

Plasma cell-free DNA (cfDNA) profiling of PTEN-PI3K-AKT pathway aberrations in two multi-institutional independent metastatic castration-resistant prostate cancer (mCRPC) cohorts

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INTRODUCTION

- Tumor tissue from mCRPC harbors frequent copy number variations (CNVs) in the PTEN-PI3K-AKT pathway, but identifying them in plasma cfDNA has proven challenging, especially *PTEN* copy number loss.
- With emerging data supporting Akt inhibition in *PTEN*-deficient mCRPC, cfDNA assays that robustly characterize PTEN-PI3K-AKT pathway aberrations are urgently needed.

AIM

Using a validated cfDNA liquid biopsy assay in two independent mCRPC cohorts totalling 231 patients, our aims were to:

- Characterize the mutational landscape of PTEN-PI3K-AKT pathway aberrations, with an emphasis on robust detection of *PTEN* loss.
- Correlate genomic aberrations with longitudinal clinical outcomes.

METHODS

Cohort description and targeted cfDNA sequencing

- Pre-treatment plasma samples were collected from mCRPC patients (pts) across two cohorts in Australia (AU; n=78) and USA (n=153).
- Plasma PTEN-PI3K-AKT pathway aberrations were characterized using the CLIA-certified Predicine targeted panel-based NGS cfDNA assay.^{1,2}
- We included *AR* aberrations recognizing reciprocal PI3K regulation.^{3,4}

Outcomes and analysis

- Kaplan-Meier curves and multivariable Cox proportional-hazards models assessed associations between PTEN-PI3K-AKT and *AR* pathway aberrations and overall survival.

RESULTS

Patient cohort

- Median follow-up was 28.0 and 80.7 months in AU and US cohorts, respectively; patient characteristics for each cohort shown in **Table 1**.
- In the AU cohort, 49 pts (63%) commenced *AR* pathway inhibitors (ARPI; abiraterone or enzalutamide) and 29 pts (37%) commenced taxane chemotherapy (docetaxel or cabazitaxel).

References: 1. Fettke H et al. *Eur Urol* 2020;78:173-80. 2. Kohli M et al. *EbioMedicine* 2020;54:102728. 3. Carver BS et al. *Cancer Cell* 2011;19:575-86. 4. Mulholland DJ et al. *Cancer Cell* 2011;19:792-804.

Table 1: Patient characteristics	AU cohort n = 78	US cohort n = 153
Age Median [interquartile range]	72 (63-78)	72 (66-77)
Gleason score		
≤ 7	19 (24)	64 (42)
≥ 8	30 (50)	75 (49)
No biopsy / unknown	20 (26)	14 (9)
Local treatment type, N (%)		
Radical prostatectomy	22 (28)	62 (41)
RT +/- adjuvant ADT	13 (16)	38 (25)
None or metastases at dx	40 (52)	53 (34)
Primary ADT	3 (4)	
Prior treatment, N (%)		
Salvage local treatment		41 (27)
Secondary hormonal treatment	12 (21)	110 (72)
Prior chemotherapy only	26 (46)	102 (66)
Prior ARPI only	18 (32)	
Prior chemotherapy and ARPI		
Baseline biochemistry, N (%)		
PSA (ng/ml)	46 (0.5-2720)	20 (5.0-98)
LDH (U/L)	122 (113-131)	202 (176-249)
ALP (U/L)	151 (94-346)	98 (73-155)

ARPI, androgen receptor pathway inhibitor; ADT, androgen deprivation therapy; ALP, alkaline phosphatase; Hb, haemoglobin; RT, radiotherapy.

Detection and clinical associations of PTEN-PI3K-AKT pathway aberrations

- PTEN* loss was observed in 37%** (85/231) of pts (**Fig 1**) and was *independently associated* with OS in AU and US cohorts (**Fig 2 & Table 2**).
- PIK3CA* gain was observed in 17%** (39/231) of pts (**Fig 1**) and was *independently associated* with poor survival in the AU but not the US cohort (**Table 2**).

- In a subset of AU samples with additional plasma (n=46), **low-pass WGS confirmed panel *PTEN* loss in 90%** (28/31), and ***PIK3CA* gain in 84%** (16/19), with **high correlation** for absolute copy number between methods (R=0.85 and R=0.80, respectively).

- Of 146 *PTEN*-neutral pts, **31 (21%) had alternate PTEN-PI3K-AKT aberrations (Fig 1)**.

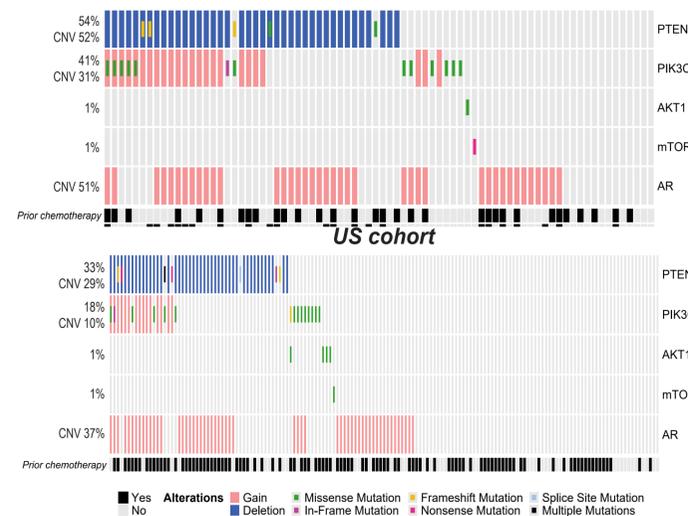


Fig 1: Genomic landscape of PTEN-PI3K-AKT and AR pathway aberrations in AU (top) and US (bottom) cohorts.

Cumulative CNVs in PTEN-PI3K-AKT and AR pathways

- Considering *PTEN* loss, *PIK3CA* gain and *AR* gain, cumulative CNVs (0 vs 1 vs ≥2 CNVs) in the PTEN-PI3K-AKT and AR pathways were significantly associated with worse clinical outcomes (**Fig 2 & Table 2**).

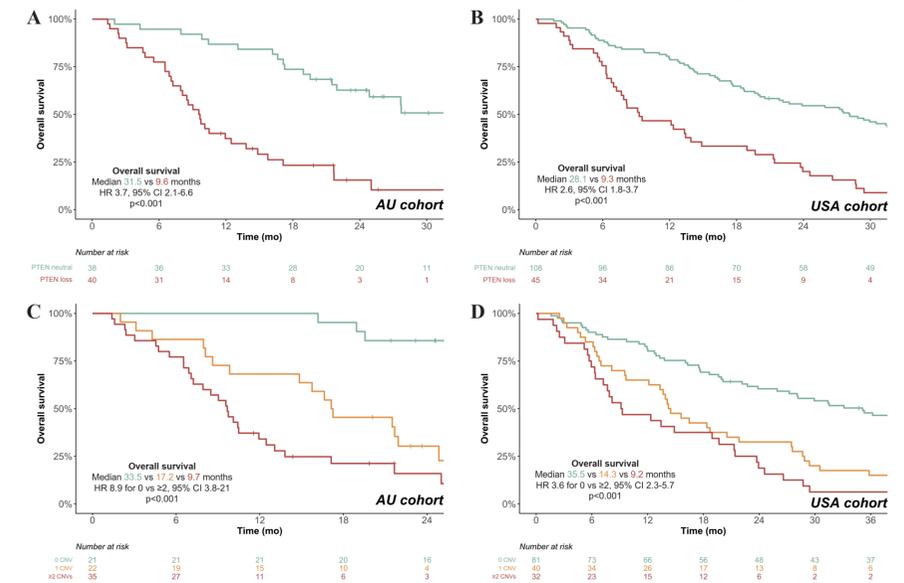


Figure 2: Kaplan-Meier analysis of OS according to *PTEN* copy number status (A,B) and cumulative CNVs in PTEN-PI3K-AKT and AR pathways (C,D).

Table 2: MVA	AU cohort (n = 78) ^a			US cohort (n = 153) ^b		
	HR	95% CI	p	HR	95% CI	p
CNVs						
<i>PTEN</i> loss	3.0	1.5-5.7	0.001	1.9	1.3-2.9	0.002
<i>PIK3CA</i> gain	2.9	1.5-5.5	0.001	1.7	0.92-3.0	0.09
<i>AR</i> gain	2.2	1.2-4.1	0.02	2.3	1.5-3.4	<0.001
Cumulative PTEN-PI3K-AKT and AR pathway CNVs						
0	REF	-	-	REF	-	-
1	6.2	2.3-17	<0.001	1.8	1.2-2.8	0.006
≥2	9.3	3.5-25	<0.001	3.2	2.0-5.3	<0.001

^a Covariates in multivariable variable analysis (MVA): ctDNA% ≥2%, prior chemotherapy, prior ARPI, visceral metastases, baseline pain and ECOG PS ≥2. ^b Covariates in MVA: ctDNA% ≥2%, prior chemotherapy, alkaline phosphatase (log₁₀).

CONCLUSION

- PTEN-PI3K-AKT CNVs were readily detected using Predicine cfDNA assay, with prevalence of *PTEN* loss comparable to tissue studies.
- Over one-fifth of *PTEN*-neutral patients had other activating aberrations in the PTEN-PI3K-AKT pathway.
- Plasma cfDNA profiling of PTEN-PI3K-AKT and AR pathway aberrations may identify a poor-risk cohort primed for dual AR/Akt targeted therapy.