

Methylation-based signature to distinguish indolent and aggressive prostate cancer

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Background

Prostate cancer management faces significant challenges in distinguishing indolent from aggressive disease, particularly since most patients are intermediate-risk and therefore hinders the ability to recommend standardized treatment recommendations. Moreover, current prognostic tools including Gleason scoring and tumor staging demonstrate limited accuracy for predicting disease progression and tumor recurrence. DNA methylation serves as a stable epigenetic modification that directly regulates gene expression, making it an ideal biomarker for cancer prognosis.

Methods

This study leveraged whole-genome enzymatic methylation sequencing (EM-Seq) on 120 patients to develop a novel prognostic signature for aggressive prostate cancer progression. We analyzed 20,849 differentially methylated regions (DMRs) and employed multiple machine learning approaches to identify optimal biomarkers.

Results

Our analysis revealed a 14-region DNA methylation signature that can serve as independent prognostic prediction factors outperforming traditional clinical indices. When combined into a risk score we observed a clinically meaningful odds ratio.

Conclusion

Our findings suggest our methylation-based approach provides actionable information for treatment decisions and surveillance strategies, representing a significant advancement toward precision medicine in prostate cancer management.

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Conflicts of Interest

Christopher Maher has a licensing agreement with Tempus.