Posterior fossa ependymoma group PFB

Posterior fossa ependymoma comprise three distinct molecular variants, termed PF-EPN-A (PFA), PF-EPN-B (PFB), and PF-EPN-SE (subependymoma) [1].

Group A patients are younger, have laterally located tumors with a balanced genome, and are much more likely to exhibit recurrence, metastases at recurrence, and death compared with Group B patients

EPN_PFB tumors occur more frequently in old children and adults, resulting in a more favorable outcome (compared with EPN_PFA tumors), and have many broad copy number changes with no recurrent somatic nucleotide variants [2].

Group B ependymomas are much less likely to recur, metastasize, or result in the death of the patient, validation of our results in additional cohorts of patients would suggest that Group B patients could be treated less aggressively than Group A patients. Conversely, the poor outcome for Group A patients underlines the need for rapid development of adjuvant therapies for these patients.

We anticipate that analysis of additional cohorts of posterior fossa ependymoma will further support the existence of at least two divergent molecular variants that are demographically, genetically, transcriptionally, and clinically distinct. The antibodies described for LAMA2 and NELL2 are both commercially available and therefore should be widely available across the globe for validation of our results and eventually for use in prognostication and stratification of PF ependymoma patients. We would also suggest that future clinical trials should prospectively validate IHC staining for LAMA2 and NELL2 on formalin-fixed, paraffin-embedded tumor material. Importantly, to further improve our understanding of the molecular biology of these posterior fossa subgroups, prospective investigations into the cell-of-origin and genetic driver mutations are desperately needed, including modeling of PF ependymoma in the mouse. Finally, the distinct molecular characteristics of these two groups of PF ependymoma suggest that subgroup-specific targeted therapies against subgroup-specific deregulated pathways are needed in future treatments of these tumors [3].

Posterior fossa ependymoma comprises two distinct molecular entities, ependymoma_posterior fossa A (EPN_PFA) and ependymoma_posterior fossa B (EPN_PFB), with differentiable gene expression profiles. As yet, the response of the two entities to treatment is unclear. To determine the relationship between the two molecular subgroups of posterior fossa ependymoma and treatment, we studied a cohort of 820 patients with molecularly profiled, clinically annotated posterior fossa ependymomas. We found that the strongest predictor of poor outcome in patients with posterior fossa ependymoma across the entire age spectrum was molecular subgroup EPN_PFA, which was recently reported in the paper entitled “Therapeutic impact of cytoreductive surgery and irradiation of posterior fossa ependymoma in the molecular era: a retrospective multicohort analysis” in the Journal of Clinical Oncology. Patients with incompletely resected EPN_PFA tumors had a very poor outcome despite receiving adjuvant radiation therapy, whereas a substantial proportion of patients with EPN_PFB tumors can be cured with surgery alone [4].

1)

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