

PD27-11

COMPARISON OF PROSTATE BIOPSY GRADE OBTAINED BY HUMAN PATHOLOGISTS VERSUS AN ARTIFICIAL INTELLIGENCE ALGORITHM FOR PREDICTING BIOCHEMICAL RECURRENCE AFTER RADICAL PROSTATECTOMY

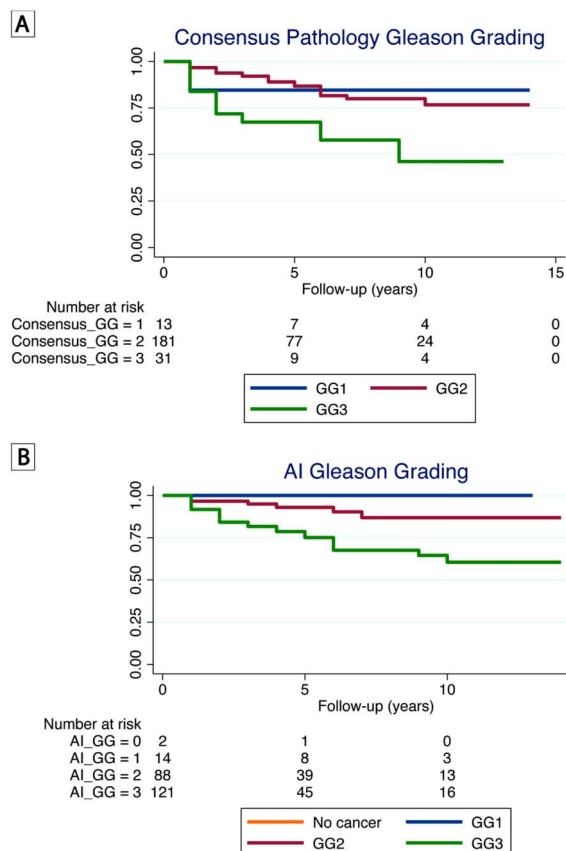
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INTRODUCTION AND OBJECTIVE: Several artificial intelligence (AI) algorithms have been developed to streamline biopsy Gleason grading, but most have not been challenged with predicting oncologic outcomes. In this study, we leveraged a cohort of patients with biopsy-detected Grade Group (GG) 2 prostate cancer (PCa) and examined the association of biopsy grade by contemporary pathologist consensus grade or AI algorithm with time to biochemical recurrence (BCR) after radical prostatectomy (RP).

METHODS: We identified 286 patients originally diagnosed with GG2 PCa on biopsy who underwent RP at our institution from 2000 to 2014. All biopsies were re-graded by two expert genitourinary pathologists (pathologist 1 and 2). For cases with discrepant reads, a third expert genitourinary pathologist determined the consensus pathology read. GG was also obtained using a previously validated and published AI algorithm. Concordance between pathologist and AI GG was quantified using the quadratic kappa. BCR was defined as two consecutive PSAs ≥ 0.2 ng/mL. Kaplan-Meier BCR free survival estimates by GG were compared using the log-rank test.

RESULTS: After RP median follow-up was 4 years (range 1-14). To date, 16% of the men have had BCR and median time to BCR was 2 years (range 1-10). Biopsy grading between pathologist 1 and 2 generated a kappa of 0.17. Grading between the consensus pathology read and the AI algorithm generated a kappa of 0.33. Grading by consensus pathology read was associated with time to BCR-free survival (log-rank $p=0.003$) as was the grading by the AI algorithm (log-rank $p=0.004$; Figure 1).

CONCLUSIONS: The AI algorithm Gleason grading demonstrated poor agreement with the consensus contemporary pathology read, but the agreement was also poor between the two pathologists. Yet, our cohort was only comprised of men originally diagnosed with GG2 PCa, a GG usually associated with poor inter-pathologist agreement. Remarkably, both the consensus pathology and the AI algorithm grades on the biopsy stratified patients well for subsequent BCR after RP, suggesting that AI algorithms could be developed to stratify for oncologic outcomes instead of attempting to replicate somewhat subjective human grading.



Note: Two patients were downgraded to 'no cancer' by the AI algorithm. Neither recurred.

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PD27-12

CORRELATION OF POST-PROSTATECTOMY DECIPHER GENOMIC CLASSIFICATION TO CLINICAL OUTCOMES IN PROSTATE CANCER OVER 8 YEAR FOLLOW-UP

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INTRODUCTION AND OBJECTIVE: Decipher genomic classification (DGC) has been developed to predict disease severity in prostate cancer. This study seeks to evaluate how well Decipher scores predicted actual clinical outcome in 192 patients that underwent robotic prostatectomy (RALRP) with 8-year follow-up of survival outcomes.

METHODS: Data is collected from an IRB-approved, prospectively-maintained database of 192 patients who underwent RALRP with DGC testing of the post prostatectomy specimens with mean 8 year follow-up outcomes. The Decipher prediction signatures were Metastasis Risk, Androgen Deprivation Therapy (ADT) Response, Post-Operative Radiation Response, Docetaxel Sensitivity, Seminal Vesicle Invasion, Genomic Gleason Score of Primary 4 or 5, Genomic CAPRA-S Score of High (>5), Pathology Stage T3 (pT3 Disease), Tumor Cell Proliferation, and Androgen Receptor (AR) Signaling Activity. A logistic regression analysis test evaluated these signatures with the actual clinical outcomes of metastatic castration-resistant prostate cancer (mCRPC), metastasis, ADT use, overall mortality (OM), and disease-specific mortality (DSM).

RESULTS: Higher Decipher scores for pT3 Disease was the most significant predictor of requiring ADT. The odds of ADT were 1.8 times greater for every 25-unit increase in pT3 Disease (95% CI 1.84-4.96, $p<0.001$). A negative relationship was seen between the Decipher prediction of Genomic Gleason Score of Primary 4 or 5 and no disease progression. The odds of no progression was 0.6 times lower for every 25-unit increase in Genomic Gleason Score of Primary 4 or 5 (95% CI 0.41-0.82, $p=0.002$). Higher Decipher scores for Post-Operative