A novel blood-based mRNA genomic test for screening, early detection, prognosis, and monitoring of prostate cancer: A multicenter study.

Yutaka Hashimoto, Shiv Verma, Guoren Deng, Dharam P Chauhan, Sujit Nair, Hirofumi Yoshino, Junya Arima, Yutong Liu, Koji Hatano, Yogesh Shivakumar, Raghunath S. Krishnappa, Chitra Chandran, Narasimhan Ragavan, Hideki Enokida, Norio Nonomura, K C Balaji, Sudhir K Rawal, Ashutosh K. Tewari, Rajvir Dahiya, Sanjay Gupta; VA San Francisco Health Care and UCSF School of Medicine, San Francisco, CA; Case Western Reserve University and University Hospitals Cleveland Medical Center, Cleveland, OH; Geneverify Inc, Hayward, CA; Tisch Cancer Institute, Icahn School of Medicine at Mount Sinai, New York, NY; Kagoshima University Hospital, Kagoshima, Japan; Osaka University Graduate School of Medicine, Osaka, Japan; HCG Cancer Hospital, Bengaluru, India; Apollo Cancer Center Hospital, Chennai, India; University of Florida College of Medicine, Jacksonville, FL; Rajiv Gandhi Cancer Institute & Research Centre, New Delhi, India; University of California, San Francisco School of Medicine, San Francisco, CA

Background: Current screening tools, including prostate-specific antigen (PSA) and clinico-pathologic parameters, have limitations in the diagnosis and prognosis of prostate cancer. This study examined whether genomic biomarkers can improve screening and monitoring of prostate cancer. Methods: We identified a panel of 25 prostate cancer-related genes through rigorous bioinformatics, computational analyses and genetic testing. These tests, developed by Geneverify Inc. (Hayward, CA; U.S. patent # 10801072 and 10822661) were utilized and optimized by qRT-PCR to determine the diagnostic and prognostic ability of prostate cancer using blood and tissues. The log2-fold increase in gene expression was used to assign the risk score to individual patients. ROC (receiver operator characteristic), AUC (area under ROC curve), and calibration curves were generated to display the overall performance and discrimination ability to separate cancer and non-cancer specimens. Results: A total of 419 prostate cancer patients (135 blood and 284 tissue samples) and 130 normal samples were analyzed in this study. The eligibility criteria were to collect blood and surgical specimens from patients with prostate cancer from 9 hospitals. The study endpoints were to analyze mRNA genomic profiling and correlate with clinicopathologic parameters of the patients. In the blood, a 25-panel gene-set separated prostate cancer patients (n=135) from non-cancer (n=30), AUC = 0.906 [sensitivity = 90% and specificity = 91%]. Assessment of tissue specimens from benign (n=100) and cancer patients (n=284) showed similar results with AUC = 0.9514 [sensitivity = 95% and specificity = 94%]. Interestingly, patients with Gleason grades (GS) >7 showed higher expression of these genes compared to GS <7, suggesting the prognostic ability of the gene-set. When we compared the gene expression in blood verses tissues, there were similar patterns, suggesting that blood can be used for screening, diagnosis and risk assessment of prostate cancer. Conclusions: To our knowledge, this is the first study to investigate the role of mRNA-based genomic signatures for screening, early diagnosis and prognosis of prostate cancer using blood samples. Our data suggest that blood mRNA-genomic profiling developed by Geneverify has the ability to diagnose prostate cancer and stratify patients into distinct prognostic groups, which in turn help in making better treatment strategies. Research Sponsor: None.