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Methylation profiling in the contemporary management of meningioma

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Abstract

Background: The last decade has seen major international research efforts focus on better understanding disease heterogeneity in meningioma. Multiple molecular platforms have generated significant biological and clinical utility, and there is a need to translate these findings into routine clinical practice. Here we review the role of DNA methylation profiling in meningioma and advocate for its widespread adoption.

Methods: We review modern DNA methylation-based classification and outcome prediction tools in meningioma. Biological classifiers, which were constructed agnostic to outcome using unsupervised approaches, outcome predictors, and liquid biopsy models are discussed in detail.

Results: DNA methylation has been used for biological classification and outcome in meningioma with considerable success. Several groups have proposed novel molecular classification systems which share similar features with one another and outperform WHO grade in their ability to predict outcome and explain subgroup-specific biological processes. In addition, recent studies have suggested a role for methylation-based liquid-biopsy in meningioma, which represents an exciting avenue for further exploration.

Conclusions: DNA methylation profiling has been revolutionary in meningioma. There is a need for widespread adoption of these approaches to personalize care and inform clinical trial design.

Keywords: Classification; Liquid biopsy; Meningioma; Methylation; Prognostication.

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