Integrated Multi-parametric MRI Biomarkers Analysis Identifies Molecular Subtypes of Glioblastoma

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Purpose:
The goal of this study is to develop a robust radiogenic-based molecular classification of glioblastoma into classical, neural, proneural, and mesenchymal subtypes. Advanced computational methods were employed for multiparametric imaging pattern analysis to extract distinctive imaging biomarkers. Defining glioblastoma subtypes based on radiologic signatures may allow for a molecularly targeted therapy. Ultimately, this technique may assist in evaluating the spatial heterogeneity of molecular tumor characteristics and monitoring response to treatment and progression.

Materials and Methods:
A retrospective cohort study was performed on 99 de novo glioblastoma patients. Preoperative multiparametric MRI data (T1, T1-Gad, T2, T2-FLAIR, rCBV, DTI, and DSC-MRI) were analyzed to extract a rich set of multiparametric imaging features and to create an integrative predictor of molecular subtype using a machine learning method in a cross-validated study. Size of enhancing tumor, nonenhancing tumor, and edema; location of tumor, mass-effect parameters, distribution of intensities of all modalities in each region were some of the most important features that were utilized through a feature selection method to build the model. For each subtype, a separate prediction model was created and the final class was defined through voting in the models. The imaging-predicted subtypes were evaluated against the RNA isoform-based classes.

Results:
The proposed method successfully classified proneural subjects with an accuracy of 86% and AUC of 0.87; neural subjects with an accuracy of 88% and AUC of 0.92; mesenchymal subjects with an accuracy of 84% and AUC of 0.89; and classical subjects with an accuracy of 85% and AUC of 0.75. The overall accuracy for all subtypes was 76%.

Conclusions:
Multiparametric image analysis extracts informative biomarkers that correlated to the molecular subtype of glioblastoma patients. When integrated via machine learning methods, these biomarkers form patterns that are quite predictive of molecular tumor subtype. These patterns are not easily appreciated by examining individual features.

Awards:
Dyke Award
Trainee Award

Categories:
ADULT BRAIN, Neoplasms