



PROSTATE CANCER DIAGNOSTIC

Genomic Panel for Prediction of Metastatic-Lethal Prostate Cancer Progression

Brief Description of Technology

Diagnostic combination panel of single nucleotide polymorphisms [SNP], epigenetic, and genetic markers to identify metastatic-lethal prostate cancer.

BUSINESS OPPORTUNITY

Exclusive license
Sponsored research

TECHNOLOGY TYPE

Diagnostic
Biomarker

STAGE OF DEVELOPMENT

Discovery studies complete;
validation studies partially complete

PATENT INFORMATION

US 9150925

INVESTIGATOR

Janet Stanford, PhD
Public Health Sciences

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Tech ID: 16-085
partnering@fredhutch.org
206-667-4304

Technology Overview

Dr. Stanford's group has identified panels of SNP, DNA methylation sites, and gene expression that classify metastatic-lethal vs. indolent prostate cancer. Prostate cancer is a clinically heterogeneous disease that often has an indolent course, but certain patients progress to metastatic-lethal disease. Additional markers are needed to improve the accuracy of prognosis for prostate cancer tumors. Dr. Stanford profiled primary tumor tissues from a population-based (n=383-430) and replication (n=78-80) cohort of patients followed prospectively for at least five years. Eight differentially methylated CpGs and 23 differentially expressed mRNAs have been identified that distinguish metastatic-lethal tumors from indolent tumors. These novel prognostic biomarkers can identify those patients who need closer monitoring for metastatic progression and/or may benefit most from aggressive therapeutic options such as adjuvant therapy.

Applications

- Identify patients with high risk for metastatic-lethal prostate cancer vs. non-recurrent disease

Advantages

- Novel diagnostic markers that combine SNP, DNA methylation, and gene expression for a combination panel
- Improves upon Gleason sum to identify higher risk patients and drive future clinical decisions

Market Overview

Prostate cancer is the most common cancer in males in the United States and in other Western countries. Prostate cancer is a biologically and clinically heterogeneous disease with approximately 240,000 new diagnoses each year. There is an unmet need for technology that can provide accurate prognosis of disease following surgical resection, in order to guide clinical decision-making and determine maximum benefit from targeted therapies.