CCP SCORE STRATIFIES RISK FOR PROSTATE CANCER PATIENTS AT BIOPSY: INITIAL COMMERCIAL RESULTS

E. David Crawford, Neal Shore, Peter T. Scardino, John W. Davis, Jonathan D. Tward, Lowndes Harrison, Kelsey Moyes, Lisa Fitzgerald, Steven Stone, Michael K. Brawer

University of Colorado Health Science Center, Aurora, CO; Carolina Urologic Research Center, Myrtle Beach, SC; Memorial Sloan-Kettering Cancer Center, New York, NY; The University of Texas MD Anderson Cancer Center, Houston, TX; University of Utah Huntsman Cancer Institute, Salt Lake City, UT; Gadsden Regional Cancer Center, Gadsden, AL; Myriad Genetic Laboratories, Inc., Salt Lake City, UT; Myriad Genetics, Inc., Salt Lake City, UT

BACKGROUND

- New prognostic markers for prostate cancer play an important role in addressing the controversies of over diagnosis and over/under treatment.
- The cell cycle progression score (CCP) (Prolaris®, Myriad Genetic Laboratories, Inc.) is a RNA—based marker which improved the prediction of prostate cancer aggressiveness in eight separate cohorts.
- Each one—unit increase in CCP score corresponds with approximately a doubling of the risk of the studied event (recurrence or death from prostate cancer).
- In this analysis, we characterized the results of CCP testing from our initial commercial testing.

METHODS

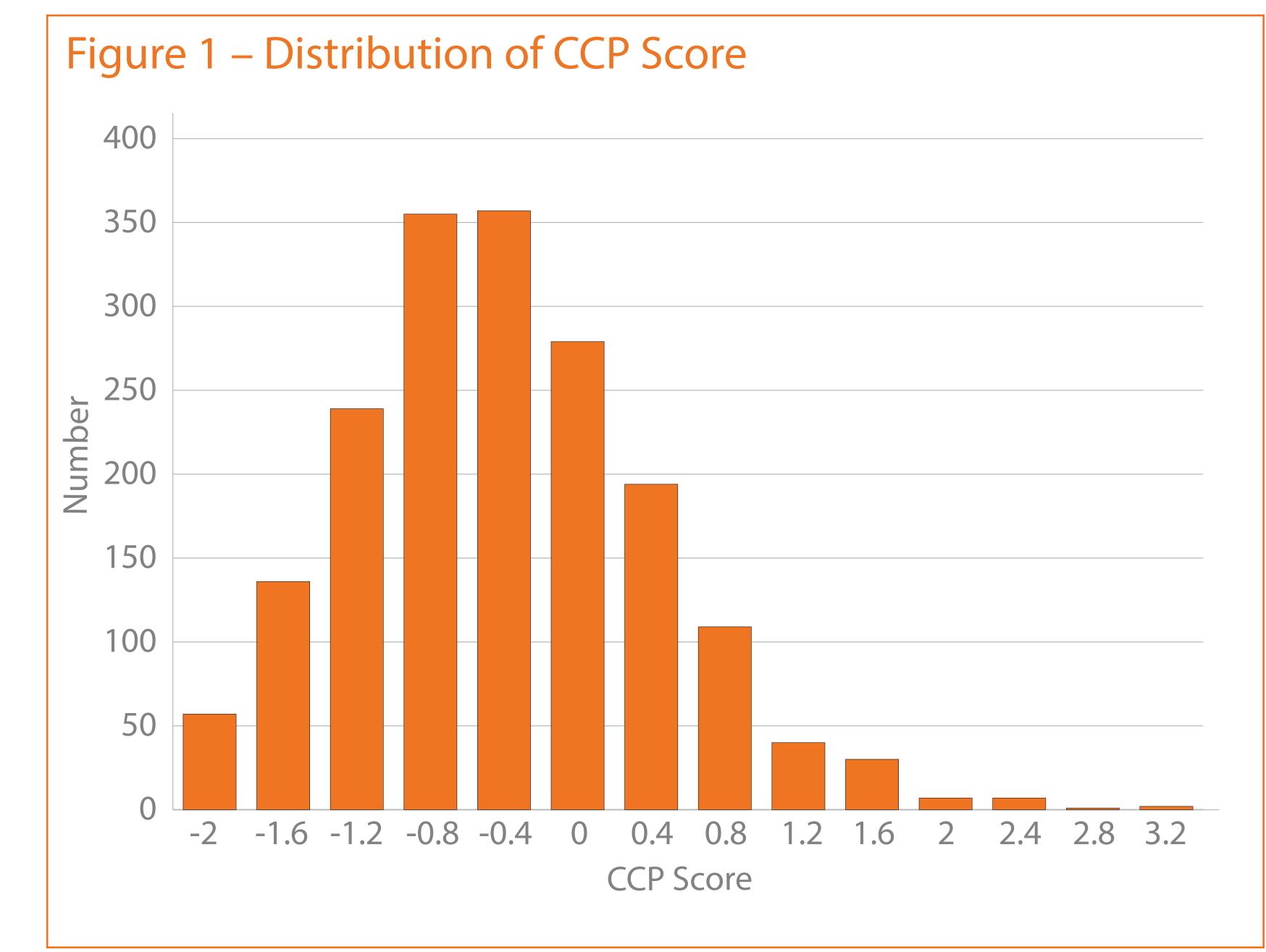
- The Myriad laboratory database was evaluated for patients:
- Biopsy analyzed with the CCP test
- Clinicopathologic data provided by ordering physician
- All commercially-ordered tests from August 2012 to September 2013
- Formalin fixed, prostate biopsy tissue from patients diagnosed with adenocarcinoma.
- The CCP score was calculated by measuring the RNA expression of 31 cell cycle progression genes normalized to 15 housekeeping genes.
- A relative classification of cancer aggressiveness based on the CCP scores of ≈1200 patients from multiple cohorts was developed to interpret how the patient's CCP score compared to that of patients within the same AUA risk category. The thresholds between each of the five intervals are one unit of CCP score apart, with the 'consistent' interval centered at the median CCP score.

RESULTS

- Test ordered by 393 physicians
- 1813/1853 (97.8%) samples yielded quality RNA
- Normal distribution for the CCP score (−2.9 to 3.1)
- Based on the CCP score, 28.96% of men had a less aggressive cancer compared to the clinicopathologic prediction
- 26.64% of patients had a more aggressive cancer

Table 1- Clinical/Pathologic Characteristics

CCI SCOIE		1013	
	mean -0.56 <u>+</u> 0.82		
	min-max	(-2.9 to 3.1)	
Age at Diagnosis	n	1813	
(yrs)	mean	68.3 <u>+</u> 8.16	
	min-max	(40 - 93)	
PSA (ng/mL)	0 - 4	312 (17.2%)	
	4.01 - 10.0	1184 (65.3%)	
	>10	317 (17.5%)	
Positive Cores (%)	n	1804	
	mean	32.15 ± 22.95	
	min-max	(Up to 100.0)	
Gleason Score	4	1 (0.1%)	
	5	3 (0.2%)	
	6	839 (46.3%)	
	3+4=7	631 (34.8%)	
	4+3=7	198 (10.9%)	
	8	89 (4.9%)	
	9 47 (2.6%)		
	10	4 (0.2%)	
Clinical Stage	T1a	34 (1.9%)	
	T1b	18 (1.0%)	
	T1c	1223 (67.5%)	
	T2a	229 (12.6%)	
	T2b	184 (10.1%)	
	T2c	113 (6.2%)	
	T3a	9 (0.5%)	
	T3b	3 (0.2%)	



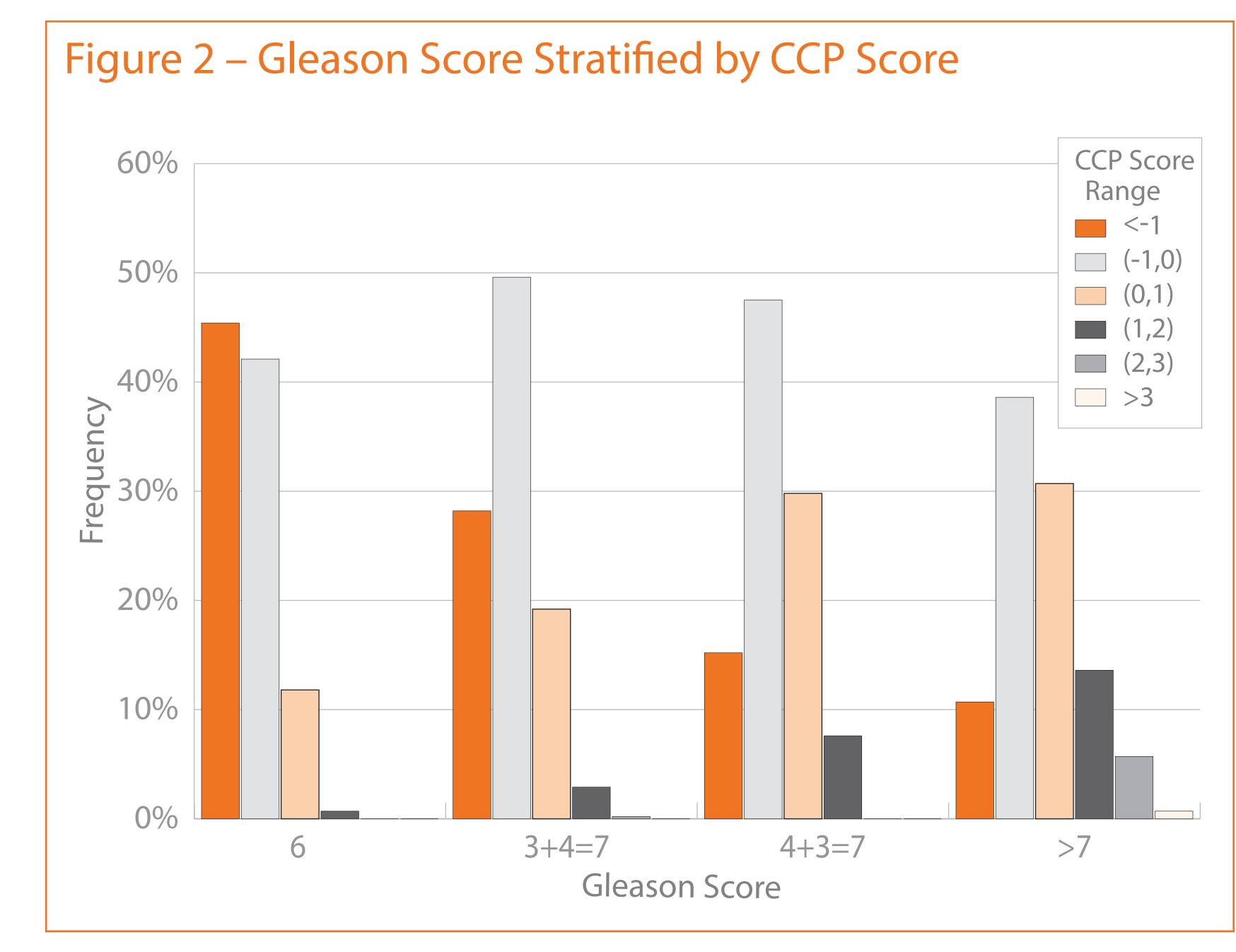


Table 2 – Correlation with CCP Score

Variable	Pearson Correlation Coefficients
Patient age at diagnosis	0.23
PSA	0.18
Gleason Score	0.35

Table 3 - Cancer Aggressiveness Based on CCP Scores

AUA Risk Classification	Considerably Less Aggressive	I ASS	Consistent	IVIORE	Considerably More Aggressive	Totals
Low	12 (1.73%)	182 (26.26%)	324 (46.75%)	158 (22.80%)	17 (2.45%)	693
Intermediate	19 (2.9%)	222 (26.71%)	374 (45.01%)	183 (22.02%)	33 (3.97%)	831
High	13 (4.5%)	77 (26.64%)	107 (37.02%)	69 (23.88%)	23 (7.96%)	289
Totals	44 (2.43%)	481 (26.53%)	805 (44.40%)	410 (22.61%)	73 (4.03%)	1813

CONCLUSIONS

- The CCP test is a novel assay that can improve risk stratification for men with prostate adenocarcinoma independent of the Gleason score and PSA level.
- Over 50% of men initially tested in the commercial assay had cancer that was more or less aggressive than suggested by clinicopathologic features alone.
- The CCP test allows for personalized risk stratification. It identifies:
 - Low-risk patients who are good candidates for active surveillance.
- High-risk patients likely to fail mono therapy who require more aggressive management.