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

Paul L. Nguyen¹, Zaid Haddad², Qiqi Wang², Lucia L.C. Lam², Kaye Ong², Christine Buerki², Samineh Deheshi², Kasra Yousefi², Elai Davicioni², Jeffrey J. Tosoian³, Tamara L. Lotan³, Felix Y. Feng⁴, Bruce J. Trock³, Ashley E. Ross³, Eric A. Klein⁵

1. Department of Radiation Oncology, Dana-Farber/Brigham and Women’s Cancer Center and Harvard Medical School, Boston, MA, USA
2. GenomeDx Biosciences Inc. Vancouver, BC, Canada
3. James Buchanan Brady Urological Institute, Johns Hopkins Hospital, Baltimore, MD, USA
4. Department of Radiation Oncology, University of California at San Francisco, San Francisco, CA, USA
5. Glickman Urological and Kidney Institute, Cleveland Clinic, Cleveland, OH, USA

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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