

P-score in preoperative biopsies accurately predicts P-score in final pathology at radical prostatectomy

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Conclusion

In this exploratory study, we illustrated the prognostic accuracy of MRI/TRUS fusion-guided core needle biopsy (CNB) based-Prostatype® algorithm (P-score) in prostate cancer (PCa) patients. We have also found a high concordance of P-score between paired pre-operative biopsies and radical prostatectomy (RP) specimens. In addition, we elucidated the same high concordance of P-score in the paired index and concomitant non-index tumour foci in the same RP specimens.

The observed high degree of concordances between these tumour tissues adds meaningful clinical information for untreated patients presenting with CNBs. This study demonstrated that determination of P-score results from CNBs is reliable, providing results that are closely aligned with those obtained from specimens and could be used for treatment decision support. It also suggested that P-score have been developed previously and validated using CNBs may also be applied to RP specimens.

Background

Preoperative CNB has been considered to be the gold standard for obtaining histological information, which helps with PCa diagnosis and treatment decision. However, CNB was also noted to provide less accurate results than specimens owing to multi-foci and intratumoural heterogeneity feature of PCa.

Prostatype® is a tissue-based multigene assay for predicting prognosis in PCa patients. This assay analyses the expression of 3 genes (IGFBP3, F3, and VGLL3) in PCa CNB¹⁻³. P-score based on the patient-specific 3-gene signature and clinical parameters was further developed and validated in a total of around 1000 patients. P-score has shown to outperform D'Amico score, CAPRA score as well as NCCN score⁴⁻⁵. The goal of this study was to assess the concordance of P-score between paired specimens and CNB samples as well as between different tumor foci from the same RP specimens.

Aims

1. Explore the association of P-score from CNB with the final pathological outcomes.
2. Explore the concordance of P-score between the paired CNB and the RP specimens.
3. Explore the concordance of P-score between the index and concomitant non-index tumour foci in the same RP specimens.



Results

Figure 1. Flow chart for cohort selection in this validation study. Preoperative biopsies yielded sufficient and technically analyzable materials for comparison with the RP specimens in 71 PCa patients.

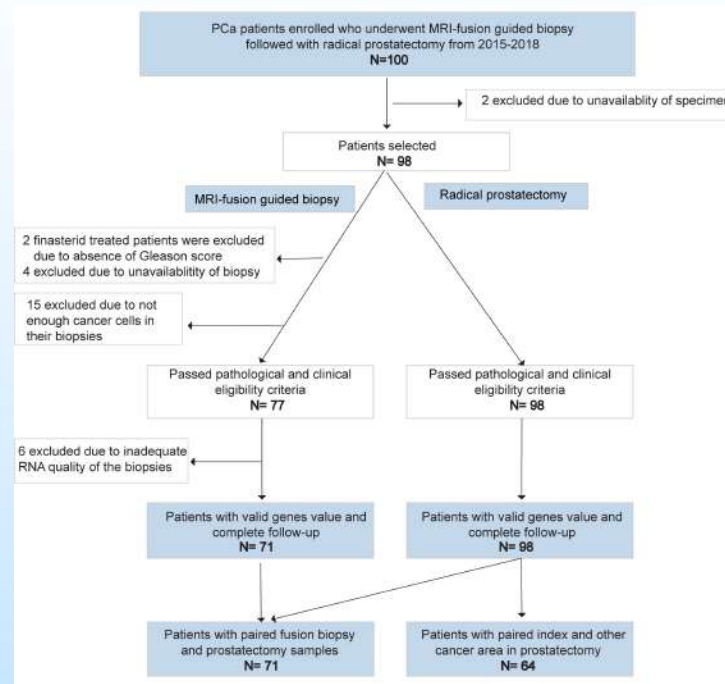


Figure 2. A. Significant correlation of P-score in paired RP and MRI/TRUS fusion-guided CNB (Spearman's rank correlation: 0.84, 95%CI: 0.74-0.91, p-value<0.0001). **B. Significant correlation of P-score in paired index and concomitant non-index tumor area from prostatectomy specimens** (spearman's rank correlation: 95%CI: 0.75-0.91, p-value<0.0001).

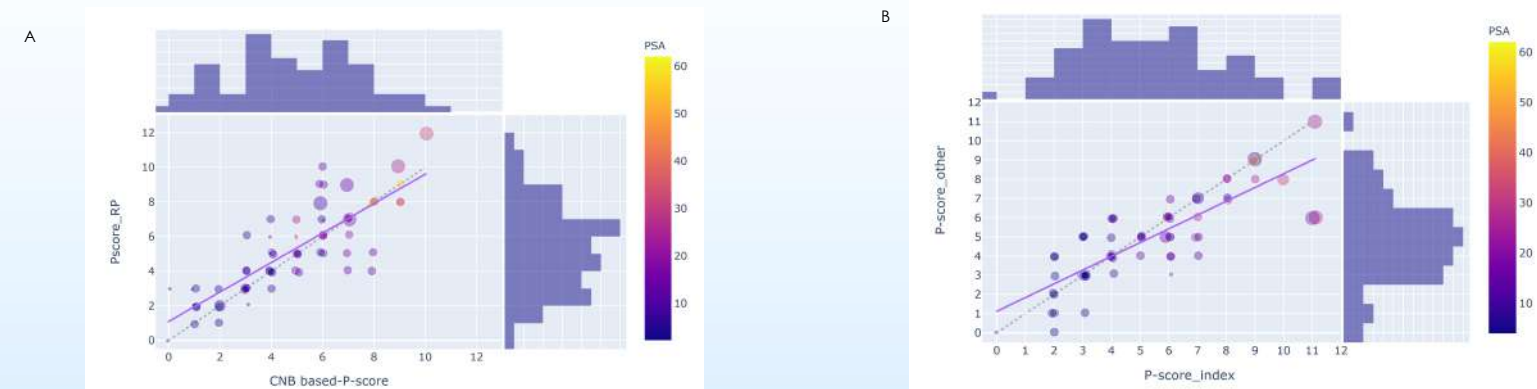
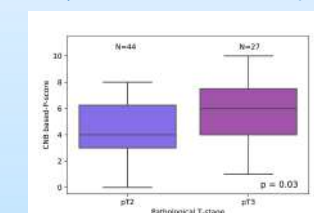


Table 1. High degree concordance of P-score between the paired PCa cases (MRI guided fusion CNB and RP) and the paired specimen cases (index tumor and concomitant non-index tumor in the same RP).

P-score in CNB	P-score in RP			Weighted quadratic kappa-score (95% CI)	P-score in index tumor	P-score in concomitant cancer			Weighted quadratic Kappa-score (95% CI)
	Low	Intermediate	High			Low	Intermediate	High	
Low	8	4	0	0.83 (0.70-0.96)	Low	6	3	0	0.81 (0.67-0.95)
Intermediate	1	21	6		Intermediate	1	22	3	
High	0	6	25		High	0	8	21	

Figure 3. P-score in preoperative biopsy has a significant association with pathological T-stage of RP specimens. (Kruskal-statistic: 4.635, p-value=0.03).



Methods

In this study, we enrolled 100 men with localized PCa, all diagnosed by MRI/TRUS fusion-guided biopsies, and afterwards underwent robot-assisted RP at Uppsala University Hospital in Sweden. Patients were operated on between 2015-2018 and diagnosed a couple of months before.

All prostatectomy specimens were whole-mounted and tumour maps were drawn. From all formalin-fixed paraffin-embedded CNB biopsies and from the index and non-index tumour foci of the corresponding prostatectomy specimens, RNA was extracted. Gene expression was determined by the Prostatype® RT-qPCR analysis and was then combined with clinical parameters (Gleason score, PSA, and T-stage at diagnosis) to calculate a previously reported P-score. This P-score was calculated in a range of 0-15 with one as the smallest unit and categorised into three risk groups by using previously defined cut-offs.

Future plan

We plan to carry out a study in a larger cohort, e.g. 250 patients, where we compare the P-score between cribriform and intraductal PCa foci, the latter is considered to have a worse prognosis.

Disclosure

The presenter has no financial interests or relationships with Prostatype Genomics AB to disclose.



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