HSD112

Real-World Patterns of Homologous Recombination Repair Testing of Patients with Metastatic Castration-Sensitive Prostate Cancer (mCSPC) in the US Community Oncology Setting

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Objective

To conduct a landscape analysis of mCSPC, with a focus on HRR testing among patients who initiated frontline systemic therapy for mCSPC.

Conclusions

HRR testing capture among patients with mCSPC in this community oncology setting was low (<30%) in structured EHR data.

These findings highlight an important unmet need for earlier and broader guideline-concordant germline and somatic HRR testing to better understand the hereditary cancer risk and prognosis of mCSPC and inform eligibility for HRR-targeted treatments.

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References: 1. NCCN Clinical Practice Guidelines in Oncology: Prostate Cancer. Version 5.2026. January 23, 2026. **2.** Barata PC, et al. *J Clin Oncol*. 2025;43(5_suppl):102. **3.** Barata PC, et al. *JAMA Oncol*. 2024;10(7):975-977. **4.** Shevach JW, et al. *J Natl Compr Canc Netw*. 2024;22(4):237-243. **5.** The US Oncology Network. https://usoncology.com/our-company/. Accessed April 13, 2026.

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Background

- Multigene tumor testing for alterations in homologous recombination repair (HRR) genes is recommended by NCCN guidelines in patients with high-/very high-risk localized, regional, or metastatic prostate cancer (mPC),[1] including:
  - Germline testing at diagnosis of metastatic, regional, very-high-risk localized, or high-risk localized PC, and/or for patients with a positive family history of certain cancers (including PC) or familial cancer risk mutation.[1]
  - Somatic testing at mPC diagnosis.[1]
- Previous studies of patients with metastatic castration-resistant prostate cancer (mCRPC) have found:
  - Higher odds of testing among patients with a family history of prostate cancer and/or Gleason ≥8.[2]
  - Lower odds of testing among higher age, worse performance status, recurrent metastatic disease, Medicaid insurance and/or lower socioeconomic status (including race-related disparities mediated by income).[3-4]
- However, HRR testing patterns remain heterogenous in the metastatic castration-sensitive prostate cancer (mCSPC) setting, and real-world studies are needed to evaluate predictors of HRR testing.

Materials and Methods

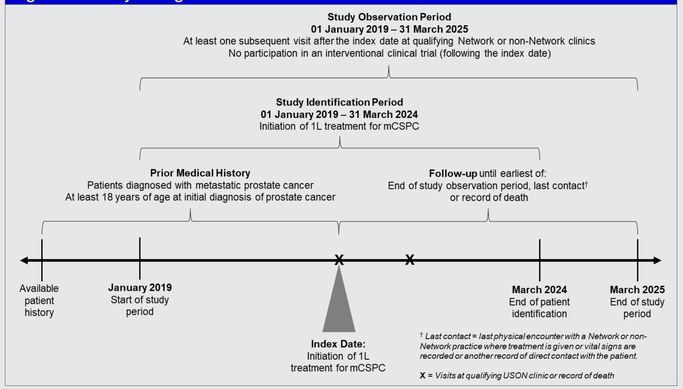
STUDY DESIGN

- This was a retrospective observational cohort study of patients with a provider-documented mCSPC diagnosis who initiated systemic therapy (index) between 1/1/2019 and 3/31/2024 in The US Oncology Network or non-Network practices and were followed through 3/31/2025 (**Figure 1**).

DATA SOURCES

- Data were sourced from structured fields of The US Oncology Network's iKnowMed (iKM) electronic health record (EHR).
- The US Oncology Network includes over 2,700 providers in over 600 sites of care across the US, and ~50 non-Network clinics that have adopted the iKM EHR and participate in real-world research activities with Ontada.

Figure 1. Study Design



ANALYSIS & VARIABLE DEFINITIONS

- Baseline characteristics were assessed within 60 days pre-index.
- All available results prior to the end of follow-up (3/31/2025) for the following HRR genes were included: ATM, ATR, BRCA1, BRCA2, CDK12, CHEK2, FANCA, MLH1, MRE11A, NBN, PALB2, and RAD51C.
- Descriptive analyses of patient characteristics were presented overall and by HRR testing/mutation status.
- HRR testing and mutation rates were described, and a multivariable logistic regression model was used to assess predictors of HRR testing.
  - Covariates were selected based on clinical and epidemiologic subject matter expertise, with consideration of the timing and missingness of each covariate.

Results

PATIENT CHARACTERISTICS

- Overall, 5,973 patients who initiated frontline systemic therapy for mCSPC between January 2019 - March 2024 were included (median follow-up: 21 months).
- Among patients with available data at baseline, most were ECOG 0-1 (93.0% of N=1,113), Gleason ≥8 (65.7% of N=1,020) and PSA >4 ng/mL (74.0% of N=3,826) (**Table 1**).

Table 1. Demographic and Clinical Characteristics

Variable	Total N=5,973	HRR Tested, w/ Mutation N=615	HRR Tested, Mutation Not Documented N=1,100	HRR Test and/or Results Not Documented N=4,258
Median (IQR) age at index	72 (65-79)	71 (63-78)	70 (63-77)	73 (66-80)
Race, n (%)				
White	3,748 (62.7)	414 (67.3)	748 (68.0)	2,586 (60.7)
Black or African American	559 (9.4)	60 (9.8)	115 (10.5)	384 (9.0)
Asian	111 (1.9)	18 (2.9)	18 (1.6)	75 (1.8)
Other Race	314 (5.3)	30 (4.9)	58 (5.3)	226 (5.3)
Not documented	1,241 (20.8)	93 (15.1)	161 (14.6)	987 (23.2)
Ethnicity, n (%)				
Hispanic or Latino	427 (7.1)	34 (5.5)	49 (4.5)	344 (8.1)
Not Hispanic or Latino	4,400 (73.7)	479 (77.9)	872 (79.3)	3,049 (71.6)
Not documented	1,146 (19.2)	102 (16.6)	179 (16.3)	865 (20.3)
Practice Region, n (%)				
West	2,523 (42.2)	211 (34.3)	380 (34.5)	1,932 (45.4)
South	1,960 (32.8)	229 (37.2)	376 (34.2)	1,355 (31.8)
Midwest	1,415 (23.7)	172 (28.0)	334 (30.4)	909 (21.3)
Northeast	75 (1.3)	3 (0.5)	10 (0.9)	62 (1.5)
Practice Rurality, n (%)				
Urban	5,498 (92.0)	576 (93.7)	973 (88.5)	3,949 (92.7)
Rural	475 (8.0)	39 (6.3)	127 (11.5)	309 (7.3)
Practice Volume (patients per year), n (%)				
Small (1-499)	258 (4.3)	11 (1.8)	45 (4.1)	202 (4.7)
Medium (500-999)	206 (3.4)	24 (3.9)	45 (4.1)	137 (3.2)
Large (1,000-4,999)	3,519 (58.9)	416 (67.6)	736 (66.9)	2,367 (55.6)
Very Large (5,000+)	1,990 (33.3)	164 (26.7)	274 (24.9)	1,552 (36.4)
Disease Stage at Initial Diagnosis (if available), or at Oncologist Referral, n (%)				
Stage 0-III	170 (2.8)	20 (3.3)	31 (2.8)	119 (2.8)
Stage IVA	635 (10.6)	61 (9.9)	94 (8.5)	480 (11.3)
Stage IVB or IV NOS	2,656 (44.5)	332 (54.0)	590 (53.6)	1,734 (40.7)
Not documented	2,512 (42.1)	202 (32.8)	385 (35.0)	1,925 (45.2)
Median (IQR) weeks from mPC diagnosis to index	0.1 (0.1-1.1)	0.1 (0.1-2.0)	0.1 (0.1-1.6)	0.1 (0.1-1.0)
Gleason Score within 60 days Prior to Index, n (%)				
N with available data	1,020	112	230	678
<8	350 (34.3)	31 (27.7)	67 (29.1)	252 (37.2)
≥8	670 (65.7)	81 (72.3)	163 (70.9)	426 (62.8)
ECOG Performance Status within 60 Days Prior to Index, n (%)				
N with available data	1,113	113	181	818
0-1	1,035 (93.0)	104 (92.0)	174 (96.1)	756 (92.4)
2+	78 (7.0)	9 (8.0)	7 (3.9)	62 (7.6)
PSA Category within 60 Days Prior to Index, n (%)				
N with available data	3,826	436	746	2,644
≤4.0 ng/mL	996 (26.0)	87 (20.0)	156 (20.9)	753 (28.5)
>4.0 ng/mL	2,830 (74.0)	349 (80.0)	590 (79.1)	1,891 (71.5)

Note: demographics and clinical characteristics associated with HRRm testing (**Table 2**) are highlighted above.

HRR TESTING & MUTATION STATUS

- Testing for ≥1 BRCA and/or non-BRCA HRR gene prior to the end of follow-up was documented in 1,715 (28.7%) patients, and the HRR mutation-positive rate among patients with documented results was 35.9% (n=615) (**Figure 2**).
  - Testing for ≥1 BRCA and ≥1 non-BRCA HRR genes were documented in 13.6% (n=815/n=5,973) of the overall cohort.
- BRCA1 and BRCA2 testing were documented in 24.2% and 24.3% overall, and the mutation-positive rates were 6.7% (n=97/n=1,447) and 14.6% (n=213/n=1,454), respectively (**Figure 3**).
  - Testing for both BRCA1 and BRCA2 were documented in 23.2% (n=1,385/n=5,973) of the overall cohort.
- Non-BRCA HRR testing was documented in 17.0% overall, and the non-BRCA HRR mutation-positive rate was 44.0% (n=446/n=1,014) (**Figure 3**).

Figure 2. (A) HRR Testing Rates (Overall) & (B) HRR Mutation-Positive Rates (Among Tested), Any HRR Test/Positive Result

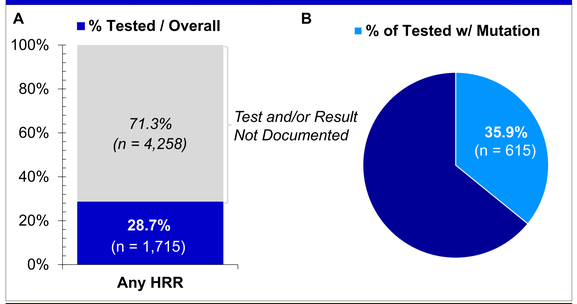
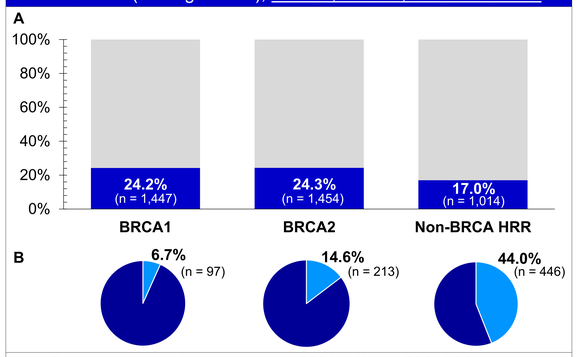


Figure 3. (A) HRR Testing Rates (Overall) & (B) HRR Mutation-Positive Rates (Among Tested), BRCA1, BRCA2, non-BRCA HRR



Note: Patients may have positive mutations to >1 BRCA and/or non-BRCA HRR gene.

PREDICTORS OF HRR TESTING

- Factors associated with more HRR testing included stage IVB/IV-NOS (OR: 1.68, 95%CI: 1.49-1.90, P<0.0001) and PSA >4 ng/mL (OR: 1.47, 95%CI: 1.23-1.77, P<0.0001) (**Table 2**).
- Geographical variation was also observed with lower rates of HRR testing in the West (OR: 0.61 95%CI: 0.52-0.72, P<0.0001) and South (OR: 0.66, 95%CI: 0.56-0.79, P<0.0001) relative to the Midwest (**Table 2**).
- Less HRR testing was observed among patients with age ≥70 years (OR: 0.59, 95%CI: 0.52-0.67, P<0.0001) and Hispanic ethnicity (OR: 0.72, 95%CI: 0.54-0.96, P=0.0242) (**Table 2**).
- Distinct trends in HRR testing rates, increasing practice volume, and increasing comorbidity burden were not observed.

Table 2. Multivariable Logistic Regression of Predictors of HRR Testing

Covariate	Level	N, Patients	N, Events	OR (95% CI)	P-value
Age Group	<70 years (ref.)	2,331	728		
	≥70 years	3,642	808	0.591 (0.523-0.669)	**<0.0001**
Race	White (ref.)	3,748	1,034		
	Black or African American	559	158	0.834 (0.667-1.028)	0.0890
	Asian	111	34	1.207 (0.79-1.844)	0.3853
	Other	314	81	0.885 (0.67-1.169)	0.3897
	Not reported	1,241	229	0.770 (0.634-0.936)	0.0085
Ethnicity	Not Hispanic or Latino (ref.)	4,400	1,217		
	Hispanic or Latino	427	70	0.720 (0.541-0.958)	**0.0242**
	Not documented	1,146	249	0.916 (0.761-1.103)	0.3554
Practice Rurality	Urban (ref.)	5,498	1,382		
	Rural	475	154	1.187 (0.956-1.472)	0.1202
Practice Region	Midwest (ref.)	1,415	457		
	Northeast	75	12	0.759 (0.361-1.595)	0.4671
	South	1,960	554	0.661 (0.555-0.788)	**<0.0001**
	West	2,523	513	0.611 (0.520-0.719)	**<0.0001**
Practice Volume (patients / year)	Small (1-499) (ref.)	258	47		
	Medium (500-999)	206	63	2.361 (1.438-3.877)	**0.0007**
	Large (1,000-4,999)	3,519	1,031	2.174 (1.470-3.215)	**<0.0001**
	Very Large (5,000+)	1,990	395	1.325 (0.886-1.981)	0.1703
Stage IVB/IV NOS at Diagnosis	No / Not Documented (ref.)	3,317	671		
	Yes	2,656	865	1.683 (1.488-1.904)	**<0.0001**
PSA Category (ng/mL)	≤4.0 ng/mL (ref.)	1,000	207		
	>4.0 ng/mL	2,826	843	1.472 (1.228-1.765)	**<0.0001**
	Not documented	2,147	486	1.097 (0.906-1.329)	0.3438
Time from mPC disease to index	Per 1 week increase	5,973	1,536	1.001 (1.000-1.002)	0.0553

Additional covariates included in the model were: modified Charlson Comorbidity Index, treatment for other primary cancer diagnosis. Gleason Score and ECOG Performance Status were omitted due to missingness.

Limitations

- Observed HRR testing rates may be underestimated due to incomplete documentation of HRR results in structured EHR data, highlighting an opportunity for improved data interoperability to ensure HRR results are documented and actionable for providers.
- Several covariates used as predictors of HRR testing were not complete across the entire cohort.
- Additionally, heterogeneity in HRR testing rates throughout the duration of follow-up is expected.

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