

Individual Patient Level Meta-analysis of the Performance of the Decipher Genomic Classifier in High Risk Men Post-Prostatectomy to Predict Development of Metastatic Disease

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ABSTRACT

Purpose: To perform the first meta-analysis of the performance of the genomic classifier test, Decipher, in men with prostate cancer post-prostatectomy.

Methods: MEDLINE, EMBASE, and the Decipher genomic resource information database were searched for published reports between 2011 and 2016 of men with prostate cancer treated by prostatectomy that assessed the benefit of the Decipher genomic classifier test. Multivariable proportional hazards models fit to individual patient data were performed, as well as meta-analyses by pooling the study-specific hazard ratios using random-effects modeling. Extent of heterogeneity between studies was determined with the I^2 test.

Results: Five studies (975 total patients, and 855 with individual patient level data) were eligible for analysis with a median follow-up of 8 years. Of the total cohort, 60.9%, 22.6%, and 16.5% of patients were classified as low, intermediate, and high-risk, respectively by Decipher, and had 10-year cumulative incidence rates of metastases of 5.5%, 15.0% and 26.7% ($p < 0.001$), respectively. Pooling the study-specific Decipher HRs across the 5 studies resulted in HR of 1.52 (95% CI 1.39-1.67, $I^2 = 0\%$) per 0.1 unit. In multivariable analysis of individual patient data, adjusting for standard clinicopathologic variables, Decipher remained a statistically-significant independent predictor of metastasis (hazard ratio [HR] 1.30, 95% confidence interval [CI] 1.14-1.47, $p < 0.001$) per 0.1 unit. The c-index for 10-year distant metastasis of the clinical model alone was 0.76 and increased to 0.81 with inclusions of Decipher.

Conclusion: The genomic classifier test, Decipher, has the ability to independently improve prognostication of patients post-prostatectomy, as well as within nearly all clinicopathologic, demographic, and treatment subgroups. Strong consideration should be given to incorporating the use of genomic testing in clinical decision making better individualize treatment.

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