
Malignant glioma: lessons from genomics, mouse models, and stem cells.

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Abstract
Eighty percent of malignant tumors that develop in the central nervous system are malignant gliomas, which are essentially incurable. Here, we discuss how recent sequencing studies are identifying unexpected drivers of gliomagenesis, including mutations in isocitrate dehydrogenase 1 and the NF-κB pathway, and how genome-wide analyses are reshaping the classification schemes for tumors and enhancing prognostic value of molecular markers. We discuss the controversies surrounding glioma stem cells and explore how the integration of new molecular data allows for the generation of more informative animal models to advance our knowledge of glioma’s origin, progression, and treatment.

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