ONCODAILY MEDICAL JOURNAL

abstract

DNA Methylation Profiling of Pediatric CNS Tumors: Real world experience from King Hussein Cancer Center

Maysa Al-Hussaini, Suha Fatafteh, Ala' Hejazi, Yazan Talab, Nisreen Amayiri, Mouness Obeidat, Osama Alayyan, Asem Mansour

doi.org/10.69690/ODMJ-018-0425-3249

POEM
Pediatric Oncology
East & Mediterranean

POEM, 4th Scientific Meeting,
Amman Jordan

ONCODAILY MEDICAL JOURNAL

SIOP ASIA 2025 SAUDI ARABIA

DNA Methylation Profiling of Pediatric CNS Tumors: Real world experience from King Hussein Cancer Center

Author: *Maysa Al-Hussaini, Suha Fatafteh, Ala' Hejazi, Yazan Talab, Nisreen Amayiri, Mouness Obeidat, Osama Alayyan, Asem Mansour*
Affiliation: *King Hussein Cancer Center*

DOI: *https://doi.org/10.69690/ODMJ-018-0425-3249*

Introduction: DNA-methylation-profiling has become core in the classification of CNS tumors.

Methodology: 240 CNS tumors from 220 patients were examined, including 96 samples from 90 pediatric patients. The median age was 10 years, with a mean of 8.9 years (3 months to 18 years). A calibrated score (CS) ≥0.9 was considered an optimal score for a definite diagnosis by the classifier. Concordance with the histopathology-based diagnosis was performed. Discordance was categorized as major if it resulted in a change of the entity and/or grade that impacts management, otherwise, it was considered minor. The origin of the tissue (KHCC vs. outside KHCC) was recorded to measure the impact on the success of the classification. Counts with frequencies and percentages are used to present the data.

Results: There were 74 (77.1%) concordant samples at the level of the methylation family, regardless of the CS. However, at ≥ 0.9 CS (n=60, representing 62.5% of all samples), there were 53 (88.3%) concordant cases. At a CS of ≥ 0.9, there were 30 (50.0%) gliomas, 28 of which were concordant (93.3%). There were 13 (21.6%) cases of embryonal tumors, 12 (92.3%) of which were concordant, 6 (10.0%) glioneuronal tumors, 4 of which were concordant (60%), and 5 (8.3%) ependymomas, all of which (100%) were concordant, 2 cases of choroid plexus tumors, meningioma, sarcoma, each (3.3%), all of which were concordant with the original diagnosis.

Among the discordant cases, there were 2 recent entities, including the newly described glioneuronal tumor with ATRX-alteration, kinase-fusion, and anaplastic features (one case), and PLAG amplified tumor (one case). Out of the 96 cases, there were 17(17.7%) cases from outside KHCC, including 9 samples from neighboring countries, 7 (77.8%) of which with CS of ≥ 0.9.

Conclusion: Our initial experience shows a good concordance rate between the initial histopathology-based diagnosis and the methylation profiling. DNA methylation profiling is a strong tool that helps in refining the diagnosis of CNS tumors, which might impact management.