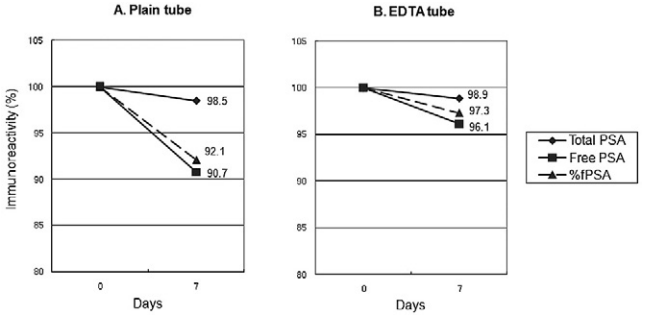
METHODS: Blood samples from 50 men were collected and processed to generate serum and EDTA plasma. Specimens were analyzed at baseline within 24 hours of collection and after 1 week of storage at 4 degrees C. Free PSA and total PSA were measured in all specimens. The changes in free PSA, total PSA and percent free PSA in serum and EDTA plasma with time were evaluated. Statistical analyses of the results were performed by paired t-test.

RESULTS: Concentrations of baseline total PSA in serum were not significantly different from those in EDTA plasma (4.83±0.45 ng/ml vs 4.81±0.44 ng/ml). In serum, however, baseline free PSA and percent free PSA were lower than in EDTA plasma (0.69±0.08 ng/ml, 14.58±0.81% vs 0.83±0.09 ng/ml, 17.89±0.93%; $p<0.001$). After 1 week, total PSA decreased slightly on average by 1.5% in serum and 1.1% in EDTA plasma, respectively. A decrease was seen in free PSA after 1 weak, with rates of 9.3% for serum and 3.9% for EDTA plasma. Similarly, there was a decrease in percent free PSA, with rates of 7.9% for serum and 2.7% for EDTA plasma. The decrease in percent free PSA in EDTA plasma was smaller than in serum significantly ($p=0.003$).

CONCLUSIONS: Free PSA is less stable with storage than total PSA in serum and EDTA plasma samples. In vitro stability of free PSA in EDTA plasma was less impaired than in serum. When using the percent free PSA in evaluation of patients with suspected prostate cancer, serum samples should be analyzed immediately after collection or EDTA plasma samples should be used.



Source of Funding: None

1918

DEVELOPMENT OF AN IMPROVED NOMOGRAM FOR PREDICTION OF THE OUTCOME OF THE INITIAL PROSTATE BIOPSY BASED ON READILY AVAILABLE CLINICAL INFORMATION

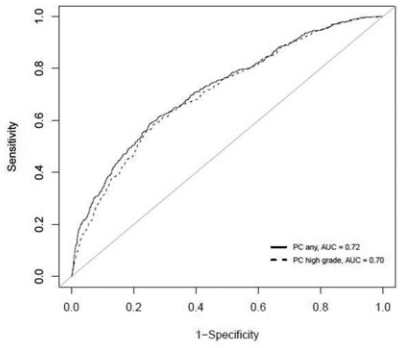
Osama Zaytoun, Ayman Moussa, Jianbo Li, Michael Kattan, Stephen Jones, Cleveland, OH*

INTRODUCTION AND OBJECTIVES: Various efforts have been attempted to develop models that improve the prediction rate of prostate cancer (PCa) on both initial and repeat biopsy settings. We aimed to construct a nomogram that can be used to estimate the risk of PCa and high grade cancer using readily available clinical information in men undergoing initial prostate biopsy.

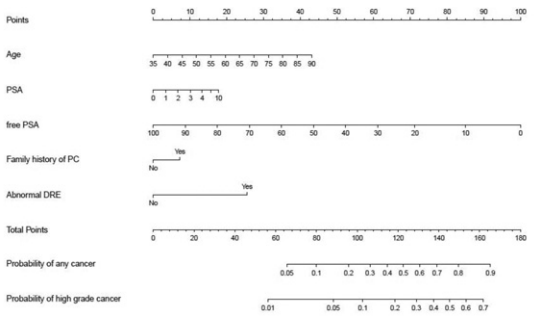
METHODS: Between March 2000 and April 2010, 1895 men with prostate-specific antigen (PSA) ≤ 10 ng/ml who underwent initial prostate biopsy were included in the study. Nomogram predictor variables were patient age, PSA, percent free PSA, family history of PCa, and digital rectal examination (DRE) findings. All transrectal ultrasound (TRUS) guided prostate biopsies were performed at our institution in an office based setting with periprostatic block. High grade PCa was defined as having a Gleason score ≥ 7. Area under the receiver operating characteristic curve (ROC AUC) was calculated as a measure of discrimination. Calibration was assessed graphically.

RESULTS: 748 men (39.5 %) were found to have PCa on biopsy. Mean values for age, PSA and percent free PSA were 63.5 y, 5.1 ng/ml and 21.09 respectively. 23.8% and 8.3% of patients with positive cancer had DRE abnormalities and positive family history, respectively. Between 748 men with detected PCa, 359 men (48 %) were diagnosed with high grade cancer. The use of univariate and multivariate analysis suggested that all five risk factors were predictors of PCa in the study cohort (p value < 0.05). The AUC for all factors in a model predicting PCa was 0.72 (95% CI, 0.70–0.74). The AUC for predicting high grade cancer was 0.70 (95% CI, 0.68–0.74). The AUC of the nomogram was found to be 75% and 71% for patients with PSA < 4 and 4 &endash; 10, respectively.

CONCLUSIONS: This predictive model allows an assessment of the risk of PCa and high grade cancer for men undergoing initial prostate biopsy using readily available, non-invasively obtained clinical data.



Receiver operating characteristic curves for the nomogram in predicting any cancer and high grade cancer



Nomogram prediction model for PCa at the time of biopsy. The nomogram is used by first locating a patient's position for each variable on its horizontal scale and then a point value is assigned according to the points scale (top axis) and summed for all variables. Total points correspond to a probability value for having PCa or aggressive PCa

Source of Funding: None

1919

NOMOGRAM FOR PREDICTING A POSITIVE PROSTATE BIOPSY BASED UPON PSA KINETIC

Luigi Benecchi, Carmelo Destro Pastizzaro, Anna Maria Pieri, Nicoletta Uliano, Michele Potenzoni, Parma, Italy*

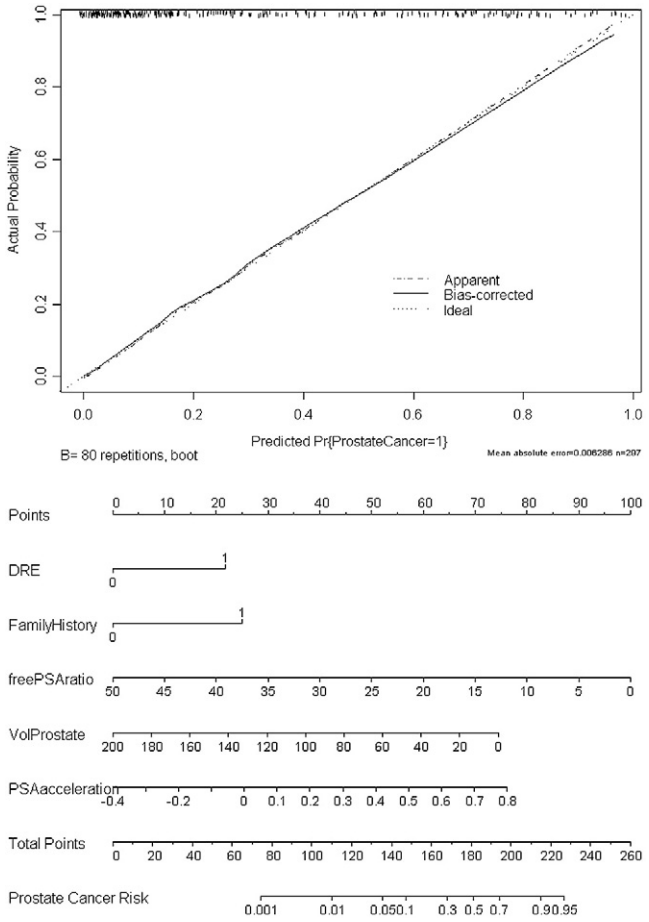
INTRODUCTION AND OBJECTIVES: A new tool for prostate specific antigen (PSA) kinetic is PSA acceleration that is the slope of logPSA versus time, where log is the natural logarithm. The aim of this study is to develop a nomogram with validation that would be useful for counseling patients in the decision to undergo prostate biopsy.

METHODS: Our prospective institutional review board-approved database of twelve core prostate biopsies performed at our institution was searched for men with at least 3 consecutive PSA measurements (done in our centralized laboratory) within 2 years or more. 602 men satisfied the inclusion criteria. A total of 182 cancers were found at the ultrasound guided prostate biopsies (30%). All logPSA (natural logarithm of PSA) were used to create the best fit line by least squares regression, the acceleration of PSA (logPSA slope) was the slope of this line.

Logistic regression model to predict the presence of prostate cancer at biopsy was fitted using age, prostate cancer family history, digital rectal examination findings (DRE), PSA, free to total PSA ratio, prostate volume and PSA acceleration.

RESULTS: All men in the study were randomly divided into 2 groups: a first group with 301 cases for multivariate logistic regression analyses and a second group with 301 patients for validation. At the multivariate logistic regression analysis, all the factors, except age and PSA, showed a significant ability to predict the outcome of a 12 -core prostate biopsy. A nomogram for a positive biopsy was developed from the final logistic regression model findings. The maximum absolute difference in predicted and calibrated probabilities was 0.018. In the validation goup the area under the curve (AUC) of the model showed a value 0.79 (95% Confidence Interval 0.739 – 0.835) better than PSA, free to total PSA ratio and PSA acceleration ($p<0.05$).

CONCLUSIONS: We successfully developed an accurate model to predict the outcome of prostate biopsy based upon free to total PSA ratio, DRE, family history, Prostate volume and PSA acceleration.



Source of Funding: None

1920

A NOMOGRAM CAN HELP PREDICT UPGRADING OR UPSTAGING IN PATIENTS THAT FIT CONVENTIONAL ACTIVE SURVEILLANCE CRITERIA

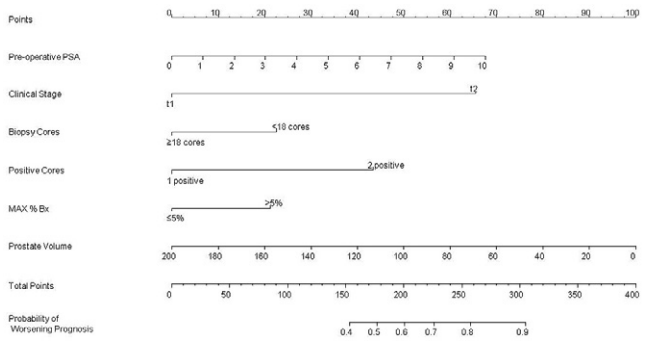
Prasanna Sooriakumaran, Abhishek Srivastava, Paul Christos, Sonal Grover, Robert Leung, Ashutosh Tewari, New York, NY*

INTRODUCTION AND OBJECTIVES: Low risk prostate cancer patients clinically eligible for active surveillance can also be managed surgically. We evaluated the pathologic outcomes for this cohort that was treated by radical prostatectomy and devised a nomogram to predict which of this cohort are at risk of upgrading or upstaging that would have then made them ineligible for active surveillance.

METHODS: 750 patients treated by radical prostatectomy from Jan 2005-present fulfilled conventional active surveillance criteria (PSA$<$10, Gleason sum 6, $\leq$cT2a) and formed the study cohort. Preoperative data on PSA, clinical stage, number of biopsy cores taken, number of positive cores, maximum percent cancer in any core, presence of high grade prostatic intraepithelial neoplasia (HGPIN), and prostate volume was available. The radical prostatectomy specimens were graded and staged, and any upgrading (Gleason sum $>$6) and/or upstaging ($\geq$pT2b) was classed as 'worsening prognosis' as these factors would be considered exclusion criteria for active surveillance if known prior to treatment. A multivariate logistic regression model was used to develop the worsening prognosis predictive nomogram.

RESULTS: 297/750 (39.6%) patients were upgraded to $\geq$Gleason 7 at final pathology; 569/750 (75.9%) were upstaged to $\geq$pT2b; overall, 597/750 (79.6%) had either upgrading or upstaging and would have been ineligible for active surveillance if known prior to treatment. All baseline variables except HGPIN were included in the best fit multivariate model. The nomogram to predict worsening prognosis was reasonably discriminatory between patients who would have been ineligible for active surveillance and those that remained eligible (bootstrap corrected c-index of 0.65).

CONCLUSIONS: Four out of five patients deemed eligible for active surveillance based on conventional criteria have worse prognostic factors in terms of histology or tumor bulk when subjected to radical prostatectomy. We suggest the use of a nomogram we have devised to adequately counsel primary prostate cancer patients deemed clinically eligible for active surveillance.



Source of Funding: None

1921

VALIDATION OF THE PROSTATE CANCER RISK CALCULATOR IN A CLINICAL SETTING

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INTRODUCTION AND OBJECTIVES: To safely adopt prediction models, their performance and applicability must be tested in other settings. We validated the European Randomized study of Screening for Prostate Cancer (ERSPC) risk calculator (www.prostatecancer-riskcalculator.com) in a clinical setting. This risk calculator has been developed to calculate the probability of a positive sextant prostate biopsy using the data of 3,624 men of the initial screening round of the ERSPC section Rotterdam.

METHODS: The ERSPC risk calculator is based on serum prostate specific antigen (PSA), digital rectal examination and transrectal ultrasound (TRUS), i.e. the presence of hypoechogenic lesions and prostate volume. This risk calculator was used to calculate the probability of a positive prostate biopsy in 220 biopsied men (mainly $>=$ 8 cores were taken), with no previous prostate biopsy, aged 55–75 years, included in 5 hospitals in the Netherlands in 2008–2010. The performance of the risk calculator was tested by comparing the observed and predicted probabilities and using the area under the curve