methylation-specific polymerase chain reaction. Blood samples from 76 patients with hormone-refractory prostate cancer were analyzed-(Table).

RESULTS: The patient charts were examined retrospectively to determine the median overall survival time, which ranged from 11 to 48 months (mean 18.4±5.9, median 19.3). Of the 76 patients, 47 (62%) had 5 or more circulating tumor cells, with a median overall survival of 12.0 months compared with 26.0 months for patients with fewer than 5 circulating tumor cells ($p < 0.001$). Circulating tumor cells were detected in 36 of 39 (92%) patients with tumor-related methylated DNA but only 11 of 37 (30%) patients without methylated DNA ($p < 0.001$). Thirty-nine (51%) patients had one or more methylated marker. Their median overall survival time was 12.0 months compared with 48.0 months or more for patients without methylated DNA ($p < 0.001$)(Figure). PSA-doubling time, circulating tumor cells and methylated DNA were independent predictors of overall survival time.

CONCLUSIONS: Patients with circulating tumor cells or tumor-related methylated DNA had a poorer outcome than those without blood markers, and patients with both markers had a worst outcome.

Table. Patient characteristics

Age, Mean (Range)	72.2(57-83)
PSA (ng/ml)	
0.2- 4.0	3 (4%)
4.1-10.0	6 (8%)
10.1-20	21(28%)
20.1-30	11(14%)
30.1-40	9 (12%)
40.1-50	10(13%)
50.1-100	7 (9%)
≥100.1	9 (12%)
Mean (Range)	19.6 (0.5-118)
CTC Mean (Range)	16 (0-225)
Gleason score	
5-7	19 (25%)
8	26 (34%)
9	20 (26%)
10	11 (14%)
EOD	
1	16 (21%)
2	31 (41%)
3	20 (26%)
4	9 (12%)
PSA doubling time (mo)	
> 6	31 (41%)
≤ 6	45 (59%)

Source of Funding: None

2050

NOMOGRAM FOR PREDICTING A POSITIVE PROSTATE BIOPSY BASED UPON PSA ACCELERATION

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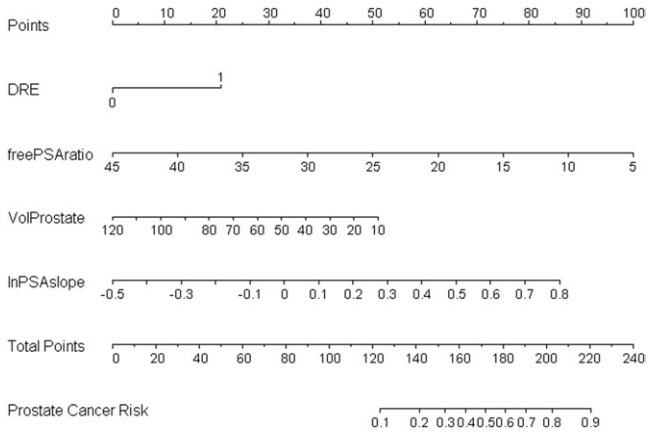
INTRODUCTION AND OBJECTIVES: A new tool for PSA kinetic is PSA acceleration that is the slope of lnPSA versus time, where ln is the natural logarithm. The aim of this study is to develop a nomogram that would be useful for counseling patients in the decision to underwent prostate biopsy.

METHODS: We analyzed data of all men with 3 or more consecutive PSA measurements in at least 730 days who underwent in our department a transrectal ultrasound-guided prostate biopsy with 12 or more cores. The factors we evaluated were age, digita rectal examination findings, PSA level, free to total PSA ratio, prostate volume and lnPSAslope.

RESULTS: 507 men entered the study that were divided random in 2 groups: a first group with 300 cases for multivariate logistic regression analyses and nomogram and a second group for validation with 207 patients. A total of 153 cancers (30.1%) were found. The stepwise multivariate logistic regression analysis showed that all the factors, except age and PSA, showed a significant ability to predict the outcome of a 12-cores prostate biopsy. A nomogram was built with the results of the model. The Area Under the Curve (AUC) of the model showed a value 0.801 (95%Confidence Interval 0.740- 0.853) better than PSA, free to total PSA ratio, prostate volume and lnPSAslope alone ($p<0.05$).

CONCLUSIONS: We successfully developed an accurate model to predict the outcome of prostate biopsy. Addition of free to total PSA ratio, DRE, Prostate volume and lnPSA slope sharply improves accuracy of our model.



	all	Prostate cancer	Non prostate cancer	P
N	507	153	354	
Age	67.2 (44.7-85.7)	67.7 (44.7-85.7)	66.9 (47.3-85.6)	0.02
Suspicious DRE	167(32.9%)	73 (47.7%)	94(26.5%)	< 0.01
PSA	6.9 (1.3-35.2)	6.9 (2.1-30.3)	6.9 (1.3 –35.2)	0.14
percent free PSA	16.5 (1.4-65)	11.3 (1.4-40.9)	18.2 (4.55-65)	< 0.01
PSA slope	0.48(-3.6-9.89)	0.68 (-1.09 – 9.89)	0.35 (-3.6 –6.8)	< 0.01
PSA acceleration (lnPSA slope)	0.08 (-0.6-0.79)	0.14 (-0.12–0.79)	0.06 (-0.6-0.65)	< 0.01
prostate volume	51 (9-330)	39 (9-137)	55.2 (16.5 – 330)	< 0.01
PSA density	0.137 (0.03-1.11)	0.201 (0.048–1.11)	0.11 (0.03 - 0.83)	< 0.01
Gleason score	6 (4-9)	6 (4-9)		

Source of Funding: None