

A novel digital pathology artificial intelligence (DPAI) score improves prognostic estimation in patients with localized prostate cancer

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Background: RNA-based genomic tests are well established to improve on standard clinical parameters in estimating prostate cancer prognosis. However, genomic tests are destructive of tissue, subject to sampling bias, and expensive to scale. Pathology artificial intelligence (AI) models offer the promise of avoiding these problems. We analyzed a novel DPAI score in the context of long-term outcomes following both radical prostatectomy (RP) and active surveillance (AS).

Methods: Under an IRB-supervised protocol we identified 3,509 patients in the UCSF prostate cancer cohort who had previously undergone Decipher testing and for whom pathology images were available. Average genomic risk (AGR) was defined as the arithmetic mean of 42 established genomic scores from Decipher Genomic Resource Information Database (GRID) data. The DPAI was defined based on recent training against distant metastasis endpoint using an attention-based multiple instance learning approach on the frozen GigaPath pathology foundation model using 34,698 GRID RWD patients (NCT02609269). The trained model was applied to 256×256-pixel tiles from whole scanned images from the UCSF cohort. We examined correlation between DPAI and AGR scores. Among the RP (N=526) and AS (N=700) sub-cohorts, we analyzed time to recurrence (defined as PSA >0.2 mg/dl) and time to development of unfavorable histology (defined as large cribriform or intraductal carcinoma), respectively, using Kaplan Meier and Cox multivariable regression, the latter adjusting for the Cancer of the Prostate Risk Assessment (CAPRA) score.

Results: DPAI scores were normally distributed and increased with Gleason grade group, though with considerable spread at each grade group (figure 1). DPAI correlated relatively well with AGR ($r=0.65$, $p<0.001$); there were more cases with high DPAI and low AGR than vice versa (figure 2). There were 39 recurrence events in the RP cohort and 87 events of progression to unfavorable histology in the AS cohort. The DPAI score was able to predict both recurrence after RP and progression to unfavorable histology, particularly at the top quartile of scores (figure 3). On multivariable regression adjusting for CAPRA score, each decile increase in DPAI was associated with a HR of 1.13 (95% CI 1.04-1.22) for progression to unfavorable histology with adjustment for CAPRA score. This was nearly identical to performance for Decipher: HR 1.17 (95% CI 1.07-1.29).

Conclusions: The novel DPAI provides independent prognostic information even with robust adjustment for clinical risk factors, in the settings of both RP and AS, and corresponds well to established genomic scores—though with enough variability to suggest both genomic and pathology AI information will yield complementary insights into prostate cancer biology and outcomes.

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Conflict of interest: YL, HYH, JP, MA, ED are employees of Veracyte. MC has received consulting fees from Veracyte.

Figure 1

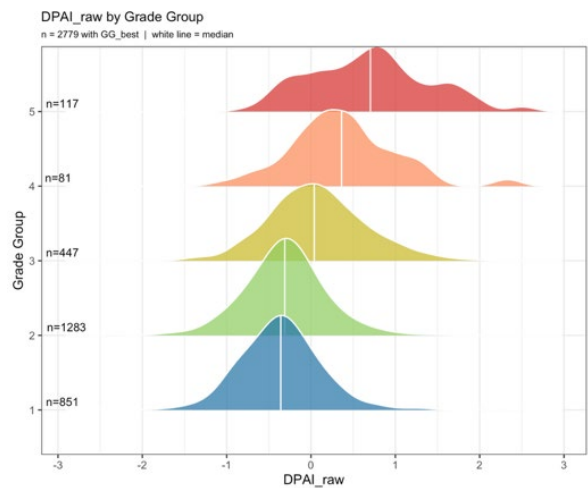


Figure 2

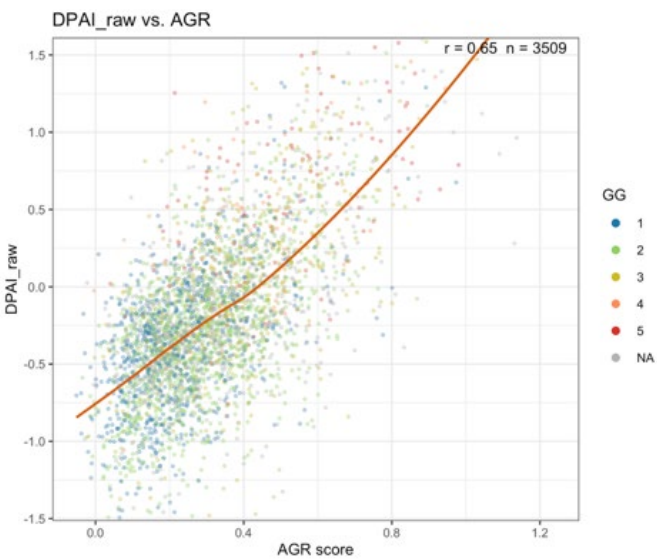


Figure 3

