

DNA methylation based molecular profiling to improve diagnostic accuracy for central nervous system

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Abstract

Central nervous system primitive neuro-ectodermal tumors (CNS-PNETs), have recently been re-classified in the most recent 2016 WHO Classification into a standby catch all category, “CNS Embryonal Tumor, not otherwise specified” (CNS embryonal tumor, NOS) based on epigenetic, biologic and histopathologic criteria. CNS embryonal tumors (NOS) are a rare, histologically and molecularly heterogeneous group of tumors that predominantly affect children, and occasionally adults. Diagnosis of this entity continues to be challenging and the ramifications of misdiagnosis of this aggressive class of brain tumors are significant. We report the case of a 45-year-old woman who was diagnosed with a central nervous system embryonal tumor (NOS) based on immunohistochemical analysis of the patient’s tumor at diagnosis. However, later genome-wide methylation profiling of the diagnostic tumor undertaken to guide treatment, revealed characteristics most consistent with *IDH*-mutant astrocytoma. DNA sequencing and immunohistochemistry confirmed the presence of *IDH1* and *ATRX* mutations resulting in a revised diagnosis of high-grade small cell astrocytoma, and the implementation of a less aggressive treatment regime tailored more appropriately to the patient’s tumor type. This case highlights the inadequacy of histology alone for the diagnosis of brain tumours and the utility of methylation profiling and integrated genomic analysis for the diagnostic verification of adults with suspected CNS embryonal tumor (NOS), and is consistent with the increasing realization in the field that a combined diagnostic approach based on clinical, histopathological and molecular data is required to more accurately distinguish brain tumor subtypes and inform more effective therapy.

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