

Validation of Canary Histological Patterns at Radical Prostatectomy with Decipher GRID Prognosis Signature Score

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Background

BMI-1 gene is a member of the polycomb group complex that functions as an epigenetic repressor by modulating chromatin structure regulating multiple genes involved in embryonic development and renewal of somatic stem cells. *BMI-1* expression has been reported across several cancer types including prostate carcinoma. Glinsky et al developed an 11-gene *BMI-1* associated stem cell-like expression pathway signature (PMID: 15931389) and demonstrated its ability to predict shorter interval to disease recurrence, distant metastasis, and mortality after treatment in 11 different tumor types. Recent work evaluating the clinical significance of morphological patterns in prostate carcinoma from the Canary Consortium has identified patterns associated with favorable, borderline and unfavorable outcomes (PMID: 38828674). In this study we sought to further validate the prognostic significance of Canary patterns with the Glinsky prognosis score available in Decipher GRID data.

Methods

Canary histological patterns were reviewed and recorded on 394 radical prostatectomy slides that underwent Decipher testing. Patterns were classified as unfavorable (Gleason pattern 5 (GP5), large cribriform (diameter >0.25 mm), intraductal carcinoma, complex intraluminal papillary architecture, anastomosing cords), borderline (glomerulations, small cribriform (diameter $\leq$ 0.25 mm), small nests, mucin, stromogenic grades 1-2), and favorable (absence of unfavorable and borderline features). The presence or absence of each of the Canary patterns was correlated with prognosis signature score from the Decipher GRID database using the student T-test. Statistical significance was defined by p-value <0.05.

Results

The mean prognosis score was 0.45 (SD 0.20, median 0.41, IQR 0.31, 0.56) across the entire cohort. All unfavorable Canary histological patterns were associated with higher prognosis scores. The p-values for each pattern were: <0.001 each for unfavorable, GP5, large cribriform, complex intraluminal papillary, solid and comedonecrosis; and 0.039 for anastomosing cords. Favorable histology and borderline glomerulations pattern were associated with lower prognosis scores (p=0.001 and 0.012 respectively) (Table 1).

Conclusions

The findings provide yet another validation of the prognostic significance of Canary histological patterns supporting higher prognosis signature score across all unfavorable patterns and lower scores for favorable and borderline glomerulation pattern.

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Table-1: Mean Prognosis Scores in Canary Patterns.

	Overall Mean (SD)	Pattern absent Mean (SD)	Pattern present Mean (SD)	p
Favorable	0.45 (0.20)	0.58 (0.27)	0.44 (0.19)	0.001
Borderline features	0.45 (0.20)	0.44 (0.24)	0.45 (0.19)	0.761
Stromogenic grades 1-2	0.45 (0.20)	0.45 (0.20)	0.44 (0.24)	0.761
Glomerulations	0.45 (0.20)	0.46 (0.21)	0.41 (0.15)	0.012
Mucinous	0.45 (0.20)	0.45 (0.20)	0.41 (0.16)	0.379
Small cribriform	0.45 (0.20)	0.41 (0.20)	0.46 (0.19)	0.029
Small nests	0.45 (0.20)	0.46 (0.19)	0.43 (0.20)	0.185
Unfavorable	0.45 (0.20)	0.33 (0.13)	0.49 (0.20)	<0.001
Anastomosing cords	0.45 (0.20)	0.44 (0.20)	0.48 (0.18)	0.039
Complex intraluminal papillary	0.45 (0.20)	0.43 (0.19)	0.54 (0.20)	<0.001
Large cribriform	0.45 (0.20)	0.36 (0.16)	0.51 (0.20)	<0.001
Gleason pattern 5	0.45 (0.20)	0.41 (0.17)	0.54 (0.22)	<0.001
Comedonecrosis	0.45 (0.20)	0.43 (0.19)	0.66 (0.21)	<0.001
Single cells/files	0.45 (0.20)	0.45 (0.19)	0.46 (0.23)	0.785
Solid	0.45 (0.20)	0.43 (0.19)	0.57 (0.23)	<0.001