Predictors of Outcome in Prostate Cancer

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Epidemiology of prostate cancer (Pca)

- **Most commonly** diagnosed cancer in men in both the United States and Europe.
- Incidence and mortality due to PCa are associated:
 - with old age
 - family history
 - race (e.g. ~60% more in African-American).
- Prostate cancer was ranked fourth in Europe among the cancers with the best prognosis. 5-year relative survival was 83%.
- Patients with metastatic prostate cancer have a poor prognosis and median survival is less than 2 years.

WHO estimated number of new cases in 2018 in Europe (all cancer, males, all ages)



Total : 11 703 936

Merseburger et al 2013 Oncologist



Clinical risk stratification: NCCN & CAPRA nomogram

Risk stratification criteria for men with localised prostate cancer						
	PSA (ng/ml)		Gleason score		Clinical stage	
Low risk	< 10	and	≤ 6	and	T1-T2a	
Intermediate risk	10-20	or	7	or	T2b-T2c	
High risk	> 20	or	8-10	or	T3-T4	

National Comprehensive Cancer Network (NCCN)



- 1. CAPRA score system added two risk factors "age at diagnosis" and "percentage of biopsy cores involved with cancer" to NCCN
- 2. Both NCCN and CAPRA risk stratification strategies are associated with recurrence-free survival of prostate cancer patients.



Survival curves for 5-year recurrence-free survival among patients with each UCSF-CAPRA score

Clinical risk stratification: AUA & EAU nomogram

AUA nomogram

Very Low Risk	PSA <10 ng/ml AND Grade Group 1 AND clinical stage T1-T2a AND <34% of biopsy cores positive AND no core with >50% involved, AND PSA density <0.15 ng/ml/cc
Low Risk	PSA <10 ng/ml AND Grade Group 1 AND clinical stage T1-T2a
Intermediate Risk	PSA 10-<20 ng/ml OR Grade Group 2-3 OR clinical stage T2b-c
	 Favorable: Grade Group 1 (with PSA 10-<20) OR Grade Group 2 (with PSA<10) Unfavorable: Grade Group 2 (with either PSA 10-<20 or clinical stage T2b-c) OR Grade Group 3 (with PSA < 20)
High Risk	PSA \geq 20 ng/ml OR Grade Group 4-5 OR clinical stage \geq T3*

Risk Groups	Gleason	5 year BCR risk free survival
1	3+3	96%
2	3+4	88%
3	4+3	63%
4	4+4	48%
5	4+5, 5+4, 5+5	26%

EAU nomogram

	Low-risk	Intermediate-risk	High-risk	
Definition	PSA < 10 ng / mL	PSA 10-20 ng /mL	PSA > 20 ng / mL	any PSA
	and GS < 7	or GS 7	or GS > 7	any GS cT3-4 or cN+
	and cT1-2a	or cT2b	or cT2c	
		Locally advanced		

PSA = prostate-specific antigen.

Risk stratification incorporating molecular tests



- Gleason score is a single independent predictor of aggressive disease
- Can molecular classifier be superior to clinical-pathologic features in predicting aggressive disease?

Molecular tests available

Table 2. Currently available tissue-based tests for prostate cancer							
Test	Platform	Molecular basis	Marketed use	CMS approved use	Useful clinical scenario		
Ki-67 Prolaris	IHC RT-PCR	Proliferation Proliferation	NA Pre and post local Tx decision making	No Yes, decision making for surveillance	Watchful waiting Watchful waiting		
PTEN	IHC/FISH	PTEN	NA	No	Active surveillance		
ProMark	Quantitative proteomics	Proteins related to PCa adverse pathology and outcomes	Pre-Tx decision making	No	Active surveillance		
OncotypeDX Prostate	RT-PCR	Transcripts related to PCa adverse pathology and outcomes	Pre-Tx decision making	No	Active surveillance		
Decipher	RNA MicroArray	Transcripts predictive of PCa metastasis	Post-Tx decision making	Yes, decision making after prostatectomy	Adjuvant radiation		
Abbreviations: FISH, fluorescence in situ hybridization; IHC, immunohistochemistry; NA, not available.							

Gene sets of genomic classifiers and its use

OncotypeDx (17 genes)						
Androgen Signaling AZGP1 FAM13C KLK2 SRD5A2	Cellular Organization FLNC GSN GSTM2 TPM2					
Stromal Response BGN COL1A1 SFRP4	Reference ARF1 GPS1 ATP5E PGK1					
Proliferation TPX2	CLTC					

Prolaris (46 genes)						
Cell CycleFOXM1DLGAP5PTTCDC20BIRC5CDCDKN3KIF20AMNCDC2PLK1PRGKIF11TOP2ADTFKIAA0101TK1CEFNUSAP1PBKRAICENPFASF1BCEFASPMC18orf24CDGBUB1BRAD54LORRRM2CC	G1 A3 M10RPL38 UBA52 PSMA1 PSMC1 RPL8 RPL4 S1 RPL37 RPL3A S1 PM A8 6LReference SLC25A3 MRFAP1 A8 SLC25A3					

Decipher (22 genes)							
Cell Structure, Adhesion & Motility THBS2 ANO7 PCDH7 MYBPC1 EEPK1	Cell Cycle Mitosis NUSAP ZWILCH UBE2C CAMK2N RABGAF	2 & 5 1 H 2 N1 21	Other/Unknown PCAT-32 GLYATL1P4/PCAT-80 TNFRS19 Intronic Non-coding transcript Coding Antisense				
Proliferation & Dif LASP1 NFI QGAP3 S1F	ferentiation B PR4	Im	mune Response TSBP PBX1				

Cuzic J.et al Lancet Onc. 2011 Erho N. et al, PLoS One 2013 Klien et al Eur Urology 2012

Risk stratification of Pca using Decipher



Adapted from Karnes et al 2013 Crawford D.E. et al Oncology 2015

Molecular subtypes in localized and metastatic PCa



TCGA 2015 *Cell* Arora et al 2018 *Curr Oncol*

Molecular drivers enriched in CRPC

CRPC

AR	AR Amplification	
	AR mutations	
aepenaent	AR splice variants	
	Abnormal AR activation	
AR	DDR genes	
independent	NEPC	
	Others	

Arora et al 2018 Curr Oncol

Reported AR-targeted therapy resistance mechanisms:

Primary:

AR-mediated: ARv7; AR amp, AR^{F877L}

non-AR-mediated: GR, TP53, RB1, MYC, MET

Acquired:

Increased testosterone levels, ARv7, AR amp, AR^{F877L}

Molecular Prognostic Markers in PCa

Prognostic marker	type	Fre	quency	Prognosis Statistics	References
Basal & Luminal (CD49)		Primary	Luminal 54% Basal 46%	 10-year DMFS freedom as whole: Luminal (0.68); Basal (0.67), p=0.29 	Zhao et al., JAMA Oncol 2017 Zhang et al. Nat Commun 2016
		mCRPC	Basal enriched	✤ 61 mCRPC subjects were analyzed (SU2C/PCF)	Simth et al., PNAS 2015
	Draganastia	Primary	LumA 33% LumB 33% Basal 34%	 10-year DMFS freedom as whole: LumA (0.73); LumB (0.53); Basal (0.73) 10-year DMFS freedom comparing ADT: LumB: ADT (33%) vs no ADT (55%); non-Lum B: ADT (37) vs no ADT (21%) 	Zhao et al., JAMA Oncol 2017
Basal & luminal Progr (PAM50) Resis	Predictive mC Resistance	mCRPC	LumA 43% LumB 14% Basal 43%	 Median OS for LumA, LumB, and Basal pts was 20.6 months, 9.5 months, and 10.4 months, respectively (p=0.04) Drug Response Signatures analyses revealed with LumA and LumB pts more sensitive to docetaxel while basal pts are more sensitive to platinums and etoposide (p<0.00001). 	Kim et al., ASCO 2018
DTEN Mutations/Loss	Progpostic	Primary	17%	 56 out of 333 primary tumors carry the genetic alterations (TCGA) 	TCGA Research Network, Cell 2015
PIEN MUTATIONS/LOSS	Prognostic	mCRPC	40%	 61 out of 150 mCRPC tumors carry the genetic alterations (SU2C/PCF) 	Robinson et al., Cell 2015
PIK3CA mutations &	Due en estis	Primary	2%	✤ 7 out of 333 primary tumors carry the genetic alterations (TCGA)	TCGA Research Network, Cell 2015
mutation and TSC1&2 CNVs	Prognostic	mCRPC	5%	8 out of 150 mCRPC tumors carry the genetic alterations (SU2C/PCF)	Robinson et al., Cell 2015

PTEN and ERG status associated with PCa progression





Molecular Prognostic Markers in PCa

Prognostic marker	type	Frequ	ency	Prognosis Statistics	References
Neuro-endocrine (histopathology)	Resistance		1-4%	25 out of 635 (4%) tumors were NEPC by histopathology, 70 gene expression signature doesn't add much to IHC	Beltran et al Can Discovery 2011, Epstein J., AJP 2014
Neuroendocrine-		Primary	5%	Small cell-like histological features were observed in 5-20% primary PCa	Rubin et al., ASCO 2015
like Re (Tp53 and Rb loss)	Resistance	mCRPC	40%	TP53 and RB1-null tumors acquire resistance under ARi selection pressure, expression is 5% in primary, 40% in mCRPC, and 75% in NEPC.	Mu et al. Science 2017
AR & NE double negative (DNPC) Re (histopathology)	Resistance mCRPC (1998- no Enz Resistance mCRPC (2012- Enaz A used)	mCRPC (1998-2011, no Enza Abi)	5.4 %	3 out of 56 mCRPC subjects were negative for both AR and NE biomarkers, while 88.4% and 6.3% are AR and NE biomarkers positive.	Bluemn et al., Cancer Cell 2017
		mCRPC (2012-2016, Enaz Abi used)	23.3%	7 out of 30 mCRPC subjects were negative for both AR and NE biomarkers, while 63.3% and 13.3% are AR and NE biomarkers positive.	Bluemn et al., Cancer Cell 2017
		Primary	19%	 62 out of 333 primary tumors carry the genetic alterations (TCGA) 	TCGA Research Network, Cell 2015
(BRCA1, BRCA2, FANCA, ATM, PALB2, CHEK2, BRIP1, HDAC2	Predictive	mCRPC	23%	 34 out of 150 mCRPC subjects carry the genetic alterations (SU2C/PCF) 	Robinson et al., Cell 2015
			33%	✤ 16 out of 49 mCRPC subjects were positive for the biomarkers. 14/16 (88%) of those patients enrolled responded to Olaparib.	Mateo et al., NEJM 2015

Conclusion

- Genomic alterations/mutational burden is increased in metastasis compared
- Genomic selection adds prognostic value on top of the clinical features across clinical risk groups.
- Combining clinical and molecular risk stratification would facilitate the development of precision medicine for improved clinical outcomes.