Changes in the EGFR amplification and EGFRvIII expression between paired primary and recurrent glioblastomas.


Abstract

BACKGROUND: The efficacy of novel targeted therapies is often tested at the time of tumor recurrence. However, for glioblastoma (GBM) patients, surgical resections at recurrence are performed only in a minority of patients; therefore, molecular data are predominantly derived from the initial tumor. Molecular data of the initial tumor for patient selection into personalized medicine trials can therefore be used only when the specific genetic change is retained in the recurrent tumor.

METHODS: In this study we determined whether EGFR amplification and expression of the most common mutation in GBMs (EGFRvIII) is retained at tumor recurrence. Because retention of genetic changes may be dependent on the initial treatment, we only used a cohort of GBM samples that were uniformly treated according to the current standard of care (ie, chemo-irradiation with temozolomide).

RESULTS: Our data show that, in spite of some quantitative differences, the EGFR amplification status remains stable in the majority (84%) of tumors evaluated. EGFRvIII expression remained similar in 79% of GBMs. However, within the tumors expressing EGFRvIII at initial diagnosis, approximately one-half lose their EGFRvIII expression at tumor recurrence.

CONCLUSIONS: The relative stability of EGFR amplification indicates that molecular data obtained in the primary tumor can be used to predict the EGFR status of the recurrent tumor, but care should be taken in extrapolating EGFRvIII expression from the primary tumor, particularly when expressed at first diagnosis.

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KEYWORDS: EGFR; EGFRvIII; glioblastoma; recurrent tumors

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