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The immunohistochemical expression of c-Met is an independent predictor of survival in patients with glioblastoma multiforme

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Abstract

Background and aims

Because the outcome of glioblastoma multiforme (GBM) remains dismal, there is an urgent need for a better molecular characterization of this malignancy. The aim of this prospective study was to investigate the prognostic impact of the expression of c-mesenchymal-epithelial transition (c-Met) a receptor tyrosine kinase implicated in expression growth, survival, motility/migration, and invasion in GMB patients managed according to the established diagnostic and therapeutic protocols.

Methods

Between May 2003 and March 2011, a total of 69 patients (33 males and 36 females; mean age: 52.2 ± 12.9 years, age range: 23–81 years) referred to our Department for the surgical removal of GBM were evaluated immunohistochemically for c-Met expression. Progression-free survival (PFS) and overall survival (OS) served as the main outcome measures.

Results

Compared with c-Met− subjects (n = 38), c-Met+ subjects (n = 31) had both a significantly lower OS (15.3 ± 2.3 vs. 22.6 ± 2.5 months, respectively, $p < 0.01$) and PFS (12.3 ± 2.1 vs. 19.1 ± 2.6 months, respectively, $p < 0.05$). After allowance for potential confounders, multivariate Cox regression analysis identified c-Met+ as an independent predictor of both OS (hazard ratio = 1.7; 95 % confidence interval = 1.2–1.9, $p < 0.01$) and PFS (hazard ratio = 1.6; 95 % confidence interval = 1.1–2.3, $p < 0.05$).

Conclusions

Our findings suggest that c-Met immunohistochemical expression is an independent predictor of outcomes in patients with GBM treated by standard of care.