

A metastatic biology gene expression assay to predict the risk of distant metastases in patients with localized prostate cancer treated with primary radical treatment

BACKGROUND

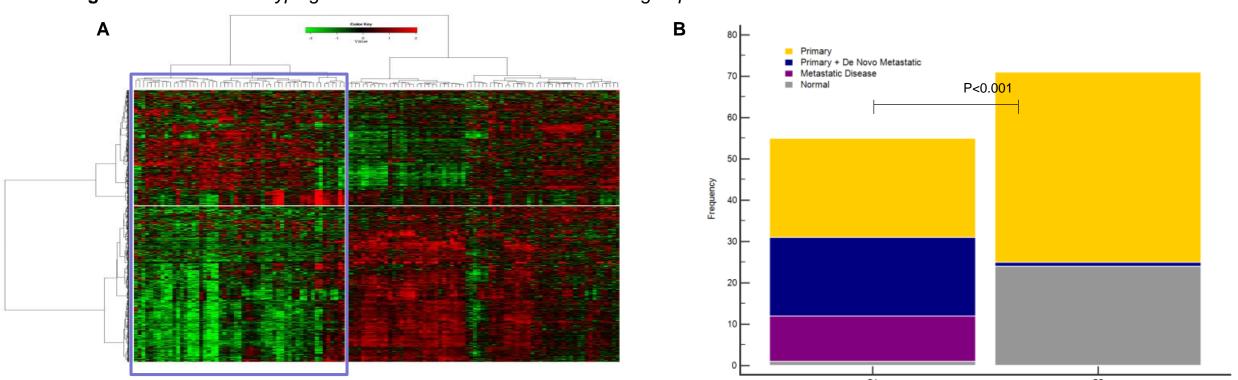
- Approximately 20% of patients with organ-confined prostate cancer (PCa) will develop disease recurrence following radical treatment (surgery or external beam radiotherapy (EBRT)).
- We hypothesized that a molecular subgroup of early PCa may have metastatic potential at presentation, resulting in disease recurrence.
- These patients may benefit from intensification of treatment such as pelvic nodal irradiation, extended lymph node dissection, extended adjuvant androgen deprivation therapy (ADT), chemotherapy or novel agents.

METHODS

- Using unsupervised hierarchical clustering of gene expression from a Discovery PCa dataset of 126 formalin-fixed and paraffin embedded (FFPE) radical prostatectomy resections including samples with known concomitant metastases, we identified a novel molecular subgroup with a transcriptional profile similar to metastatic disease (Fig. 1).
- We developed a 70-gene expression assay (Metastatic Assay) to prospectively identify patients within the subgroup from FFPE. Initial assessment found the assay to be prognostic in three independent publicly available prostatectomy datasets (Glinsky, Erho, Taylor).
- We therefore assessed the prognostic value of the assay in FFPE radical prostatectomy samples collected from multiple international sites and FFPE biopsy samples collected from patients treated with radical EBRT.
- Tumor resections and tumor biopsy specimens were obtained from 322 surgical patients (n = 61, IPCRC, Republic of Ireland; n = 142, Oslo, Norway; n = 34, Surrey, UK; n = 85, Wales Cancer Bank, UK) and 248 patients treated with radical EBRT (n = 248, Belfast, UK). The regions of highest Gleason grade were identified for macrodissection, RNA extraction and gene expression analysis.
- Samples were dichotomized as Metastatic Assay positive or negative using a pre-specified cut-off. The association of assay results with biochemical failure (BF) and distant metastases (DM) was tested on multivariate analysis (MVA).

RESULTS – Assay Development

Figure 1. Molecular subtyping and identification of the metastatic subgroup



A. Hierarchical clustering of transcriptional profiles from the discovery cohort. Specific genes which are upregulated (red) or downregulated (green) are labelled on the vertical axis within aene clusters

B. Bar chart representing the number and type of each tumor mapping to each of the two identified sample clusters within the discovery cohort.

• A proportion of primary prostate cancer clustered with the primary cancers with known concomitant metastatic disease ('Metastatic like subgroup', highlighted in purple) whilst the normal samples clustered together with the remaining primary prostate cancer ('Non-metastatic like subgroup').

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RESULTS – Surgical Cohort



Cluster ID

- On MVA, the metastatic assay was significantly associated with BF (HR 1.59 [1.11-2.29], p=0.0128) and DM (HR 3.09 [1.70-5.61], p=0.0002) in the independent surgical cohort (n=322).
- In a combined model with CAPRA-S, the assay identified patients at high risk of BF (HR 2.67 [1.90-3.75], p<0.0001) and DM (HR 7.53 [4.13-13.73, p<0.0001) better than either model alone.

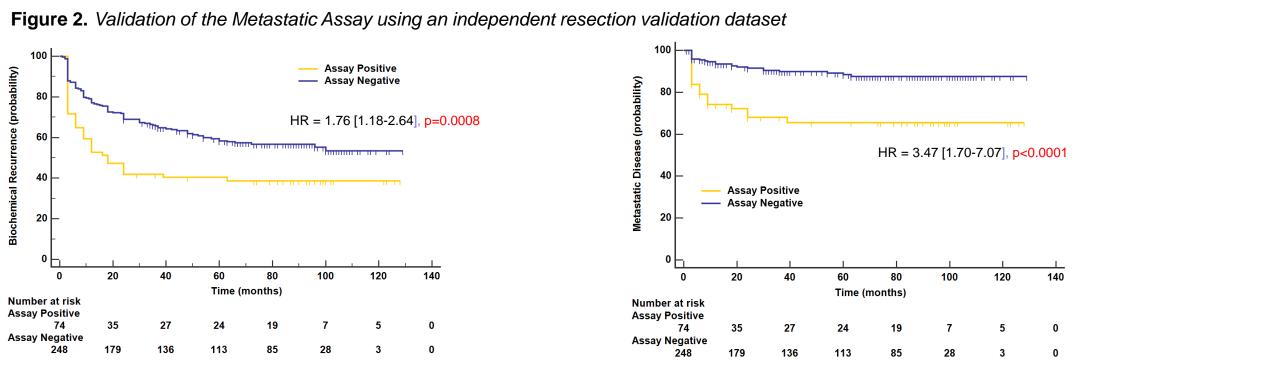
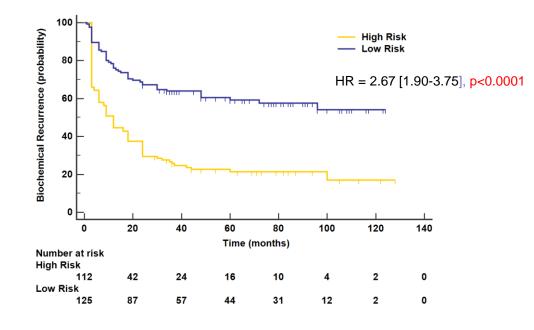
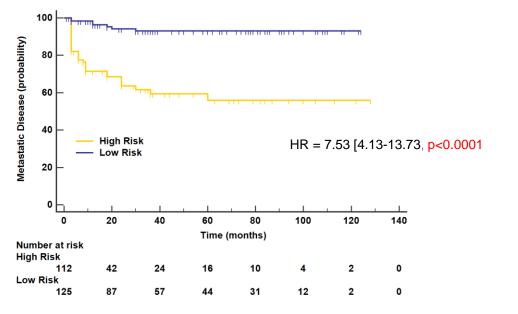
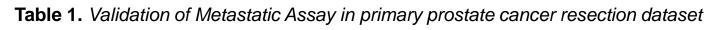


Figure 3. Validation of the Metastatic Assay in radical resections using a combined model with CAPRA-S to stratify high- and low-risk







BIOCHEMICAL RECURRENCE

METASTATIC RECURRENCE

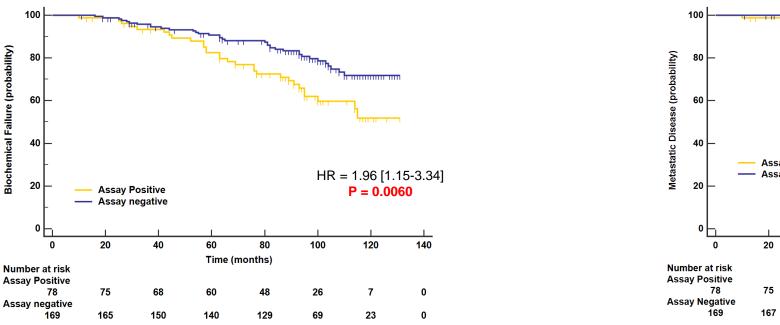
Multivariate Model 1				Multivariate Model 1			
Covariate	HR	95% CI	р	Covariate	HR	95% CI	Р
Metastatic Assay	1.59	1.11 to 2.29	0.0128	Metastatic Assay	3.09	1.70 to 5.61	0.0002
Gleason Score (3 + 4) < 6 6 4 + 3 8 - 10	2.39 0.70 1.96 2.80	0.58 to 9.87 0.40 to 1.23 1.29 to 2.96 1.82 to 4.30	0.2295 0.2173 0.0016 <0.0001	Gleason Score (3 + 4) < 6 6 4 + 3 8 - 10	5.20 0.50 4.37 6.88	0.65 to 41.86 0.11 to 2.36 1.90 to 10.01 2.94 to 16.13	0.1231 0.3850 0.0005 <0.000
Age	1.00	0.97 to 1.03	0.8733	Age	0.97	0.92 to 1.02	0.2550
PSA	1.01	1.00 to 1.01	0.0319	PSA	1.00	0.99 to 1.02	0.6413
Multivariate Model 2				Multivariate Model 2			
Covariate	HR	95% CI	р	Covariate	HR	95% CI	р
Metastatic Assay	1.72	1.19 to 2.48	0.0042	Metastatic Assay	2.94	1.60 to 5.40	0.0005
Metastatic Assay CAPRA-S	1.72 2.52	1.19 to 2.48 1.79 to 3.54	0.0042 <0.0001	Metastatic Assay CAPRA-S	2.94 4.76	1.60 to 5.40 2.46 to 9.23	0.0005
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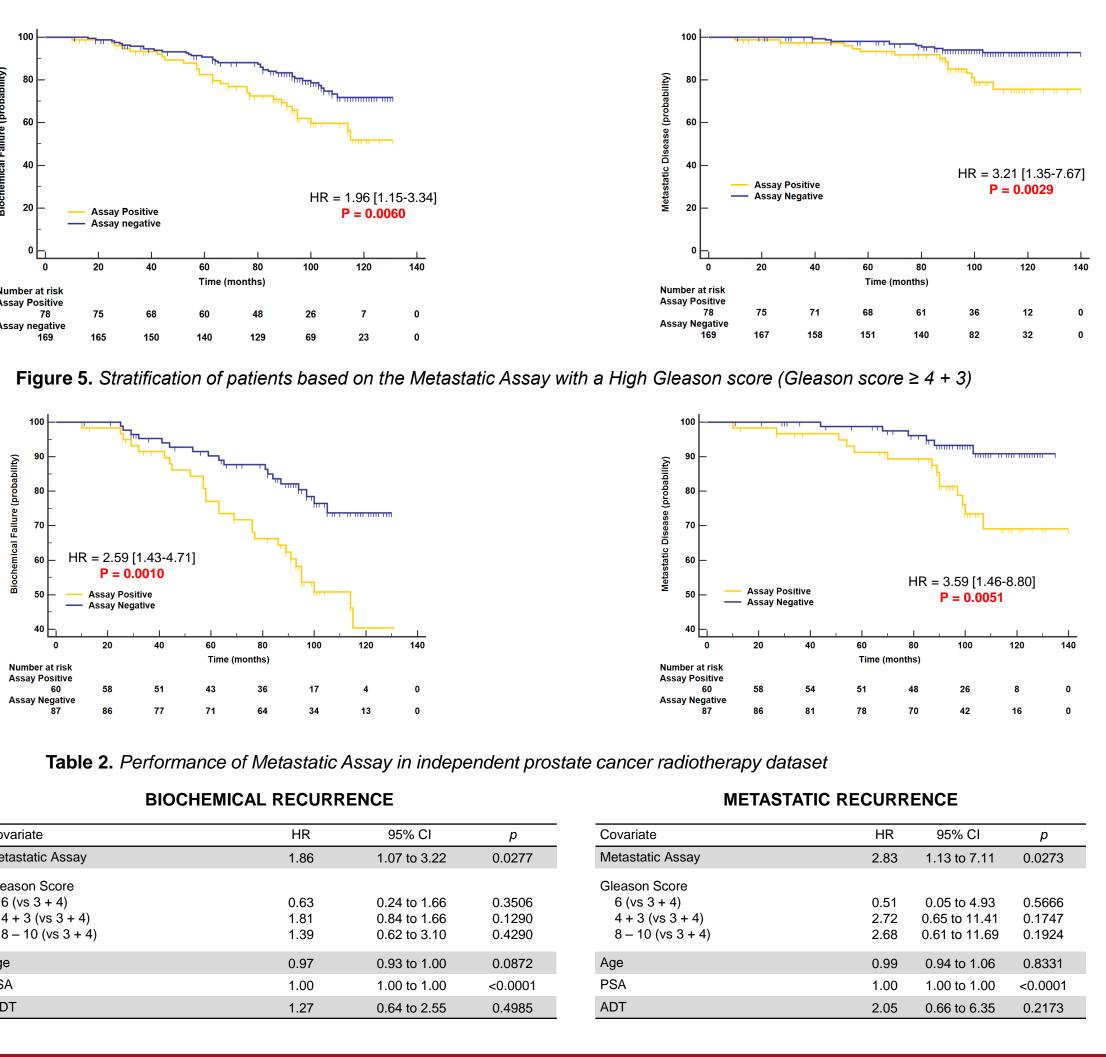
Abbreviations: HR, hazard ratio; CI, confidence intervals; PSA, prostate specific antigen; CAPRA-S, Cancer of the Prostate Risk Assessment post-surgica

RESULTS – Radiotherapy Cohort

• On MVA, the metastatic assay was significantly associated with BF (HR 1.86 [1.07-3.22], p=0.0277) and DM (HR 2.83 [1.13-7.11], p=0.0273) in the radiotherapy cohort (n=248).

Figure 4. Validation of the Metastatic Assay using an independent biopsy dataset





BIOCH	METAST			
Covariate	HR	95% CI	p	Covariate
Metastatic Assay	1.86	1.07 to 3.22	0.0277	Metastatic Assay
Gleason Score 6 (vs 3 + 4) 4 + 3 (vs 3 + 4) 8 - 10 (vs 3 + 4)	0.63 1.81 1.39	0.24 to 1.66 0.84 to 1.66 0.62 to 3.10	0.3506 0.1290 0.4290	Gleason Score 6 (vs 3 + 4) 4 + 3 (vs 3 + 4) 8 - 10 (vs 3 + 4)
Age	0.97	0.93 to 1.00	0.0872	Age
PSA	1.00	1.00 to 1.00	<0.0001	PSA
ADT	1.27	0.64 to 2.55	0.4985	ADT

CONCLUSIONS

- The Metastatic Assay predicts BF and DM in PCa patients treated with either radical surgery or EBRT.
- This assay may help to select patients at low risk of relapse, who may benefit from an active surveillance approach, and to identify those patients at high risk of metastatic disease for additional treatment aimed at preventing disease recurrence.

FASTMAN **Belfast-Manchester Movember PCUK Centre of Excellence**









