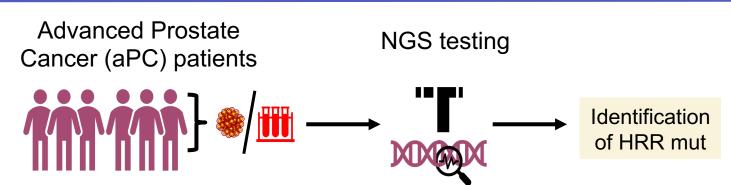
Homologous Recombination Repair (HRR) mutation concordance between liquid biopsy (LB) and tumor tissue by NGS in a real-world prostate cancer (PC) database

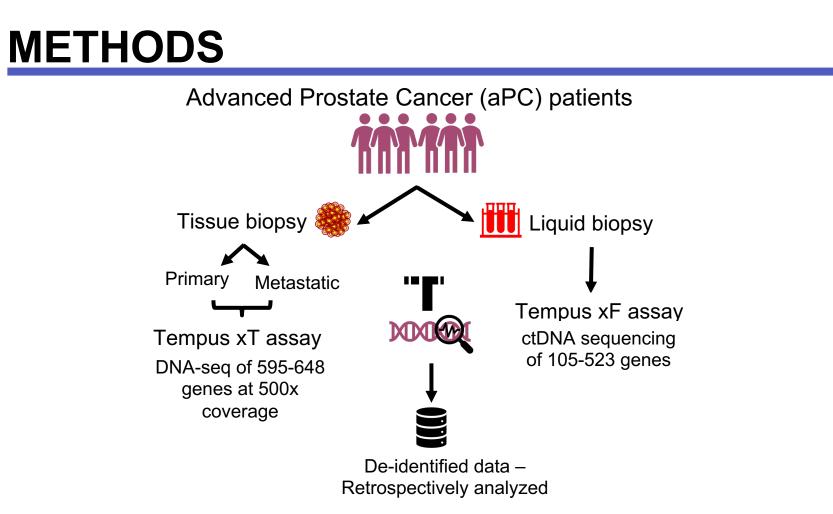
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INTRODUCTION



In a large real-world (RW) database, we determined:

- Concordance between plasma ctDNA and primary tumor tissue (PT) and/or metastatic tissue (MT) for BRCA1, BRCA2, and ATM mut in PC patients who received both LB and tissue NGS any time during standard of care (SOC) management
- The utility of LB to detect actionable mut in these HRR genes and demonstrate the utility of combined LB and tissue testing



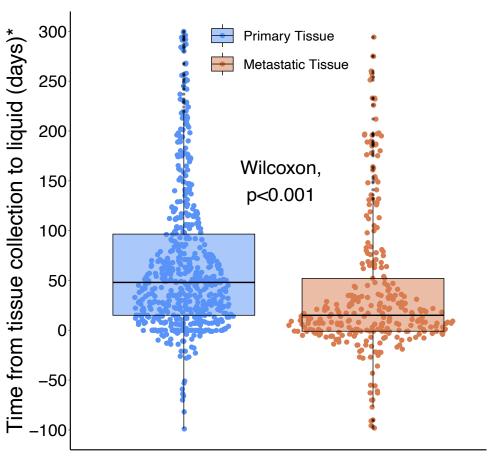
- Paired analysis from primary tumor (PT), metastatic tumor (MT) and liquid biopsy (LB) of patients: 1) PT vs LB 2) MT vs LB.
- The results from the patient's earliest PT or MT and earliest LB were used for paired analyses.
- The prevalence of a pathogenic/likely pathogenic germline and/or somatic mut in BRCA1, BRCA2, or ATM was reported as N (%), 95% Cl.
- The sensitivity of the LB to identify observed HRR mut in tissue was also reported as N (%), 95% CI.
- Concordance between pairs was evaluated by Cohen's kappa statistic with 95% CI.

SUMMARY

RESULTS

Characteristic	Matched PT - LB , N = 1074 ¹	Matched MT - LB, N = 451^{1}
Age at Diagnosis	66 (60, 72)	64 (58, 72)
Unknown	3	12
Race		
White	434 (69%)	197 (70%)
Black or African American	147 (23%)	54 (19%)
Other	27 (4.3%)	20 (7.1%)
Asian	24 (3.8%)	12 (4.2%)
Unknown	442	168
Ethnicity		
Hispanic or Latino	80 (19%)	40 (25%)
Unknown	648	291
Match Type		
tumor/normal match	975 (91%)	403 (89%)
tumor only	99 (9.2%)	48 (11%)
HRR+, tissue (PT or MT)	94 (8.8%)	46 (10%)
HRR+, liquid (LB)	67 (6.2%)	47 (10%)
1 Median (IQR), n (%)		
- - - - - - - - - -		





• Plasma ctDNA-based analysis of BRCA1, BRCA2, and ATM mut showed greater concordance between liquid biopsy and metastatic tissue than liquid biopsy and primary tumor tissue, in this large Real-World dataset, potentially influenced by greater proximity in time between the former paired samples.

• Liquid Biopsy is an effective initial tool for **HRR mut detection**, identifying 70% of HRR mutations found in metastatic tissue biopsies • When liquid biopsy results are negative, further exploration with tissue-based testing may identify additional HRR mut to guide clinical decisions

Figure 1 – Time from tissue collection to liquid was significantly shorter in MT vs LB analyses compared to PT vs LB analyses (median 21 vs 174 days, respectively)

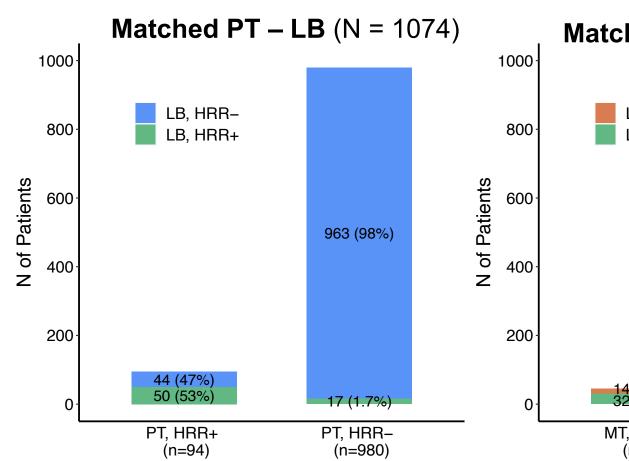


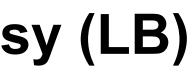
Figure and Table 2 – Agreement of HRR detection between tissue and liquid Sensitivity: N LB, HRR+/N PT (or MT), HRR+, Specificity: N LB, HRR-/N PT (or MT), HRR-, Positive predictive value: N PT (or MT), HRR+/N LB, HRR+, Negative predictive value: N PT (or MT), HRR-/N LB, HRR-

Key Results

- 7.6%-13%). Table 1
- analyses, respectively). **Table 1**

Acknowledgments: We thank Minxuan Huang, Ph.D for data analysis, Rachel Berg, MS, and Amrita A. Iyer, Ph.D, for poster preparation & review Correspondence: JohnShen@mednet.ucla.edu

*y-axis truncated at 300 and -100





ched MT – LB (N = 451)		Characteristic	PT vs LB ¹ , N = 1074	MT vs LB ¹ , N = 451
LB, HRR–		Sensitivity	53% (43%-64%)	70% (54%-82%)
LB, HRR+	Specificity	98% (97%-99%)	96% (94%-98%)	
		+ve Predictive Value	75% (63%-84%)	68% (53%-81%)
		-ve Predictive Value	96% (94%-97%)	97% (94%-98%)
		Cohen's Kappa	0.59 (0.50 – 0.68)	0.65 (0.54 – 0.77)
200 (06%)	390 (96%)	1statistic (95% C.I)		
14 (30%) 32 (70%)	15 (3.7%)			
MT, HRR+	MT, HRR-			
(n=46)	(n=405)			

• HRR+ was identified in 8.8% of primary tissue (95% CI (7.2%-11%) and 10% of metastatic tissue (95%

• HRR+ was identified in 6.2% (95% CI 4.9%-7.9%) and 10% (7.8%-14%) of liquid samples (PT vs MT

• Liquid biopsy demonstrated higher concordance of HRR+ detection with metastatic tissue compared to primary tissue (Cohen's kappa 0.65 vs 0.59, respectively, **Table 2**), potentially influenced by reduced time between tissue and liquid collection (Figure 1) and increased tumor burden in metastatic patients.