RadioGenomics and Glioblastoma Multiforme: Update from the TCGA Glioma Phenotype Research Group

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Purpose

Imaging features of cancers are phenotypic expressions of the tumors genomic blueprint. The term “radiogenomics” or the phrase “genomic imaging” has been applied to the concept of bridging these relationships between imaging and genomics in clinical research. Opportunities to systematically marry the rich imaging features provided by MR imaging to genetics of cancer have been limited to small cohorts and exploration of limited imaging features. The Cancer Genome Atlas (TCGA) has been banking large volumes of tumors for comprehensive genomic analysis. The first tissue line collected by TCGA was glioblastoma multiforme (GBM). Concurrently, the Cancer Imaging Program (CIP) collected baseline MRI studies on each of the TCGA submissions into a secure repository known as the Cancer Imaging Archive (TCIA). The purpose of this exhibit is to summarize the collective work of the TCGA Glioma Phenotype Research Group - an ad hoc volunteer committee focused on advancing the complementary role of imaging in understanding the biological and clinical behavior of GBM.

Approach/Methods

The TCGA Glioma Phenotype Research group initially developed, vetted and tested a controlled vocabulary of comprehensive MRI features of GBM. This VASARI featureset captures 30 unique imaging characteristics that are familiar to neuroradiologists in the evaluation of brain tumors. Using this methodology, the baseline imaging features of over 130 glioblastomas have been recorded by three or more independent observers. Subsets of physiologic imaging characteristics such as dynamic susceptibility contrast (DSC perfusion) and diffusion tensor imaging (DTI) were utilized for related analyses.

Findings/Discussion

Through this unique collaborative effort, eight other distinct research arms have been initiated from this single project that focused on the interrelationship of the 30 subjective MRI features (VASARI featureset) and the genetics of GBM. These include: (1) DSC T2* MR perfusion analysis which examines the combination of perfusion metrics and molecular characteristics to improving ability to predict survival; (2) Forecasting disease-free interval and survival using combined modeling of clinical parameters, imaging and genomics; (3) Mapping of edema/cellular invasion to MR phenotypes using MRI volumetrics and large-scale gene and microRNA expression profiling in GBM; (4) A growth kinetic study to predict growth pattern of GBM based upon features on baseline MRI, (5) Man-machine correlation of cardinal MR imaging features scored between human and machine observers; (6) Prediction of histopathologic, genomic and clinical features from DTI characteristics of GBM; (7) A computer-aided detection (CAD) texture analysis which uses multispectral features including intensity, texture and morphology to identify important features that predict genetic patterns; and (8) Supervised and unsupervised clustering of GBM into semantically distinct categories using imaging derived features.

Summary/Conclusion

Imaging has a much greater role to play in oncology than just diagnosis and staging. There is a complementary role between clinical parameters, imaging and genetics that can improve upon current methods to predict disease type, response to treatment and overall survival in GBM. The collective work of the TCGA Glioma Phenotype Working Group serves as a model for efficient collaboration and discovery.