Chromosomal anomalies and prognostic markers for intracranial and spinal ependymomas.

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Abstract

Ependymomas are neoplasms that can occur anywhere along the craniospinal axis. They are the third most common brain tumor in children, representing 10% of pediatric intracranial tumors, 4% of adult brain tumors, and 15% of all spinal cord tumors. As the heterogeneity of ependymomas has severely limited the prognostic value of the World Health Organization grading system, numerous studies have focused on genetic alterations as a potential basis for classification and prognosis. However, this endeavor has proven difficult due to variations of findings depending on tumor location, tumor grade, and patient age. While many have evaluated chromosomal abnormalities for ependymomas as a whole group, others have concentrated their efforts on specific subsets of populations. Here, we review modern findings of chromosomal analyses, their relationships with various genes, and their prognostic implications for intracranial and spinal cord ependymomas.

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