudied populations. D. Establish if the presence of SNPs associated with WAA are associated with PCA presence or aggressive features among a prostate biopsy cohort. E. Establish the role of novel serum (fPSA, PHI) and urine, biomarkers (PCA3 and TMPRSS2: ERG alone and in combination) along with epidemiologic variables in the prediction of PCA biopsy findings. <p>Expected outcomes for Aim3</p> <ol style="list-style-type: none"> F. Establish the association between time to disease recurrence and patients' clinical characteristics, genotyping, SES and lifestyle factors. G. Accrue and analyze a variety of data that will describe clinical characteristics, progression, and outcomes of PCA (along with epidemiologic, anthropomorphic, comorbidities etc.) among a significant cohort of both PR and AA men undergoing RP in a comprehensive focused manner by the same research team. 	<ol style="list-style-type: none"> H. In collaboration with BEBiC, it will construct software to correlate presence of risk loci with disease presence and aggressiveness, and to efficiently query the known biological function of regions in proximity of affected loci. Using techniques borrowed from class-discovery and biological function assessment of microarray data, it will generate testable hypothesis of which mechanisms lead to PCA presence and aggressiveness in AA and PR men. 	<ol style="list-style-type: none"> I. The long-term goal is to characterize features of PCA and its aggressive phenotype among at risk PR and AA men as a step toward decreasing PCA mortality among the two populations.

Process Evaluation

Outcome Evaluation