Genomic Analysis of Childhood Brain Tumors: Methods for Genome-Wide Discovery and Precision Medicine Become Mainstream.

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Abstract
Recent breakthroughs in next-generation sequencing technology and complementary genomic platforms have transformed our capacity to interrogate the molecular landscapes of human cancers, including childhood brain tumors. Numerous high-throughput genomic studies have been reported for the major histologic brain tumor entities diagnosed in children, including interrogations at the level of the genome, epigenome, and transcriptome, many of which have yielded essential new insights into disease biology. The nature of these discoveries has been largely platform dependent, exemplifying the usefulness of applying different genomic and computational strategies, or integrative approaches, to address specific biologic and/or clinical questions. The goal of this article is to summarize the spectrum of molecular profiling methods available for investigating genomic aspects of childhood brain tumors in both the research and the clinical setting. We provide an overview of the main next-generation sequencing and array-based technologies currently being applied in this field and draw from key examples in the recent neuro-oncology literature to illustrate how these genomic approaches have profoundly advanced our understanding of individual tumor entities. Moreover, we discuss the current status of genomic profiling in the clinic and how different platforms are being used to improve patient diagnosis and stratification, as well as to identify actionable targets for informing molecularly guided therapies, especially for patients for whom conventional standard-of-care treatments have failed. Both the demand for genomic testing and the main challenges associated with incorporating genomics into the clinical management of pediatric patients with brain tumors are discussed, as are recommendations for incorporating these assays into future clinical trials.

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