

INTERNATIONAL SYMPOSIUM

GU-Alliance for Research and Development



PRESENCIAL RETRANSMITIDO EN DIRECTO FACE-TO-FACE AND LIVE STREAMING

26-27 JUNIO 2025

Espacio Maldonado, Madrid



¿HA LLEGADO LA MEDICINA DE PRECISIÓN AL CÁNCER DE PRÓSTATA HORMOSENSIBLE METASTÁSICO?

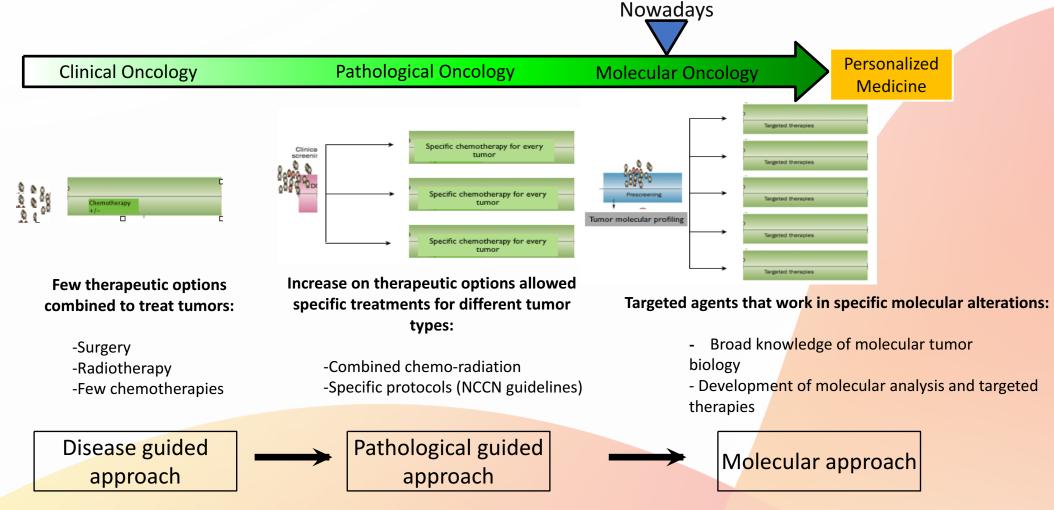
Dr. Joan Carles Jefe de Sección Hospital Universitario Vall d'Hebron Barcelona

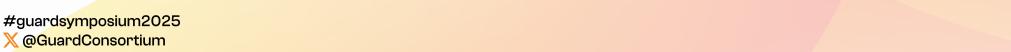
Disclosures

- Employee: Vall d'Hebron University Hospital, Teknon Oncology Department
- Consultant and scientific advisory board attendee: Amgen, Astellas, Bayer, BMS, MSD, Johnson & Johnson, Sanofi,
 Pfizer, Novartis (AAA)
- Speaker bureau: Asofarma, Astellas, Bayer, Johnson & Johnson, Sanofi
- Others: CAMDHA Agency
- Institutional Studies Collaborations: AB Science, Aragon Pharmaceuticals, Arog Pharmaceuticals, INC, Astellas Pharma, Astrazeneca AB, Aveo Pharmaceuticals INC, Bayer AG, Blueprint Medicines Corporation, BN Immunotherapeutics INC, Boehringer Ingelheim España, S.A., Bristol-Myers Squibb International Corporation (BMS), Clovis Oncology, INC, Cougar Biotechnology INC, Deciphera Pharmaceuticals LLC, Exelixis INC, F. Hoffmann-La RocheLTD, Genentech INC, Glaxosmithkline, SA, Incyte Corporation, Janssen-Cilag International NV, Karyopharm Therapeutics INC., Laboratoires Leurquin Mediolanum SAS, Lilly, S.A., Medimmune, Millennium Pharmaceuticals, INC., Nanobiotix SA, Novartis Farmacéutica, S.A., Pfizer, S.L.U, Puma Biotechnology, INC, Sanofi-Aventis, S.A., SFJ Pharma LTD. II, TevaPharma S.L.U.



Conceptual evolution of cancer treatment







Conceptual evolution of cancer treatment

Nowadays Personalized Molecular Oncolog Medicine

Clinical Oncology

Pathological Oncology

First "magic bullets":

- BCR/ABL Translocation-imatinib
- HER 2 Amplification –Trastuzumab

Push in Molecular Biology of Cancer

ARTICLE

Signatures of mutational processes in human cancer

A list of authors and their affiliations appears at the end of the pape

Social attention (Nixon declares war on cancer)













Pharma expands the pipeline









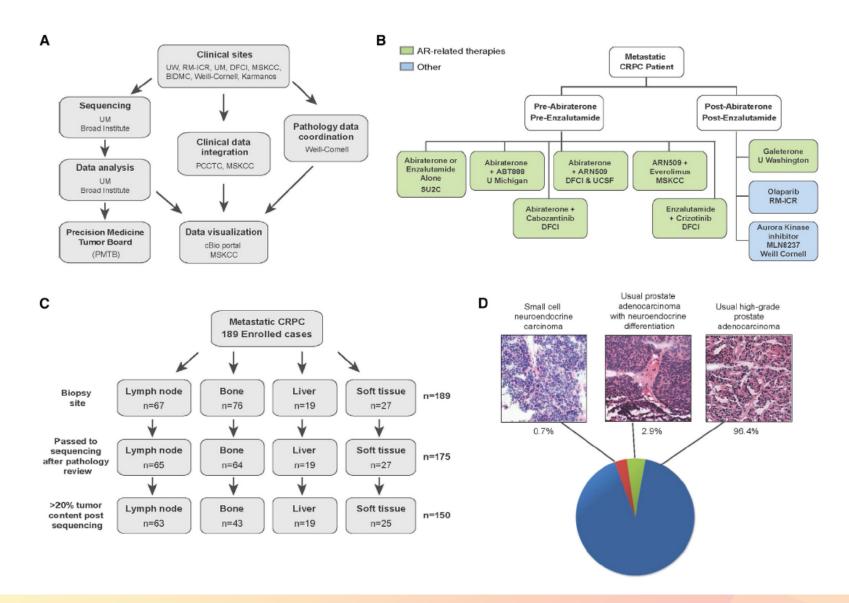




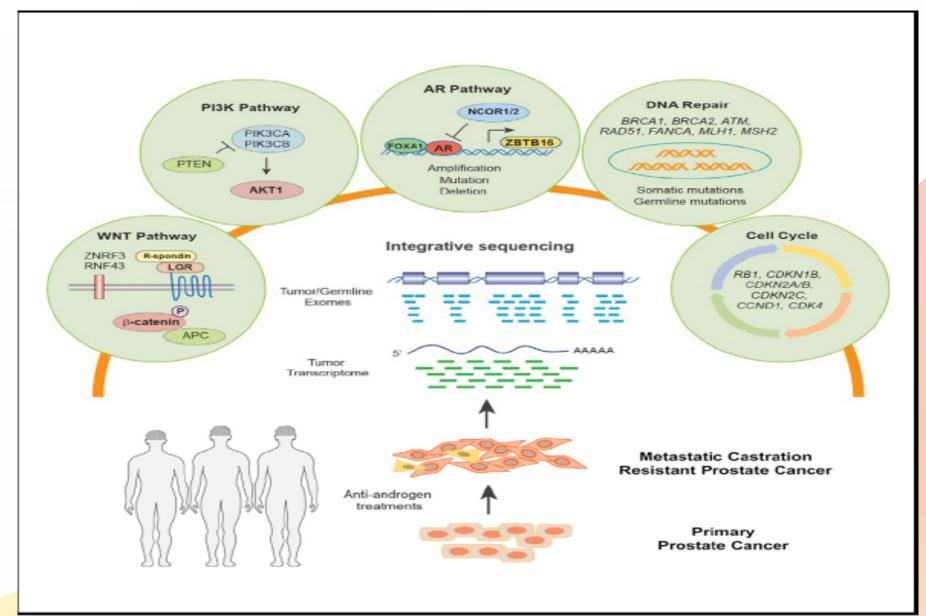


Changes in the last 15 years



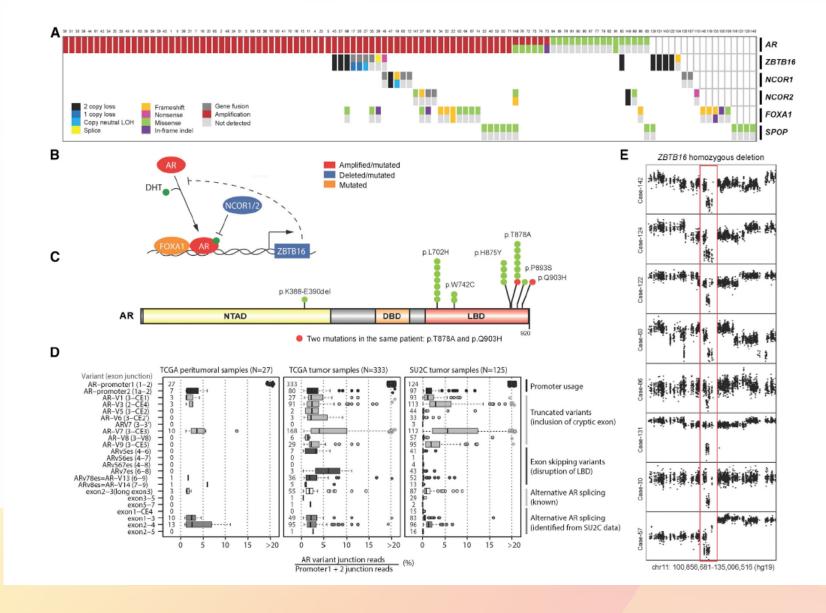






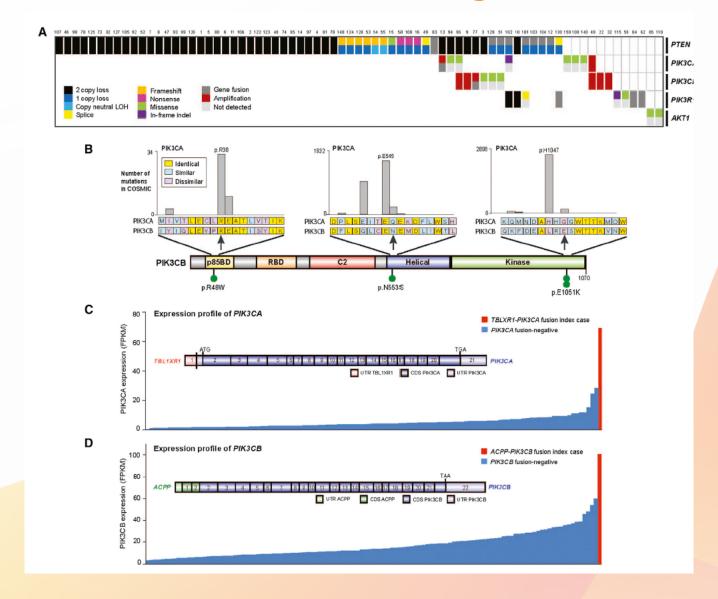


Aberrations in AR



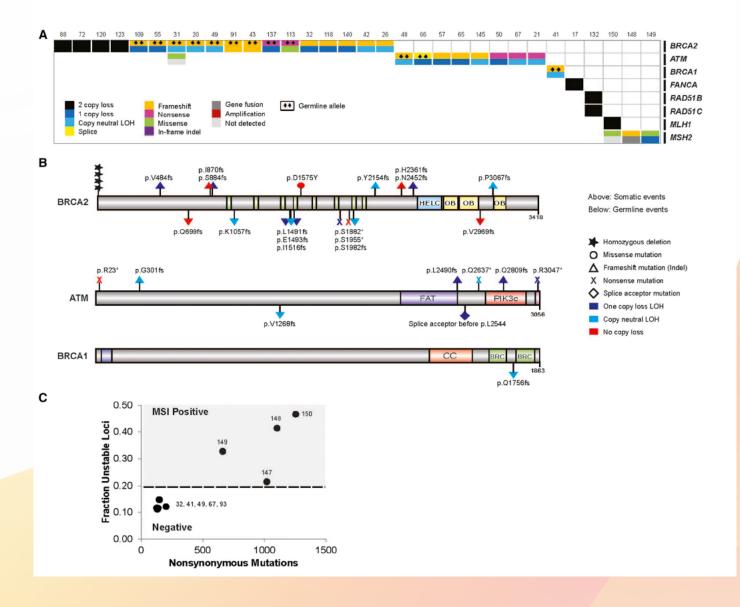


Aberrations on PI3k Pathway



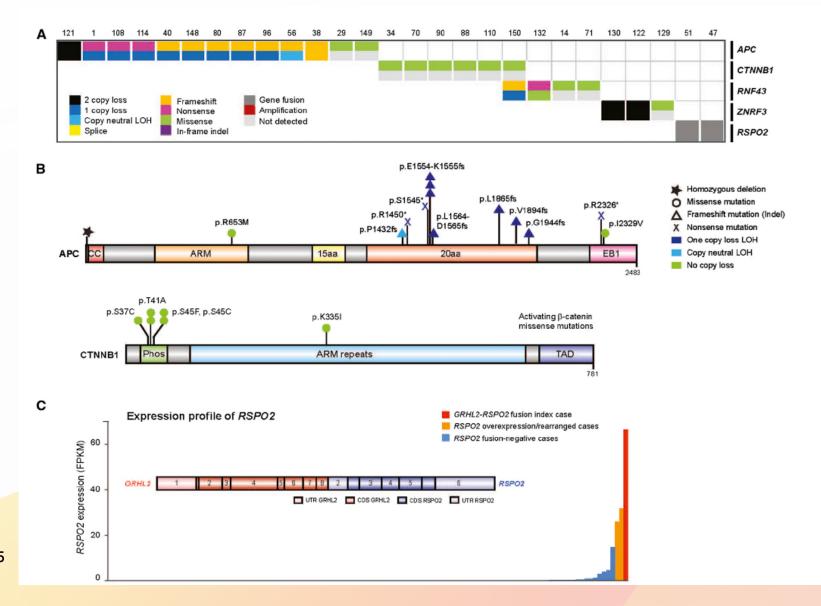


Aberrations in DNA repair pathway





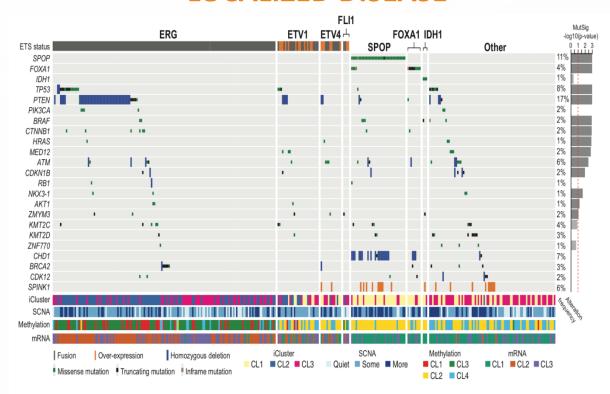
Aberrations in Wnt pathway





The genomic landscape of prostate cancer

LOCALIZED DISEASE

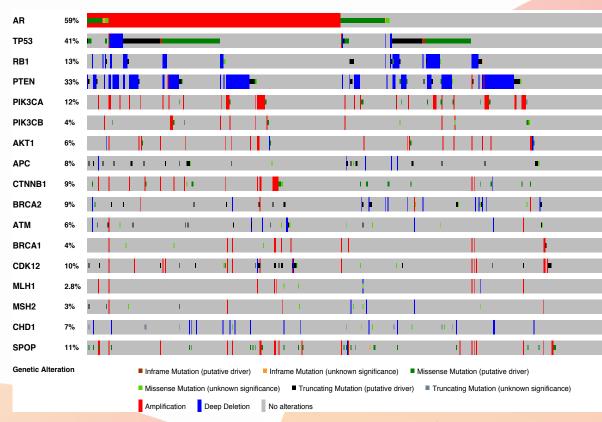


TCGA. Abehouse et al Cell 2015

333 PRIMARY TUMORS

#guardsymposium2025
X @GuardConsortium

METASTATIC DISEASE

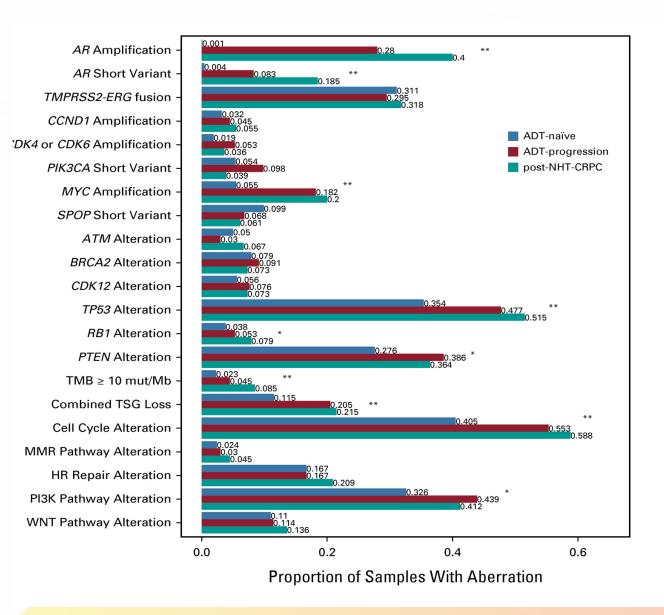


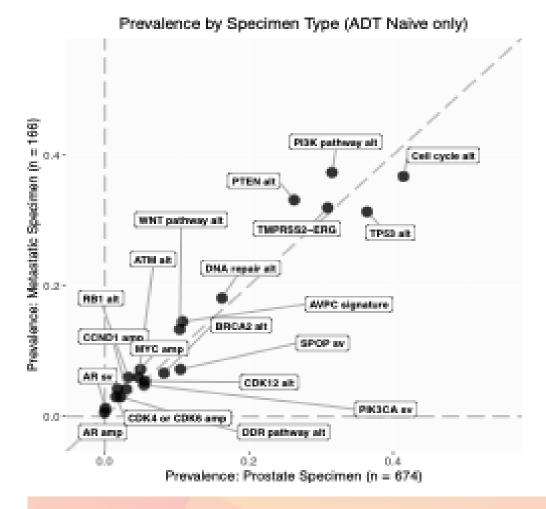
SU2C-PCF mCRPC Dream Team Study n=432 (Abida et al, PNAS 2019)

First published at Robinson et al, Cell 2015 (n=150)



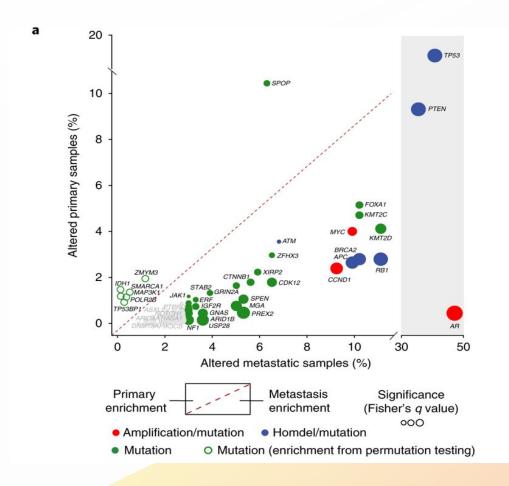
Genomics of HSPC vs CRPC

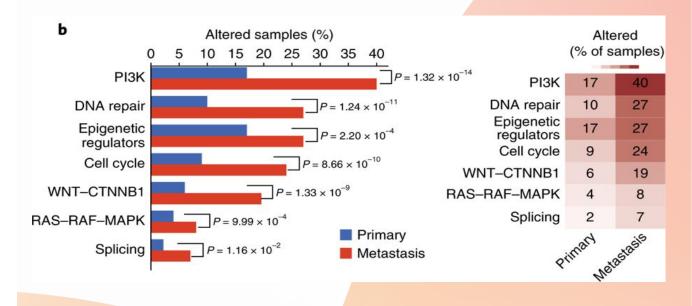






Genomics of locoregional vs lethal prostate cancer









But...

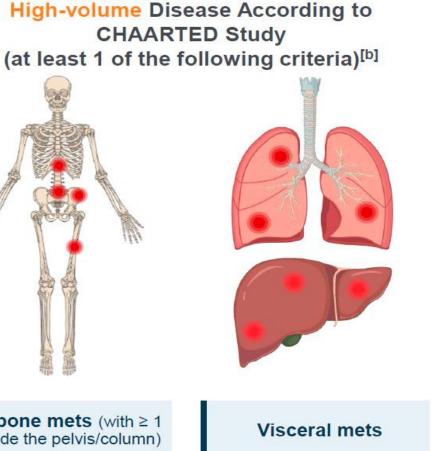


Prognostic classification criterio of High-Risk/Volume M1 HSPC

High-risk Disease According to LATITUDE Study (at least 2 of the following criteria)[a] Gleason score ≤ 6 Gleason score 7 (3+4) Gleason score 7 (4+3) Gleason score 8 - 10

≥ 4 bone mets (with ≥ 1

outside the pelvis/column)



≥ 3 bone mets

Visceral mets

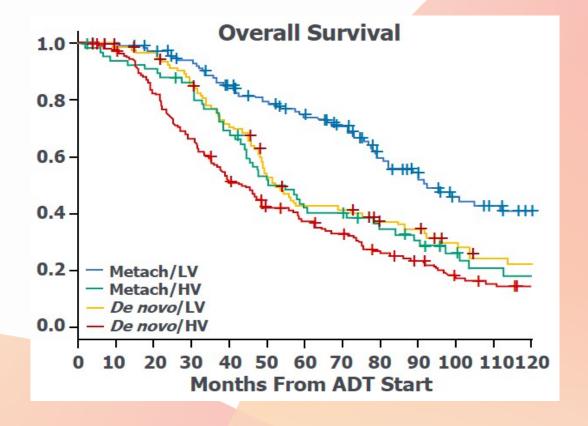
Gleason score ≥ 8



Prognosis according to volume and presentation at diagnosis

High-volumen de Novo metastatic diseases is associated with the poorest prognosis

Groups	N (% events)	mOS, years (95% CI)
Metach/ Low Vol	125 (50)	7.7 (6.7, 10.6)
Metach/ High Vol	67 (75)	4.6 (3.7, 6.7)
De novo/ Low Vol	96 (70)	4.3 (4.0, 6.5)
De novo/ High vol	148 (84)	3.6 (3.1, 4.7)





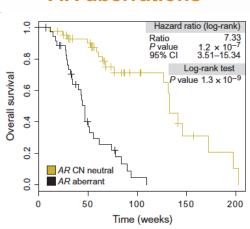


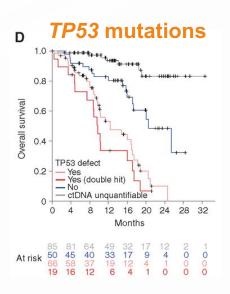
Can genomics help us to select different patient groups for different treatments?



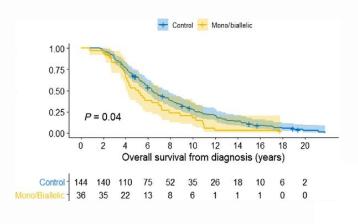
Some gonomic events are prognostic biomarkers

AR aberrations

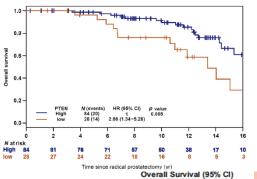


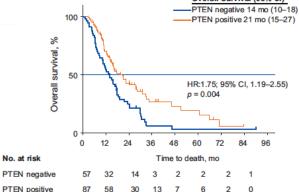


CDK12 mutations



PTEN loss





BRCA2 alterations, RB1 loss, MYC amplification

	Media	ın CSS					
	Yes	No			Hazard Ratio (95% CI)	p-value	
Germline BRCA1 carriers	13.5	17.6		-	1.84 (0.83 to 4.10)	0.136	
Germline BRCA2 carriers	9.1	17.6			2.10 (1.33 to 3.33)	0.002	
BRCA2 loss	9.0	16.9		├	2.62 (1.67 to 4.10)	<0.001	
RB1 loss	9.9	16.9		├	1.89 (1.23 to 2.90)	0.004	
BRCA2-RB1 codeletion	9.0	16.9			2.81 (1.69 to 4.70)	<0.001	
MYC amplification	6.0	17.6			5.25 (3.25 to 8.50)	<0.001	
MYC Gain	12.6	17.6			2.56 (1.31 to 4.99)	0.006	
		0.1		1	7 10		
			Better	Worse			
			beller	AAOISE			

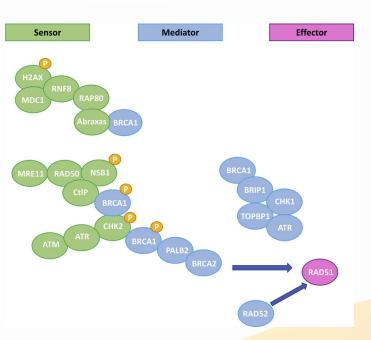


No. at risk

PARPi Monotherapy

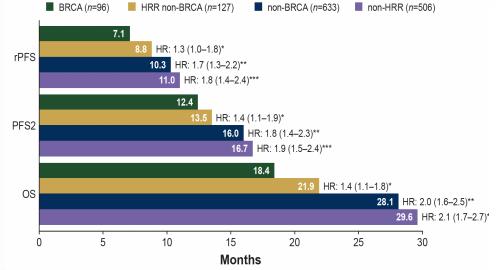
The HRR subgroup is heterogeneous

Different FUNCTIONS



Pellegrino et al, Translational Oncology, 2020

PROGNOSTIC implications



Olmos et al, Ann Oncol, 2024

Unadjusted median survival outcomes presented; HRs adjusted for differences in baseline characteristics between subgroups
*HR comparing BRCA vs HRR non-BRCA; **HR comparing BRCA vs non-BRCA; ***HR comparing BRCA vs non-HRR

SENSITIVITY to PARPI

Subgroup	Olaparib n/N	Control n/N	Overall population	HR (95% CI)
Alteration in any single HRR gene	148/239	81/120	•	0.79 (0.60-1.04)
BRCA1 (n=13)	5/8	5/5		0.42 (0.12-1.53)
BRCA2 (n=128)	39/81	32/47	⊢	0.59 (0.37-0.95)
ATM (n=86)	39/62	15/24	-	0.93 (0.53-1.75)
BARD1 (n=1)	0/0	1/1	NC	NC
BRIP1 (n=3)	1/2	1/1	NC	NC
CDK12 (n=89)	47/61	18/28	-	0.97 (0.57–1.71)
CHEK1 (n=2)	1/1	0/1	NC	NC
CHEK2 (n=12)	4/7	3/5		0.87 (0.19-4.44)
PALB2 (n=4)	2/3	1/1	NC	NC
PPP2R2A (n=10)	5/6	2/4		5.11 (1.10–35.73)
RAD51B (n=5)	2/4	1/1	NC	NC
RAD51D (n=1)	1/1	0/0	NC	NC
RAD54L (n=5)	2/3	2/2	NC	NC
			0.06 0.25 1 4 16	64 →
			Olaparib better Control bette	r

Hussain et al, NEJM, 2020





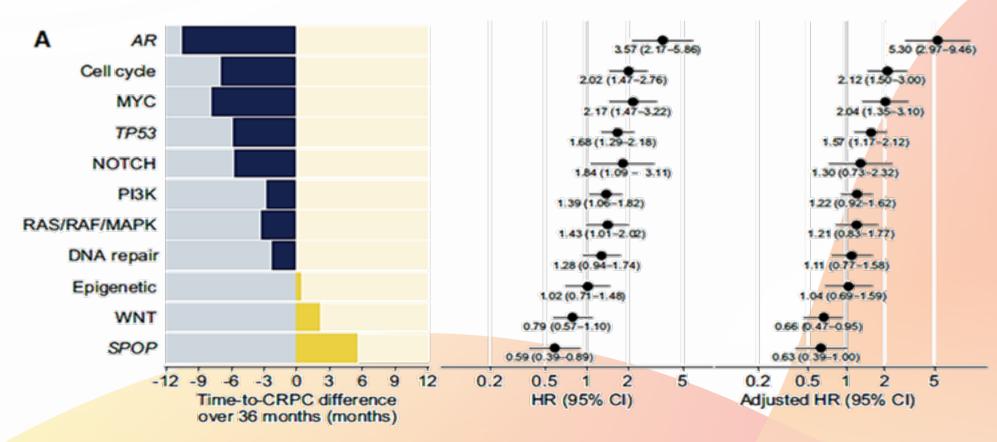


High SUV on PSMA PTEN loss, PIK3A/ Triple negative PET **AKT** mutation (PTEN loss, Rb loss, and TP53 loss) ADT + ARPI + PSMA-ADT + ARPI + AKT inhibitor targeted therapy (PSMA ADT + ARPI + docetaxel small molecule or antibody carrying beta-radioligand, ADT + cabazitaxel+ BiTEs, CAR T-cell) carboplatin Presence of HRR MSI high or TMB mutation high ADT + ARPI + PARPi ADT + ARPI + PD-1 axis inhibitors **mHSPC** Rb intact and no Presence of liver metastases SPOP mutation ADT + ARPI + CDK4/6 inhibitors ADT + ARPI **Optimal PSA** response (≤0.2 ng/mL) Deintensification





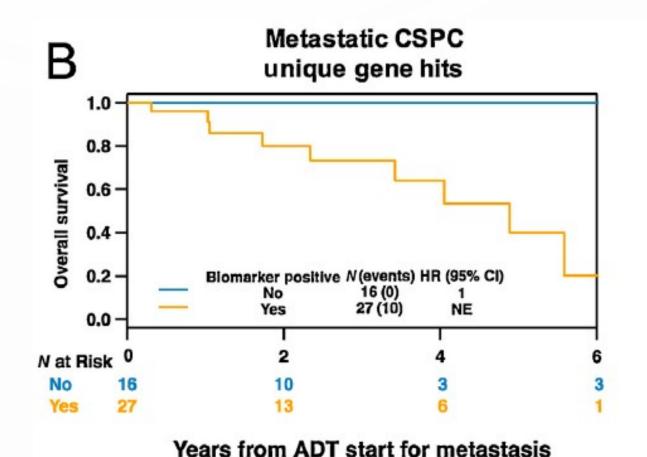
Oncogenic genomic alterarions, clinical phenotypes and outcomes in mHSPC

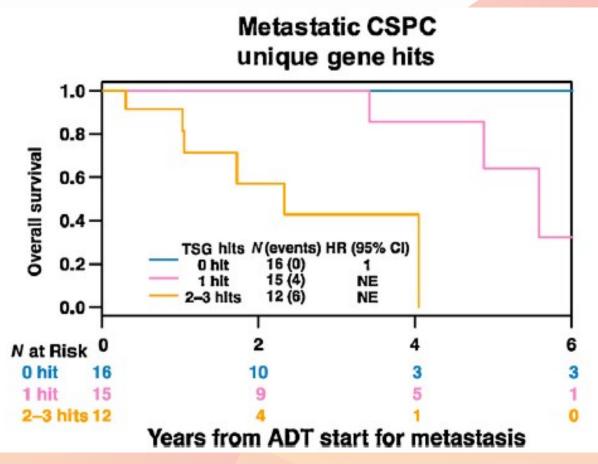






Men with prostate tumours with compound tumour suppressor gene (TP53, PTEN and RB1) mutations have poorer outcomes

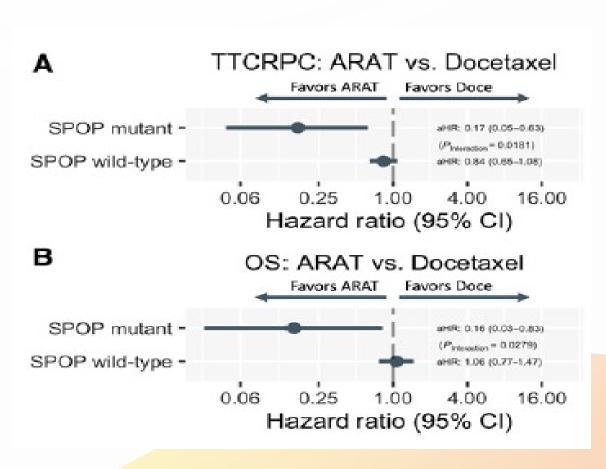


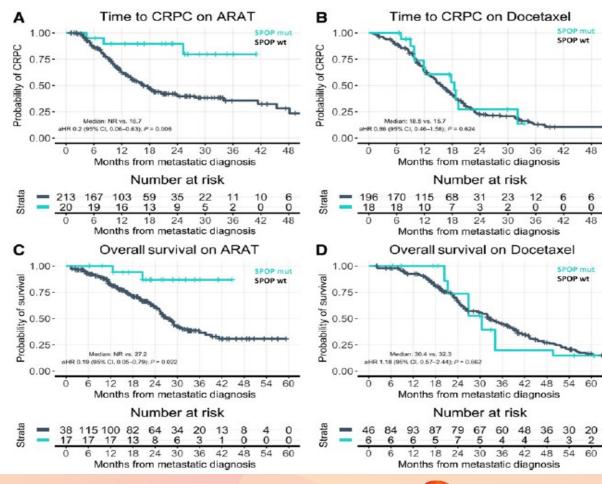


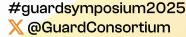




The association of SPOP mutation with outomes in men with de novo mHSPC









Transcriptome classification of PTEN inactivation to predict survival benefit from docetaxel at start of androgen deprivation therapy (ADT) for metastatic prostate cancer (PC): an ancillary study of the STAMPEDE trials

Emily Grist*, Peter Dutey-Magni*, Marina A. Parry, Larissa Mendes, Ashwin Sachdeva, James A. Proudfoot, Anis A. Hamid, Mazlina Ismail, Lia DePaula, Oliveira Oluwademilade Dairo, Sharanpreet Lall, Claire L. Amos, Mahesh K.B. Parmar, Elai Davicioni, Tamara L. Lotan, Christopher J. Sweeney, Louise C. Brown, Noel W. Clarke, Nicholas D. James, Gerhardt Attard

Presented by: Dr. Emily Grist

ClinicalTrials.gov number, NCT00268476 & Current Controlled Trials number, ISRCTN78818544 Trial conducted by Medical Research Council Trials Unit at University College London, U.K.

105 UK trial sites participated in this study

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MERIT AWARD







STAMPEDE docetaxel and abiraterone phase 3 trials

Metastatic prostate cancer

≥ 1 metastases on bone / CT scan

High-risk localised (adjuvant)
Lymph node positive OR
≥ 2 high risk features:
T3/T4, PSA ≥40ng/ml, Gleason sum 8-10

3909 directly-randomised patients

- > ADT versus ADT+ docetaxel+/-zoledronic acid
- > ADT versus ADT+ abiraterone

Aim: To link tumour multi-gene expression signatures to 14-year prospective follow-up for overall survival to identify prognostic and predictive biomarkers

STAMPEDE, Systemic Therapy in Advancing or Metastatic Prostate cancer: Evaluation of Drug Efficacy (MRC-PR08, NCT00268476) www.stampedetrial.org

95% synchronous M1

STRATOSPHERE (STratification for RAtional Treatment-Oncomarker Pairings of STAMPEDE patients starting long-term Hormone treatment) protocol overseen by the STAMPEDE trial management groups and biological research group



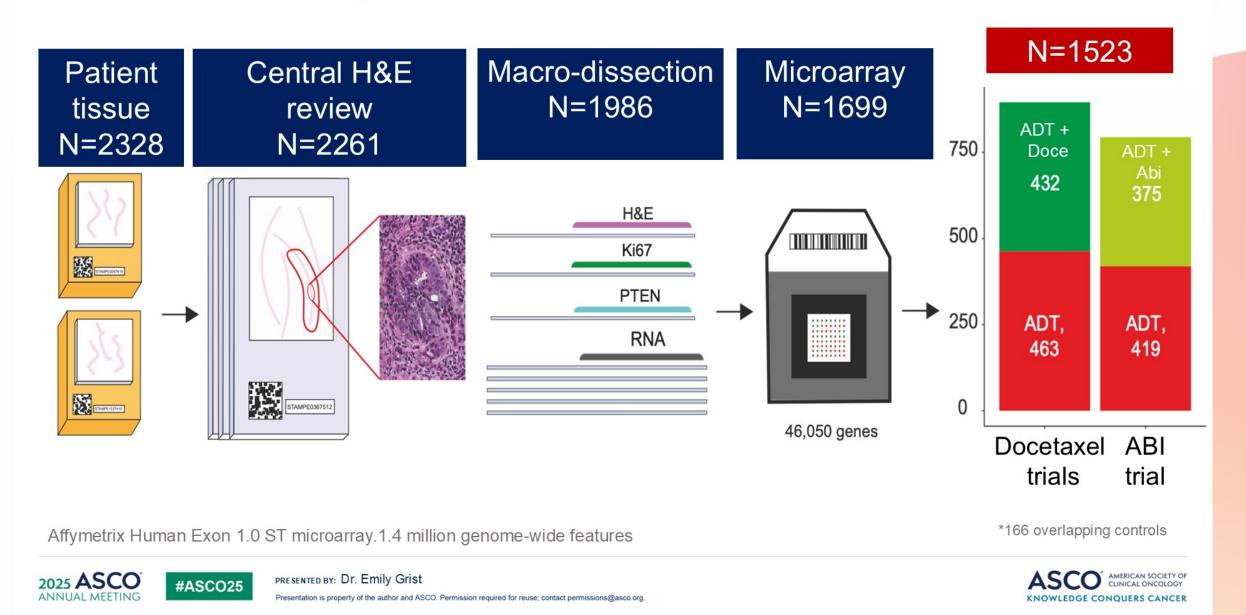


PRESENTED BY: Dr. Emily Grist

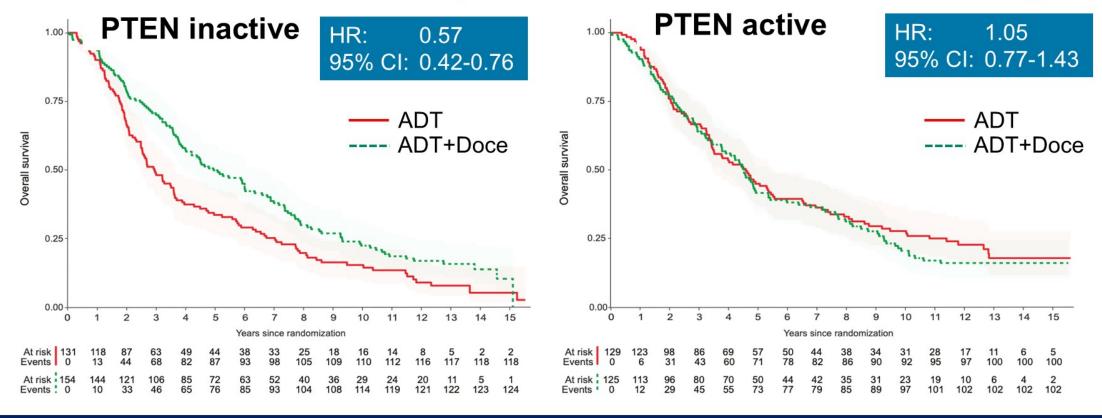
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Linking of clinical and multi-omic data



PTEN inactivation predicts docetaxel sensitivity



Tumour PTEN inactivity identifies metastatic patients most likely to benefit from docetaxel Biomarker-treatment interaction effect p value= 0.002*

Treatment effect uniform in abiraterone comparison trial (adjusted HR): PTEN inactive HR 0.52, 95% CI 0.36-0.73; PTEN active HR 0.55, 95% CI 0.39-0.77; p=0.784 Direction of treatment effect is the same in CHAARTED biomarker cohort (adjusted HR): PTEN inactive HR 0.52, 95% CI 0.31-0.87; PTEN active cancers HR 0.62, 95% CI 0.30-1.30

Kaplan-Meier estimates with 95% CI in lighter shade. HR and interaction test from multivariable model adjusted for Gleason score, disease burden, age, pre-ADT PSA, WHO PS, nodal stage, tumour stage, NSAID/aspirin use, and metastatic volume PTEN score dichotomised around 0.3 based on bimodal distribution



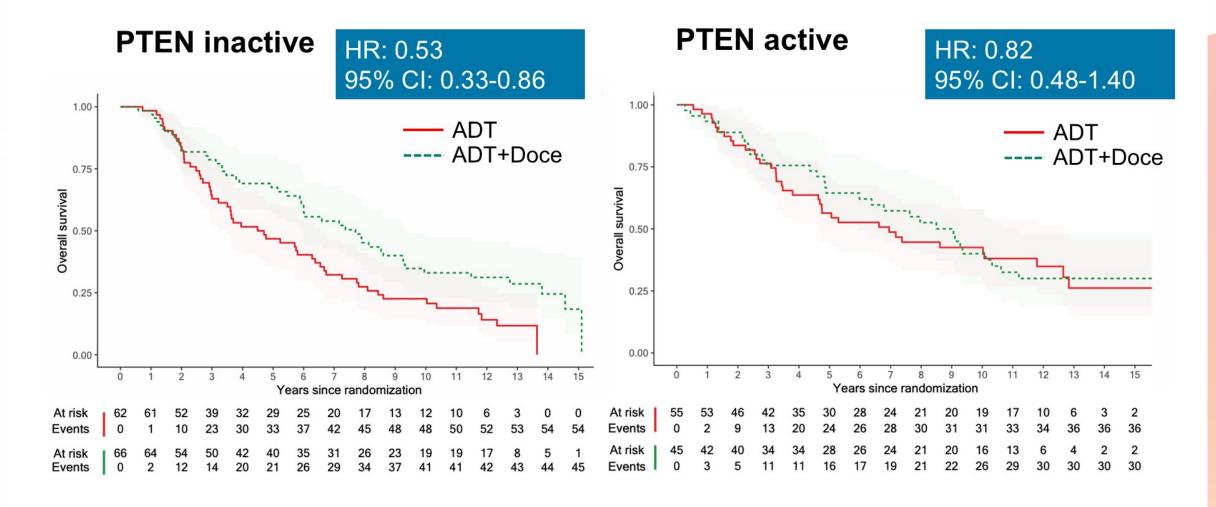


PRESENTED BY: Dr. Emily Grist

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Direction of treatment effect consistent in low volume





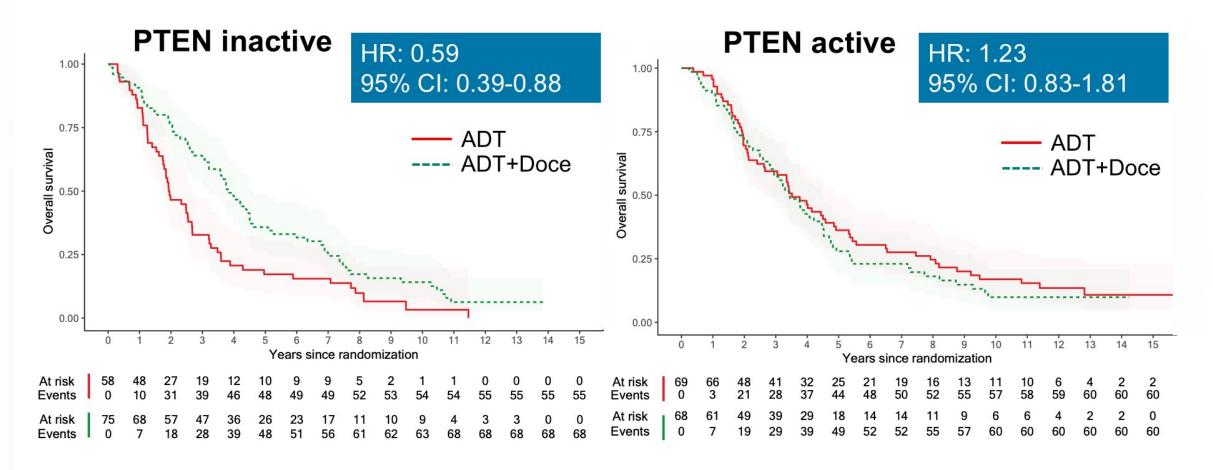








Direction of treatment effect consistent in high volume













What science can do - R&D - Our therapy areas - Our company -Sustainability -Careers - Investors -Media -

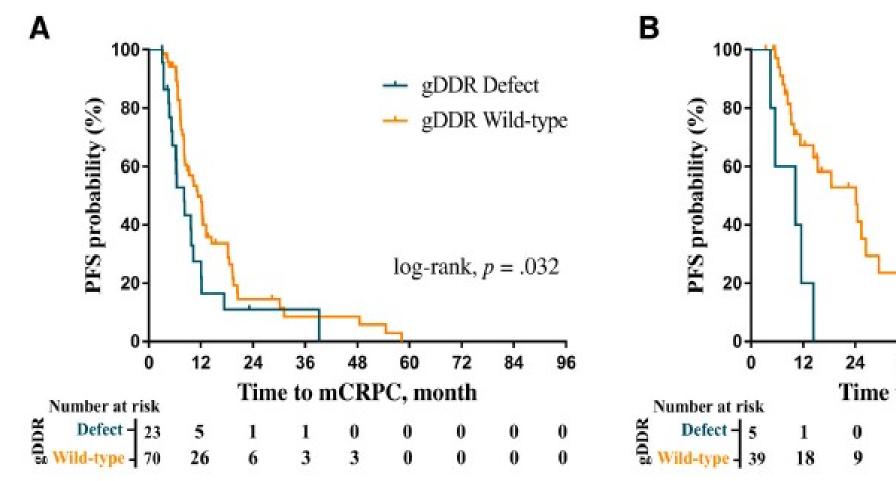
Trugap combination in PTEN-deficient metastatic hormonesensitive prostate cancer demonstrated statistically significant and clinically meaningful improvement in radiographic progression-free survival in CAPItello-281 Phase III trial

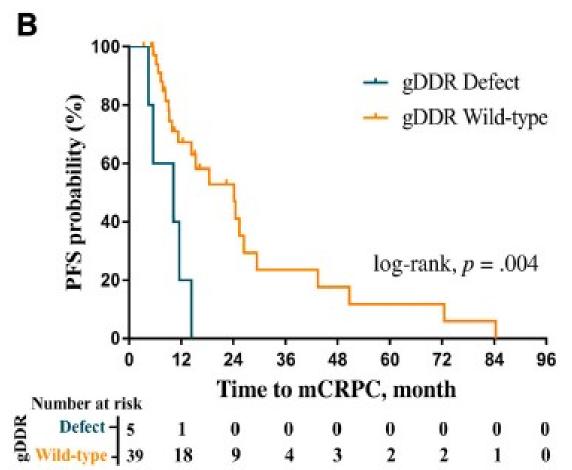
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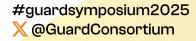
25 November 2024



Prognostic value of Germline DNA repair gene mutations in de novo metastatic and castration-sensitive prostate cancer









Study design and population

Key Inclusion Criteria.

- Male ≥18 years.
- Histologically confirmed adenocarcinoma of the prostate without predominance of small-cell or neuroendocrine features (ASCO/CAP guidelines).
- High-volume metastatic disease documented on bone scan or CT/MRI scan.
- Life expectancy ≥ 12 months.

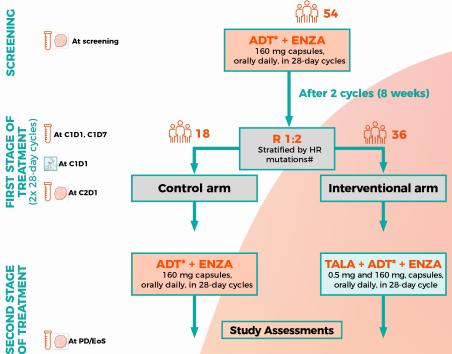
- Prior (neo)adjuvant ADT-based regimen is allowed if PD occurred while on noncastrate testosterone levels > 12 months after discontinuation.
- No prior treatment with enzalutamide, apalu-tamide, darolutamide or abiraterone acetate.
- PSA ≥ 4 ng/mL at diagnosis or before starting ADT therapy.
- No prior systemic therapy for metastatic prostate cancer.

PRIMARY ENDPOINT

• PSA-complete response (PSA-CR) (PSA<0.2 ng/mL) after 12 months of therapy in pts with mHNPC in the androgen deprivation therapy (ADT) + enzalutamide (ENZA) + talazoparib (TALA) arm. H0: 20%: H1 ≥40%.

SECONDARY ENPOINTS

- PSA-CR rate at any time point and at month 7 and 12.
- PSA progression-free survival (PSA-PFS)
- Radiologic PFS (rPFS) as per RECIST v.1.1/PCWG3
- Overall survival (OS)
- Safety and tolerability (CTCAE v.5.0).



- Tumor imaging was performed at screening, every 8 weeks for the first 6 months and every 12 weeks thereafter.
- Serum prostate-specific antigen (PSA) was assessed at screening, C1D1, and every 4 weeks during first 13 cycles, and every 8 weeks thereafter
- Whole-body diffusion-weighted magnetic resonance imaging (MRI) was performed in a subset of pts at baseline and during treatment to explore biomarkers of response and resistance in bone metastases.

Follow-up until PD, unacceptable toxicity, death. or discontinuation

* Pts to continue treatment with ADT throughout the study (except for surgical orchiectomy). #Randomization will be stratified based on HR gene alterations detected in the baseline biopsy (presence versus absence/unknown).



Primary endpoint

C13D1 PSA-CR in ENZA+TALA arm was 73% (95% CI, 55.9%-86.2%, p<0.001),

C13D1 PSA-CR in ENZA arm was 64.7%

Key secondary endpoints

Figure 2. Radiologic PFS according to RECIST v.1.1.

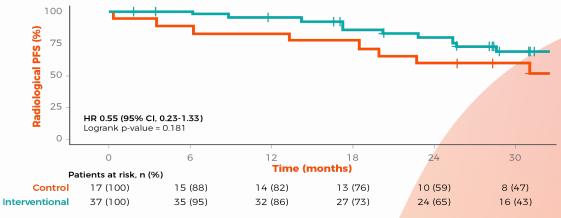
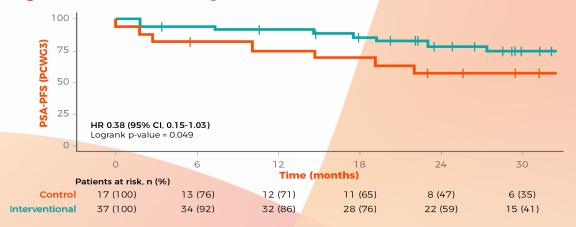


Figure 3. PSA-PFS according to PCWG3 criteria.







Phase 3 AMPLITUDE trial: Niraparib and abiraterone acetate plus prednisone for metastatic castrationsensitive prostate cancer patients with alterations in homologous recombination repair genes

Gerhardt Attard¹, Neeraj Agarwal², Julie N Graff^{3,4}, Shahneen Sandhu⁵, Eleni Efstathiou⁶, Mustafa Özgüroğlu⁷, Andrea J Pereira de Santana Gomes⁸, Karina Vianna⁹, Hong Luo¹⁰, Heather H Cheng^{11,12}, Won Kim¹³, Carly R Varela¹⁴, Daneen Schaeffer¹⁴, Shiva Dibaj¹⁵, Susan Li¹⁴, Fei Shen¹⁴, Suneel D Mundle¹⁶, David Olmos¹⁷, Kim N Chi¹⁸ Dana E Rathkopf¹⁹, on behalf of the AMPLITUDE investigators

¹Cancer Institute, University College London, London, UK, ²Huntsman Cancer Institute, University of Utah, Salt Lake City, UT, USA; ³Oregon Health & Science University and Knight Cancer Institute, Portland, OR, USA; ⁴Veterans Affairs Portland Health Care System, Portland, OR, USA: 5Peter MacCallum Cancer Centre, Melbourne, Australia: 6Houston Methodist Cancer Center, Houston, TX, USA: 7Istanbul University, Cerrahnasa, Cerrahnasa, Faculty of Medicine, Istanbul Türkiye, BLiga Norte Riograndense Contra o Cancer, Natal, Brazil, Centro Integrado de Oncologia de Curitiba, Curitiba, Brazil; Chongging University Cancer Hospital, Chongging, China; University of Washington, Seattle, WA, USA;

AMPLITUDE: Randomized, Double-Blind, Placebo-**Controlled Trial in HRRm mCSPC**

First and final rPFS analysis and first interim analysis of time to symptomatic progression and overall survival. Median follow-up: 30.8 months

Key inclusion criteria: • mCSPCª

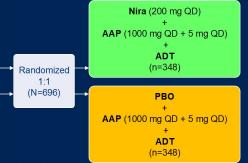
- Alteration in ≥1 HRR eligible gene BRCA1, BRCA2, BRIP1, CDK12, CHEK2, FANCA, PALB2, RAD51B, RAD541 b
- ECOG PS 0-2

Kev exclusion criteria:

- Any prior
- PARPi
- · ARPI other than AAP

Prior allowed treatments in mCSPC:

- · ADT ≤6 months
- Docetaxel ≤6 cycles^c
- AAP ≤45 days
- Palliative RT



Primary end point · rPFS by investigator review

Key secondary end points

- Time to symptomatic progression
- Safety

Clinical data cutoff: January 7, 2025

ASCO AMERICAN SOCIETY CLINICAL ONCOLOG

Stratification factors:

- BRCA2 vs CDK12 vs all other alterations
- Prior docetaxel (yes vs no)

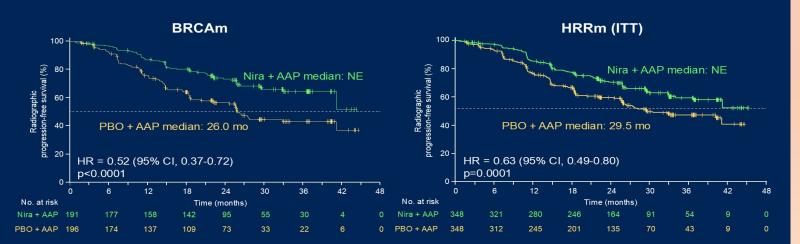
Patients with lymph node—only disease are not eligible. HRR gene panel was fixed prior to trial initiation based on MAGNITUDE trial and external data from the published literature. I ast dose 3 months prior to randomization

2025 **ASCO**

#ASCO25

PRESENTED BY: Prof. Gerhardt Attard, MD, FRCP, Phil

Primary End Point: Radiographic Progression-Free Survival



AMPLITUDE met the primary end point: Nira + AAP significantly reduced the risk of radiographic progression or death by 48% in BRCAm group and by 37% in HRRm population

erPFS by investigator review; rPFS improvement by blinded independent central review was as large: HR = 0.51 (95% CI, 0.37-0.72) for BRCAm group and 0.61 (95% CI, 0.47-0.79) for HRRm group



#ASCO25

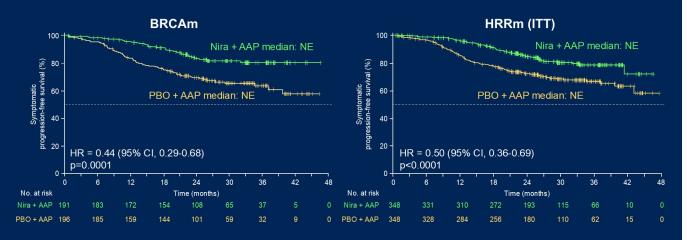
PRESENTED BY: Prof. Gerhardt Attard, MD, FRCP, PhD





#guardsymposium2025 X @GuardConsortium

Secondary End Point: Time to Symptomatic Progression



Nira + AAP significantly reduced the risk of symptomatic progression by 56% in BRCAm group and by 50% in HRRm population

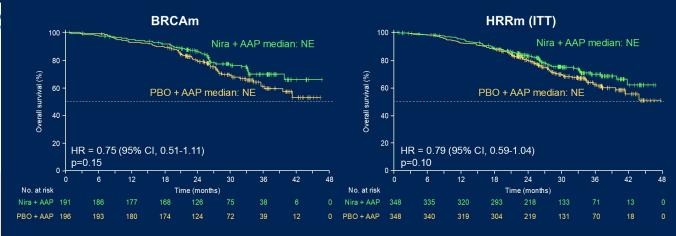
2025 ASCO



PRESENTED BY: Prof. Gernardt Attard, MD, PRCP, PhD

KNOWL

Secondary End Point: Overall Survival (First Interim Analysis)

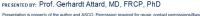


This first interim analysis (≈50% of total needed events) estimates show Nira + AAP reduced risk of death by 25% in BRCAm group and by 21% in HRRm population

The first interim analysis for OS was conducted when 193 patients had died (of a target of 389, an information fraction of 50%), 85 of 348 (24%) in the Nira + AAP arm and 108 of 348 (31%) in the PBO + AAP arm









There are several mHSPC Trials implementing molecular biomarkers that either recruiting already or being planned

- BRCA2/DRD: AMPLITUDE (NCT037486641), TALAPRO-3 (NCT04821622), and STAMPEDE (NCT00268476)
- PTEN loss: CAPItello-281 (NCT04493853)
- PSMA positive: PSMAddition (NCT04720157)
- Cell cycle: CYCLONE 3 testing abiraterone + prednisone +/- LY2835219 (NCT05288166)



Can we improve the results with a better selection?



How to perform all these studies?

Primary Tumor

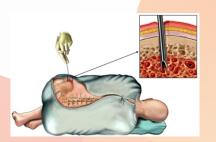
Liquid Biopsy

- CTCs
- cfDNA
- Exosomes

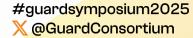
CT Guided Bone Marrow Biopsy





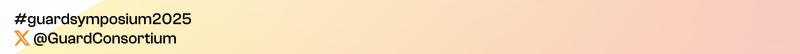






Different diagnostics strategies can be considered to assess for HRR alterations

	Advantages	Disadvantages
Tumour tissue testing	Gold standard (High clinical sensitivity) Fresh or archival tumour samples can be used (but older samples can have lower success rates) Can detect both germline and somatic mutations	High failure rate, especially for older samples Tissues for sampling may be in locations that are not safe or amenable to biopsy Single-site biopsies do not capture intra-individual heterogeneity (across metastases in an individual or changes over time or with disease progression)
Plasma ctDNA testing	Non-invasive, safer, serial analysis Can detect both germline and somatic mutations Useful where no tissue is available or when re-biopsy is undesirable Capture relative contribution of metastases in different anatomical sites	Low levels of tumour fraction can lead to false negative results CHIP may lead to false positives Blood collection must be timed in order to evaluate progressive disease Relative sensitivity at a prospective cohort level is unknown (clinical validation in PC still limited)
Germline testing (Blood or saliva)	Assess familial risk Easy to obtain samples from blood, saliva or buccal swabs	Misses alterations of somatic origin (≃ 50% of HR alterations)





BRCA 1/2 and other DDR alterations are likely early events

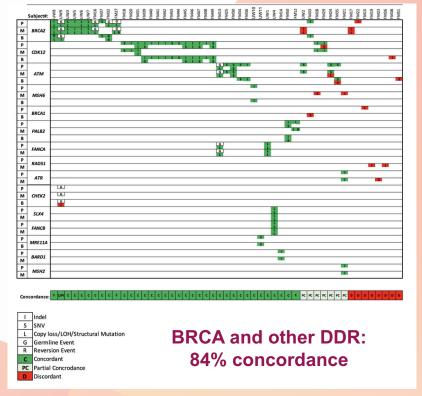
High concordance in DDR mutational status between primary prostate and metastatic tissue/ctDNA

	HHR gene alteration prevalence %
All patients	27.9
All primary tumors	27
Archived primary	27
Newly collected primary	26.5
All metastatic tumors	32.3
Archived metastatic	33.9
Newly collected metastatic	29.7

BRCA1/2: 99% Overall concordance

Table 1. Patients with BRCA mutation in primary tumor				
Pt #	BRCAm primary	Interval	BRCAm cfDNA 1	
1	Detected	3.13 months	Not Detected	
2	Detected	0.93 months	Detected	
3	Detected	0.2 months	Detected	
4	Detected	97.93 months	Not Detected	
5	Detected	40.77 months	Detected	

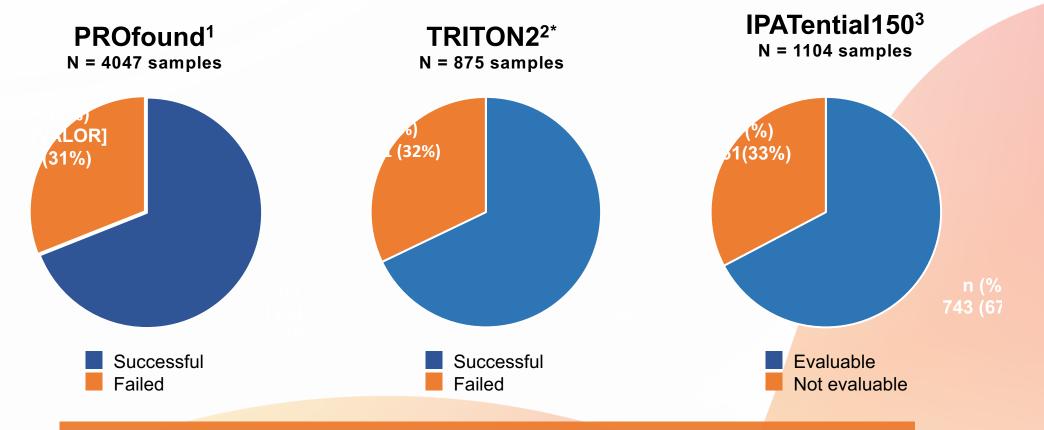
Table 2. Patients with no BRCA mutation in primary tumor					
Matched CGP	Median (range)	New BRCA1	New BRCA2		
Primary test to 1st cfDNA (n=191)	23.6 months (0.1 - 232)	None	None		
Primary test to 2 nd cfDNA (n=27)	58.9 months (7.23 - 211)	None	None		
Primary test to 3 rd cfDNA (n=2)	65.5 months (21.9 - 109)	None	None		







TISSUE is the ISSUE



Sample selection and optimisation of tissue collection is critical, since 30–50% of prostate cancer samples fail NGS^{1–3}



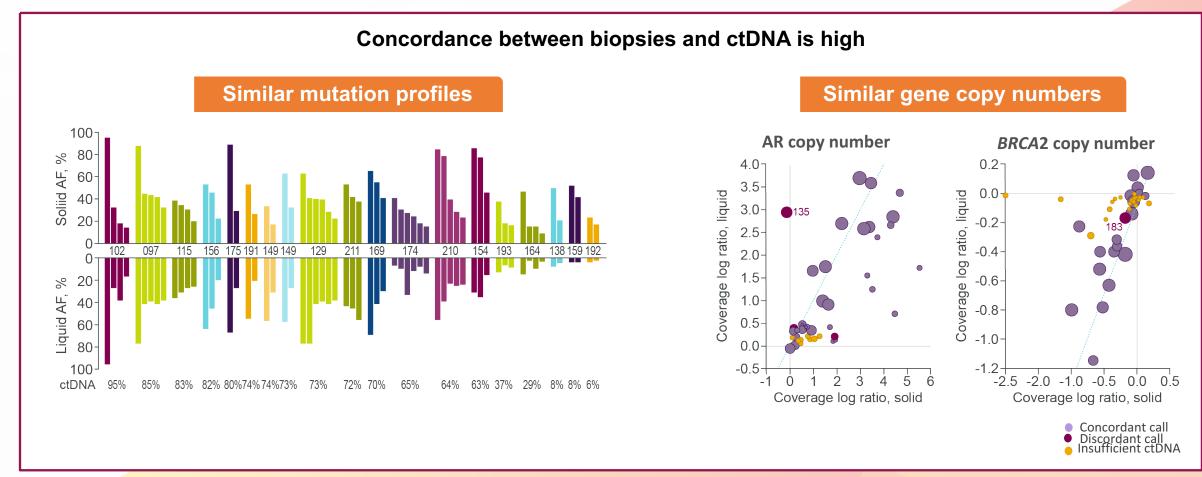


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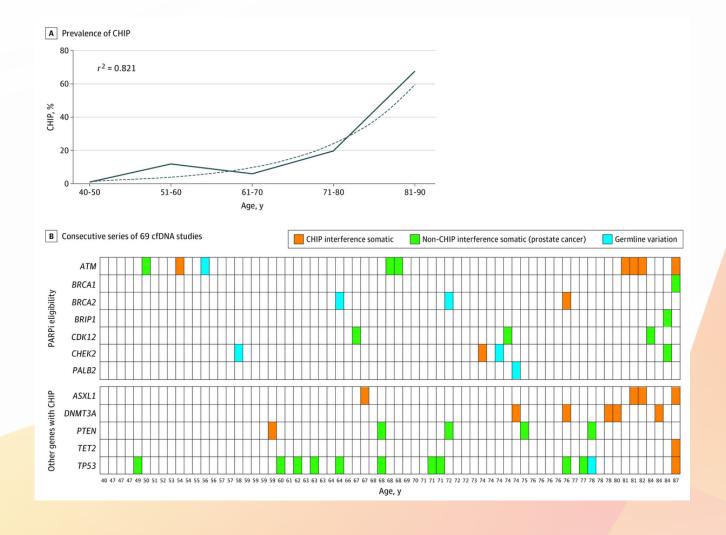


Assessment of genomic alterations of tumor in ctDNA





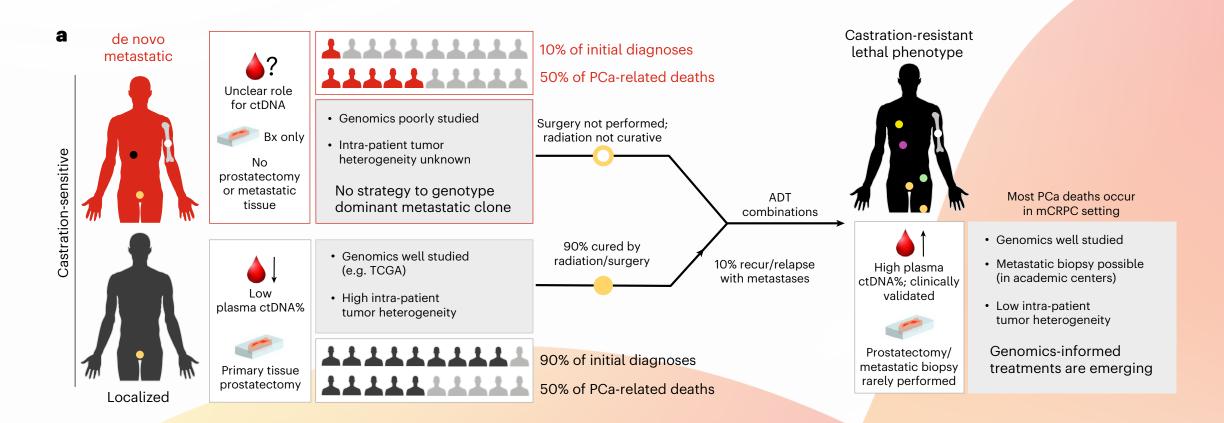
Clonal hematopoiesis of indeterminat potencial may lead to false positives







The biological and clinical challenge of the novo mCSPC







Why should we think about the de-escalation?

Living Longer



- But with more side-effects
- No significant improvement in HRQoL
- A substantial increase in cost

A tale of Efficacy vs. value for the Patients and the health care system





Why should we think about de-escalation?



For patients

 To live better and longer, avoid burdensome further treatment, and improve quality of life.

For payers

- Is it acceptable cost-wise? Can we afford it?
- Incremental cost-effectiveness ratio (ICER)





Conclusiones

- A mi juicio todavía es pronto para afirmar que hemos entrado en la época de la implementación de la medicina de precisión en la enfermedad hormonosensible metastásica.
- Si bien es cierto que los resultados presentados este año nos permiten decidir / intuir el mejor de los tratamientos para nuestros enfermos.
- •La intensificación terapéutica ha permitido mejorar los resultados globales de nuestros enfermos, sin embargo, ahora tenemos un problema que es seleccionar aquellos que nos podemos permitir desescalarlos.



¡Gracias!

