

Brain Tumors: Challenges and Opportunities to Cure

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Tumors of the CNS are among the most challenging malignancies to treat. Despite surgery, radiation, and chemotherapy, many patients have incurable cancers and suffer disabling symptoms. The median survival of patients with glioblastoma, the most common malignant adult brain tumor, remains less than 2 years, and brain tumors include the most common and difficult-to-treat malignancies in children. Although these statistics are daunting, recent advances in the understanding of brain tumor biology have fueled a new sense of optimism that more effective and less toxic treatments can be developed. This Special Series summarizes progress across a variety of adult and pediatric CNS malignancies with an eye toward future therapeutic opportunities. Some articles review current standard-of-care and practice-changing clinical trials among specific brain tumor types. Others summarize research findings that are shaping the way we think about brain tumors and that hold promise to advance novel treatments.

Whole-genome and RNA sequencing, as well as global epigenetic profiling, have revolutionized our understanding of pediatric brain tumors—they explain why these diseases, once regarded as histologically homogeneous cancers, display discrepant behaviors.¹⁻¹¹ This new knowledge could improve the treatment of patients by pinpointing good-prognosis cohorts for reduced-treatment trials (which ultimately spares tissue from toxicity) and by targeting relatively poor-prognosis subtypes for novel treatment studies. In this regard, Mack and Northcott¹² provide an overview of approaches to supplement the current histopathologic classification of pediatric brain tumors with a variety of -omics approaches. Among malignant pediatric brain tumors, medulloblastoma is the most common and, arguably, the best understood. DNA and RNA microarray profiling techniques first demonstrated that these tumors comprise molecularly and clinically distinct tumor types, each marked by a unique transcriptional profile.¹³⁻¹⁵ Subsequent cross-species genomic studies demonstrated that these transcriptional profiles likely echo those of the corresponding originating cell type in the developing hindbrain.¹⁶ Armed with these and subsequent whole-genome sequencing data, Ramaswamy and Taylor¹⁷ review changes in the classification, risk stratification, and treatment of medulloblastoma. Similar approaches have been used to better understand the cellular and molecular origins of ependymoma, the third most common type of pediatric brain tumor; however, treatment of this disease has been limited significantly by chemotherapy resistance.^{18,19} Merchant²⁰ discusses the evolution of ependymoma therapy and, in particular, the efforts to reduce iatrogenic complications

and increase disease control. Although less common than their adult counterparts, pediatric high-grade gliomas are among the most frequent and lethal childhood brain tumors. These highly heterogeneous tumors have provided some of the most intriguing sequencing results of any cancer to date, not least of which is the identification of recurrent somatic mutations in *H3F3A*, which encodes histone H3.3, or in the related *HIST1H3B*, which encodes histone H3.1.^{8,9} These data have stimulated studies that provide insights into the basic biology of DNA metabolism and of brain tumor biology.^{21,22} In another review, Sturm et al²³ discuss this complex set of pediatric brain tumors and explore new insights into tumor biology and clinical management. As well as being driven by sporadic somatic mutations, pediatric and adult brain tumors may arise in the context of germline tumor predisposition syndromes. Campian and Gutmann²⁴ review the spectrum and treatment of central nervous system tumors that arise in individuals with neurofibromatosis type 1 and neurofibromatosis type 2.

Gliomas represent the most common malignant brain tumors in adults and are highly heterogeneous in their clinical presentation. Integrated genomic profiling has substantially advanced our understanding of this group of malignancies, including the identification of glioma core pathways in glioblastoma and isocitrate dehydrogenase mutations in low-grade gliomas.²⁵⁻²⁷ These studies have provided a foundation for the additional classification of low-grade gliomas into distinct disease subgroups^{28,29} and for an update of the WHO Classification of Tumors of the Central Nervous System.³⁰ Several articles in this series review this remarkable progress and its clinical implications. Diamandis and Aldape³¹ summarize key insights from the molecular profiling of adult glioma and potential strategies for their clinical implementation. van den Bent et al³² describe how the treatment of adult low-grade gliomas has evolved in recent years on the basis of results of recent clinical trials and reappraisal of prognostic disease biomarkers. Alexander and Cloughesy³³ review the current treatment of glioblastoma and highlight novel directions and opportunities for innovative clinical drug development. Two other articles in this series shed light on exciting progress in adult CNS tumors. Grommes and DeAngelis³⁴ provide an update on primary CNS lymphoma and strategies to incorporate molecularly targeted agents, such as inhibitors of deregulated B-cell receptor signaling, into the treatment of this disease. Barzilai et al³⁵ describe a state-of-the-art multidisciplinary approach toward spinal metastasis, an increasingly common problem in adults with cancer.

Four final reviews address important concepts in the biology, diagnosis, and treatment of brain tumors that are applicable to

both pediatric and adult cancers. The concept that cancers may be propagated by stem-like cells stretches back decades, and some of the first evidence that such cells exist in solid tumors was provided by studies of brain tumors.^{36,37} Parada et al³⁸ review evidence for and against brain tumor stem cells and their implications for treatment. The intimate relationship of brain tumors to critical structures in the CNS renders imaging particularly important in disease management. Exciting advances in several new modalities are likely to provide real-time evaluation of the metabolism, treatment response, and microenvironment of brain tumors. Brindle et al³⁹ review existing and novel approaches to neuroimaging-based diagnosis, and Wen et al⁴⁰ review the use of imaging to evaluate brain tumor treatment. Finally, long-anticipated evidence that the immune system could be harnessed for therapeutic gain in the treatment of cancers has been provided by studies of various liquid and solid cancers.⁴¹ Here, Sampson et al⁴² provide insights into how immunotherapy might be developed for brain tumors.

All of the articles in this Special Series were graciously contributed by leaders in the field and highlight areas of substantial progress and extraordinary opportunity in neuro-oncology. However, we must learn from previous decades of failed drug development. Translation of new knowledge into effective therapies will require a much deeper understanding of actionable genetic alterations, of the contribution of drug targets to tumor

maintenance, and of how best to integrate novel treatments with existing standard of care. Given the uncertainty of drug delivery across the blood-brain barrier and the lack of experimental models to reliably predict drug penetration in the CNS, the clinical evaluation of investigational agents also should include documentation of target inhibition in on-treatment biopsies and quantitative evaluation of drug-related effects on tumor growth rates, tumor metabolism, and tumor evolution. More extensive and comprehensive evaluation of cerebrospinal fluid for liquid biopsies may be informative in this regard.^{43,44} And let us not forget to measure treatment effects that are perhaps less obvious to the oncologist but very real to the patient—for example, changes in seizure frequency, reductions in corticosteroid doses, avoidance of treatment-related cognitive changes. Although much work remains, the roadmap provided by recent biology and clinical advances provides us with the tools needed to generate real impact for patients.

AUTHORS' DISCLOSURES OF POTENTIAL CONFLICTS OF INTEREST

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REFERENCES

- Fontebasso AM, Papillon-Cavanagh S, Schwartzentruber J, et al: Recurrent somatic mutations in *ACVR1* in pediatric midline high-grade astrocytoma. *Nat Genet* 46:462-466, 2014
- Jones DT, Hutter B, Jäger N, et al: Recurrent somatic alterations of *FGFR1* and *NTRK2* in pilocytic astrocytoma. *Nat Genet* 45:927-932, 2013
- Jones DT, Jäger N, Kool M, et al: Dissecting the genomic complexity underlying medulloblastoma. *Nature* 488:100-105, 2012
- Mack SC, Witt H, Piro RM, et al: Epigenomic alterations define lethal CIMP-positive ependymomas of infancy. *Nature* 506:445-450, 2014
- Parker M, Mohankumar KM, PUNCHIHEWA C, et al: C11orf95-RELA fusions drive oncogenic NF-κB signalling in ependymoma. *Nature* 506:451-455, 2014
- Pugh TJ, Weeraratne SD, Archer TC, et al: Medulloblastoma exome sequencing uncovers subtype-specific somatic mutations. *Nature* 488:106-110, 2012
- Robinson G, Parker M, Kranenburg TA, et al: Novel mutations target distinct subgroups of medulloblastoma. *Nature* 488:43-48, 2012
- Schwartzentruber J, Korshunov A, Liu XY, et al: Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. *Nature* 482:226-231, 2012
- Wu G, Broniscer A, McEachron TA, et al: Somatic histone H3 alterations in pediatric diffuse intrinsic pontine gliomas and non-brainstem glioblastomas. *Nat Genet* 44:251-253, 2012
- Wu G, Diaz AK, Paugh BS, et al: The genomic landscape of diffuse intrinsic pontine glioma and pediatric non-brainstem high-grade glioma. *Nat Genet* 46:444-450, 2014
- Zhang J, Wu G, Miller CP, et al: Whole-genome sequencing identifies genetic alterations in pediatric low-grade gliomas. *Nat Genet* 45:602-612, 2013
- Mack SC, Northcott PA: Genomic analysis of childhood brain tumors: Methods for genome-wide discovery and precision medicine become mainstream. *J Clin Oncol* doi:10.1200/JCO.2017.72.9921
- Pomeroy SL, Tamayo P, Gaasenbeek M, et al: Prediction of central nervous system embryonal tumour outcome based on gene expression. *Nature* 415:436-442, 2002
- Thompson MC, Fuller C, Hogg TL, et al: Genomics identifies medulloblastoma subgroups that are enriched for specific genetic alterations. *J Clin Oncol* 24:1924-1931, 2006
- Northcott PA, Korshunov A, Witt H, et al: Medulloblastoma comprises four distinct molecular variants. *J Clin Oncol* 29:1408-1414, 2011
- Gibson P, Tong Y, Robinson G, et al: Subtypes of medulloblastoma have distinct developmental origins. *Nature* 468:1095-1099, 2010
- Ramaswamy V, Taylor MD: Medulloblastoma: From myth to molecular. *J Clin Oncol* doi:10.1200/JCO.2017.72.7842
- Khatua S, Ramaswamy V, Bouffet E: Current therapy and the evolving molecular landscape of paediatric ependymoma. *Eur J Cancer* 70:34-41, 2017
- Pajtler KW, Mack SC, Ramaswamy V, et al: The current consensus on the clinical management of intracranial ependymoma and its distinct molecular variants. *Acta Neuropathol* 133:5-12, 2017
- Merchant TE: Current clinical challenges in childhood ependymoma: A focused review. *J Clin Oncol* doi:10.1200/JCO.2017.73.1265
- Funato K, Major T, Lewis PW, et al: Use of human embryonic stem cells to model pediatric gliomas with H3.3K27M histone mutation. *Science* 346:1529-1533, 2014
- Lewis PW, Müller MM, Koletsky MS, et al: Inhibition of PRC2 activity by a gain-of-function H3 mutation found in pediatric glioblastoma. *Science* 340:857-861, 2013
- Sturm D, Pfister SM, Jones DTW: Pediatric gliomas: Current concepts on diagnosis, biology, and clinical management. *J Clin Oncol* doi:10.1200/JCO.2017.73.0242
- Campian J, Gutmann DH: CNS tumors in neurofibromatosis. *J Clin Oncol* doi:10.1200/JCO.2016.71.7199
- Parsons DW, Jones S, Zhang X, et al: An integrated genomic analysis of human glioblastoma multiforme. *Science* 321:1807-1812, 2008
- Cancer Genome Atlas Research Network: Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature* 455:1061-1068, 2008
- Yan H, Parsons DW, Jin G, et al: *IDH1* and *IDH2* mutations in gliomas. *N Engl J Med* 360:765-773, 2009
- Eckel-Passow JE, Lachance DH, Molinaro AM, et al: Glioma groups based on 1p/19q, *IDH*, and TERT promoter mutations in tumors. *N Engl J Med* 372:2499-2508, 2015
- Brat DJ, Verhaak RG, Aldape KD, et al: Comprehensive, integrative genomic analysis of diffuse lower-grade gliomas. *N Engl J Med* 372:2481-2498, 2015
- Louis DN, Perry A, Reifenberger G, et al: The 2016 World Health Organization Classification of Tumors of the Central Nervous System: A summary. *Acta Neuropathol* 131:803-820, 2016
- Diamandis P, Aldape KD: Insights from molecular profiling of adult glioma. *J Clin Oncol* doi:10.1200/JCO.2017.73.9516

32. van den Bent MJ, Smits M, Kros JM, et al: Diffuse infiltrating oligodendroglioma and astrocytoma. *J Clin Oncol* doi:[10.1200/JCO.2017.72.6737](https://doi.org/10.1200/JCO.2017.72.6737)
33. Alexander BM, Cloughesy TF: Adult glioblastoma. *J Clin Oncol* doi:[10.1200/JCO.2017.73.0119](https://doi.org/10.1200/JCO.2017.73.0119)
34. Grommes C, DeAngelis LM: Primary CNS lymphoma. *J Clin Oncol* doi:[10.1200/JCO.2017.72.7602](https://doi.org/10.1200/JCO.2017.72.7602)
35. Barzilai O, Laufer I, Yamada Y, et al: Integrating evidence-based medicine for treatment of spinal metastases into a decision framework: Neurologic, oncologic, mechanical stability, and systemic disease. *J Clin Oncol* doi: [10.1200/JCO.2017.72.7362](https://doi.org/10.1200/JCO.2017.72.7362)
36. Visvader JE, Lindeman GJ: Cancer stem cells in solid tumours: Accumulating evidence and unresolved questions. *Nat Rev Cancer* 8: 755-768, 2008
37. Singh SK, Hawkins C, Clarke ID, et al: Identification of human brain tumour initiating cells. *Nature* 432:396-401, 2004
38. Parada LF, Dirks PB, Wechsler-Reya RJ: Brain tumor stem cells remain in play. *J Clin Oncol* doi: [10.1200/JCO.2017.73.9540](https://doi.org/10.1200/JCO.2017.73.9540)
39. Brindle KM, Izquierdo-Garcia JL, Lewis DY, et al: Brain tumor imaging. *J Clin Oncol* doi:[10.1200/JCO.2017.72.7636](https://doi.org/10.1200/JCO.2017.72.7636)
40. Wen PY, Chang SM, Van den Bent MJ, et al: Response assessment in neuro-oncology clinical trials. *J Clin Oncol* doi:[10.1200/JCO.2017.72.7511](https://doi.org/10.1200/JCO.2017.72.7511)
41. Gotwals P, Cameron S, Cipolletta D, et al: Prospects for combining targeted and conventional cancer therapy with immunotherapy. *Nat Rev Cancer* 17:286-301, 2017
42. Sampson JH, Maus MV, June CH: Immunotherapy for brain tumors. *J Clin Oncol* doi: [10.1200/JCO.2017.72.8089](https://doi.org/10.1200/JCO.2017.72.8089)
43. Wang Y, Springer S, Zhang M, et al: Detection of tumor-derived DNA in cerebrospinal fluid of patients with primary tumors of the brain and spinal cord. *Proc Natl Acad Sci USA* 112:9704-9709, 2015
44. Pentsova EI, Shah RH, Tang J, et al: Evaluating cancer of the central nervous system through next-generation sequencing of cerebrospinal fluid. *J Clin Oncol* 34:2404-2415, 2016

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