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Prognostic evaluation of patients with glioblastoma using a new score prediction model

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Abstract

Despite the wide reportage of prognostic factors for glioblastoma (GBM), it is difficult to determine how these factors interact to affect patients' survival. To determine the combination of prognostic factors, we retrospectively analyzed the clinic data of 248 IDH wild-type GBM patients and built a novel prediction model. The survival variables of patients were identified via univariate and multivariate analyses. In addition, the score prediction models were constructed by combining classification and regression tree (CART) analysis with Cox regression analysis. Finally, the prediction model was internally validated using the bootstrap method. Patients were followed for a median of 34.4 (interquartile range, 26.1-46.0) months. Multivariate analysis identified gross total resection (GTR) (HR 0.50, 95% CI: 0.38-0.67), unopened ventricles (HR 0.75 [0.57-0.99]), and MGMT methylation (HR 0.56 [0.41-0.76]) as favorable independent prognostic factors for PFS. GTR (HR 0.67 [0.49-0.92]), unopened ventricles (HR 0.60 [0.44-0.82]), and MGMT methylation (HR 0.54 [0.38-0.76]) were favorable independent prognostic factors for OS. In the process of building the model, we incorporated GTR, ventricular opening, MGMT methylation status, and age. The model had six and five terminal nodes in PFS and OS respectively. We grouped terminal nodes with similar hazard ratios together to form three sub-groups with different PFS and OS ($P < 0.001$). After the internal verification of bootstrap method, the model had a good fitting and calibration. GTR, unopened ventricles, and MGMT methylation were independently associated with more satisfactory survival. The novel score prediction model which we construct can provide a prognostic reference for GBM.

Keywords: Classification and regression tree; Glioblastoma; IDH wild-type; Prediction model; Survival.

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