Evaluation of the Decipher prostate cancer classifier to predict metastasis and disease-specific mortality from genomic analysis of diagnostic prostate needle biopsy specimens

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Background: Accurate risk stratification after diagnosis of prostate cancer (PCa) is key to optimal treatment decision-making. Decipher RP is an extensively validated genomic classifier used to determine biological potential for metastasis. Here, in a multi-institutional cohort, we aimed to evaluate its ability to predict metastasis and prostate cancer-specific mortality from analysis of PCa needle biopsy tumor tissue specimens.

Methods: We identified 175 patients treated with either first-line RP or first-line radiation therapy (RT) + androgen deprivation therapy (ADT) with available genomic expression profiles generated from diagnostic biopsy specimens obtained from three tertiary referral centers: Cleveland Clinic, Brigham and Women's Hospital and Johns Hopkins. The core with the highest grade was sampled and Decipher was calculated based on a locked random forest model. Cox univariable and multivariable (MVA) proportional hazards model and survival c-index were used to evaluate the performance of Decipher.

Results: Overall, 85% of patients had NCCN intermediate and high-risk disease. Of the 175 patients, 43% and 57% were treated with first-line RP and RT+ADT, respectively. With a median follow-up of 6 years, 32 patients developed metastases and 11 of these patients died of PCa. For prediction of metastasis 5 years post biopsy, Decipher had a c-index of 0.74 (95% confidence interval [CI] 0.63-0.84) compared to 0.66 (95% CI 0.53-0.77) for CAPRA and 0.66 (95% CI 0.55-0.77) for NCCN risk group.. On MVA, when modeled with CAPRA, Bx Decipher remained a significant predictor of metastasis (Decipher Bx hazard ratio [HR] 1.33 per 10% increase in score, 95% CI 1.06–1.69, P=0.01). Decipher Bx was also a significant predictor of PCSM (Decipher Bx HR 1.57 per 10%, 95% CI 1.07–2.40, P=0.02)

Conclusions: Decipher Bx was able to predict metastasis and PCSM from diagnostic biopsy specimens in a cohort of primarily intermediate and high-risk men regardless of first line treatment. This additional genomic information provides important risk stratification to help guide therapy for men with intermediate- and high-risk disease.

Conflict of Interest: ZH, QW, LL, KO, CB, SD, KY, ED are employees of GenomeDx Biosciences. BJT is a consultant for GenomeDx Biosciences.

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