Outcome Prediction in Patients with Glioblastoma by Using Imaging, Clinical, and Genomic Biomarkers: Focus on the Nonenhancing Component of the Tumor (GBM-MR-NER-Outcomes)

Description

This manuscript correlates patient survival with morphologic imaging features and hemodynamic parameters obtained from the nonenhancing region (NER) of glioblastoma (GBM), along with clinical and genomic markers. Forty-five patients with GBM underwent baseline imaging with contrast material-enhanced magnetic resonance (MR) imaging and dynamic susceptibility contrast-enhanced T2*-weighted perfusion MR imaging. See DSC T2* MR Perfusion Analysis for more information about the authors' perfusion analysis. Molecular and clinical predictors of survival were obtained. Single and multivariable models of overall survival (OS) and progression-free survival (PFS) were explored with Kaplan-Meier estimates, Cox regression, and random survival forests.

Worsening OS (log-rank test, P = .0103) and PFS (log-rank test, P = .0223) were associated with increasing relative cerebral blood volume of NER (rCBV NER), which was higher with deep white matter involvement (t test, P = .0482) and poor NER margin definition (t test, P = .0147). NER crossing the midline was the only morphologic feature of NER associated with poor survival (log-rank test, P = .0125). Preoperative Karnofsky performance score (KPS) and resection extent (n = 30) were clinically significant OS predictors (log-rank test, P = .0176 and P = .0038, respectively). No genomic alterations were associated with survival, except patients with high rCBV NER and wild-type epidermal growth factor receptor (EGFR) mutation had significantly poor survival (log-rank test, P = .0306; area under the receiver operating characteristic curve = 0.62). Combining resection extent with rCBV NER marginally improved prognostic ability (permutation, P = .084). Random forest models of presurgical predictors indicated rCBV NER as the top predictor; also important were KPS, age at diagnosis, and NER crossing the midline. A multivariable model containing rCBV NER , age at diagnosis, and KPS can be used to group patients with more than 1 year of difference in observed median survival (0.49-1.79 years). Conclusion Patients with high rCBV NER and NER crossing the midline and those with high rCBV NER and wild-type EGFR mutation showed poor survival. In multivariable survival models, however, rCBV NER provided unique prognostic information that went above and beyond the assessment of all NER imaging features, as well as clinical and genomic features.

Data Access

Data Access

Some data in this collection contains images that could potentially be used to reconstruct a human face. To safeguard the privacy of participants, users must sign and submit a TCIA Restricted License Agreement to help@cancerimagingarchive.net before accessing the data.

Data Type	Download all or Query/Filter	License
Combined Images & Maps (DICOM, 45 subjects, 68864 files, 6.85 GB)	*Download* (Download requires NBIA Data Retriever)	TCIA Restricted
Feature maps (DICOM, 45 subjects, 42.30 MB)	*Download* (Download requires NBIA Data Retriever)	TCIA Restricted
Clinical, Genomic, and Radiologist Assessments (XLSX, 33 kb)	*Download*	CC BY 3.0

Please contact help@cancerimagingarchive.net with any questions regarding usage.

Collections Used in this Third Party Analysis

Below is a list of the Collections used in these analyses:

Source Data Type	Download all or Query/Filter	License
Original Data from TCGA-GBM (DICOM, 45 subjects, 46 studies, 488 series, 67730 images, 6.81 GB)	*Download* (Download requires NBIA Data Retriever)	TCIA Restricted

- TCGA-GBM

Detailed Description

Detailed Description

	Radiology Imaging Statistics
Modalities	MR
Number of Participants	45
Number of Studies	45
Number of Series	135
Number of Images	1134
Images Size	42.30 MB

Please see DSC T2* MR Perfusion Analysis for more information about the authors' perfusion analysis.

Citations & Data Usage Policy

Citations & Data Usage Policy

Some data in this collection contains images that could potentially be used to reconstruct a human face. To safeguard the privacy of participants, users must sign and submit a TCIA Restricted License Agreement to help@cancerimagingarchive.net before accessing the data.

Data Citation

Jain R, Poisson LM, Gutman D, Scarpace L, Hwang SN, Holder CA, Wintermark M, Rao A, Colen RR, Kirby J, Freymann J, Jaffe CC, Mikkelsen T, and Flanders A. (2014). **Outcome Prediction in Patients with Glioblastoma by Using Imaging, Clinical, and Genomic Biomarkers: Focus on the Nonenhancing Component of the Tumor.** The Cancer Imaging Archive. https://doi.org/10.7937/K9/TCIA.2014.FAB7YRPZ

Publication Citation

Jain, R., Poisson, L. M., Gutman, D., Scarpace, L., Hwang, S. N., Holder, C. A., Wintermark, M., Rao, A., Colen, R. R., Kirby, J., Freymann, J., Jaffe, C. C., Mikkelsen, T., & Flanders, A. (2014). **Outcome Prediction in Patients with Glioblastoma by Using Imaging, Clinical, and Genomic Biomarkers: Focus on the Nonenhancing Component of the Tumor.** Radiology, 272(2), 484–493. https://doi.org/10.1148/radiol.14131691

TCIA Citation

Clark, K., Vendt, B., Smith, K., Freymann, J., Kirby, J., Koppel, P., Moore, S., Phillips, S., Maffitt, D., Pringle, M., Tarbox, L., & Prior, F. (2013). **The Cancer Imaging Archive (TCIA): Maintaining and Operating a Public Information Repository.** Journal of Digital Imaging, 26(6), 1045–1057. https://doi.org/10.1007/s10278-013-9622-7

Other Publications Using This Data

TCIA maintains a list of publications that leverage TCIA data. If you have a manuscript you'd like to add please contact TCIA's Helpdesk.

Versions

Version 1 (Current): 2014/07/24

Data Type	Download all or Query/Filter
Image Data (DICOM)	Download
Supplemental Data (XLS)	Download