ABSTRACT

J Neurosurg. 2022 Jan 14:1-10. doi: 10.3171/2021.10.JNS211261. Online ahead of print.

Development and external validation of a clinical prediction model for survival in patients with IDH wild-type glioblastoma.

Mijderwijk HJ(1), Nieboer D(2), Incekara F(3)(4), Berger K(1), Steyerberg EW(2)(5), van den Bent MJ(6), Reifenberger G(7), Hänggi D(1), Smits M(3), Senft C(8)(9), Rapp M(1), Sabel M(1), Voss M(10), Forster MT(8), Kamp MA(1)(9).

Author information:

(1)Departments of1Neurosurgery and.

(2)Departments of 2Public Health and.

(3)3Radiology & Nuclear Medicine, Erasmus MC, University Medical Center, Rotterdam.

(4)Departments of4Neurosurgery and.

(5)5Department of Biomedical Data Sciences, Leiden University Medical Center, Leiden, The Netherlands.

(6)6Neurology, Brain Tumor Centre, Erasmus MC Cancer Institute, University Medical Center, Rotterdam.

(7)7Neuropathology, Heinrich Heine University, Medical Faculty, Düsseldorf, Germany.

(8)8Department of Neurosurgery, and.

(9)9Department of Neurosurgery, Friedrich Schiller University, Medical Faculty, Jena, Germany.

(10)10Dr. Senckenberg Institute of Neurooncology, Goethe University, Medical Faculty, Frankfurt; and.

OBJECTIVE: Prognostication of glioblastoma survival has become more refined due to the molecular reclassification of these tumors into isocitrate dehydrogenase (IDH) wild-type and IDH mutant. Since this molecular stratification, however, robust clinical prediction models relevant to the entire IDH wild-type glioblastoma patient population are lacking. This study aimed to provide an updated model that predicts individual survival prognosis in patients with IDH wild-type glioblastoma.

METHODS: Databases from Germany and the Netherlands provided data on 1036 newly diagnosed glioblastoma patients treated between 2012 and 2018. A clinical prediction model for all-cause mortality was developed with Cox proportional hazards regression. This model included recent glioblastoma-associated molecular markers in addition to well-known classic prognostic variables, which were updated and refined with additional categories. Model performance was evaluated according to calibration (using calibration plots and calibration slope) and discrimination (using a C-statistic) in a cross-validation procedure by country to assess external validity.

RESULTS: The German and Dutch patient cohorts consisted of 710 and 326 patients, respectively, of whom 511 (72%) and 308 (95%) had died. Three models were developed, each with increasing complexity. The final model considering age, sex, preoperative Karnofsky Performance Status, extent of resection, O6-methylguanine DNA methyltransferase (MGMT) promoter methylation status, and adjuvant therapeutic regimen showed an optimism-corrected C-statistic of 0.73 (95% confidence interval 0.71-0.75). Cross-validation between the national cohorts yielded comparable results.

CONCLUSIONS: This prediction model reliably predicts individual survival prognosis in patients with newly diagnosed IDH wild-type glioblastoma, although additional validation, especially for long-term survival, may be desired. The nomogram and web application of this model may support shared decision-making if used properly.

DOI: 10.3171/2021.10.JNS211261 PMID: 35171829