

Expression of the transcription factor HEY1 in glioblastoma: a preliminary clinical study

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ABSTRACT

Aims and background. The hairy/enhancer of split (E(spl))-related family of transcription factors (HES and HEY) are established targets of the notch signaling pathway, which has been implicated in different developmental processes, tumor formation and the self-renewal of neural stem cells. We determined the expression of HEY1 in human malignant gliomas to investigate whether its expression might be related to prognosis.

Methods. The expression of HEY1 was studied by *in situ* hybridization on 62 cases of glioblastoma. Patients were treated with surgery followed by chemotherapy and radiotherapy. We considered as end points of the study the overall survival time and progression-free interval. Correlations between HEY1 expression and tumor grade/patient overall survival and free interval before recurrence were analyzed using univariate analysis.

Results. Based on the *in situ* hybridization results, HEY1 expression rate was reported as negative staining in 13 cases (20.6%), as weak staining in 11 cases (17.3%), as moderate staining in 21 cases (33.3%), and as strong staining in 17 cases. We considered in the analysis the cumulative expression of HEY1 at *in situ* hybridization (Hey Index) as negative in 13 cases and positive in 49 cases (77.78%). The overall survival ($P = 0.002$) and the free-interval ($P = 0.012$) were significantly longer in patients who were negative for HEY1 expression.

Conclusions. Our data suggest that expression of HEY1 might be used as a marker to distinguish glioblastoma patients with a relatively good prognosis from those at high-risk, and that, in the future, HEY1 might represent a therapeutic target. **Free full text available at www.tumorionline.it**

Key words: HEY1, malignant glioma, prognosis.

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