

Evaluation of a novel transcriptomic tumor signature (PROSTest) as response biomarker for ¹⁷⁷Lu-PSMA therapy in advanced prostate cancer

Authors: Alin Chirindel, Mark Kidd, Cyrill Rentsch, Frank Stenner, Arnoud Templeton, Egbert Nitzsche, Damian Wild, Guillaume Nicolas and Irvin Modlin

Background:

Radionuclide therapy targeting the prostate-specific membrane antigen (PSMA) has proven to be an effective treatment in men with metastatic castration-resistant prostate cancer (mCRPCs). Despite representing a significant therapeutic breakthrough, a critical unmet need in PSMA-targeted radionuclide therapy is a response biomarker for treatment optimization. Imaging and standard biomarkers have limited value. The PROSTest is a new 27-gene algorithmic signature originally developed for prostate cancer (adenocarcinoma) diagnosis. We hypothesized that PROSTest would be elevated in mCRPCs and could have utility as a biomarker for mCRPC management.

Methods:

Prospective enrollment of 113 mCRPC for ¹⁷⁷Lu-PSMA therapy (KIB-5338-0302021 study). Pathology, clinical, and biomarker data were available as was PSMA-PET/CT. Blood samples were collected for PROSTest prior to therapy. Target genes were isolated and amplified using qPCR. PROSTest scores (0-100) were obtained following algorithmic analysis. Scores were correlated with mCRPC diagnosis and baseline information. Scores and standard clinical measures were evaluated as prognostic factors with survival as the endpoint. Mann-Whitney U-test, Kaplan-Meier survival and Cox proportional hazards regression analysis were utilized. All data: median (IQ range).

Results:

89 (79%) patients were evaluable. Median age (range) was 75 (68-80). Disease characteristics at the time of diagnosis included Gleason scores which were predominantly 8-10 (70%) and TMM: T3-T4 tumors (67%), N1 (53%), M1 (45%). At the time of therapy, all patients were metastatic and all exhibited PSMA-positive disease.

The highest tumor SUV_{max} was 51 (28-78). PSA levels were 69ng/mL (18-305). The median PROSTest score was 89 (81-92). PROSTest scores were weakly correlated with age (r=0.33, p=0.0015) but not with baseline histopathological parameters (e.g., Gleason score, TNM) or pre-treatment imaging results (e.g., SUV_{max}). Twenty-four (27%) have perished following treatment initiation. Treatment and follow-up are ongoing: the median is 5 months (3-18). The mOS was 15 months. No factors were associated with death as an outcome except for the PROSTest score. PROSTest scores >79 were associated with significantly increased risk for mortality (HR: 2.9, 95% CI: 1.5-7.4). The mOS was 14 months in patients with pre-therapy PROSTest scores >79 compared to mOS not reached for PROSTest scores <79 (p=0.02). In the COX model, baseline PROSTest was confirmed to be significantly predictive of death despite therapy ($\beta = 1.51, p=0.01$).

Conclusions:

The PROSTest blood gene expression score is elevated in mCRPCs. Levels are not associated with baseline clinical, histopathological, or pretreatment PSA or imaging parameters. Elevated expression (>79) of this biomarker prior to treatment was associated with a lower survival and could be used to predict survival in those patients undergoing ¹⁷⁷Lu-PSMA.

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