Computer-aided Visual Image Analysis of Glioblastomas and Genomic Features

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E-Mail: snhwang@alum.mit.edu Primary Category: Neuroradiology/Head and Neck Secondary Category: Brain: Neoplastic Computer-aided Visual Image Analysis of Glioblastomas and Genomic Features S N Hwang, PhD, MD, Atlanta, GA; C A Holder, MD; E Huang, PhD; R A Clifford; D Hammoud, MD; P Raghavan, MD; et al. (snhwang@alum.mit.edu)

PURPOSE

Investigate quantitative computer-aided and qualitative visual imaging characteristics of primary glioblastomas that may predict genomic features.

METHOD AND MATERIALS

As part of The Cancer Genome Atlas (TCGA) MRI characterization project of the National Cancer Institute (NCI), methods for image analysis were developed as macros for NIH ImageJ. Preprocessing with 3D Slicer (software partially sponsored by NIH/NCI) included anisotropic diffusion noise reduction, N4 intensity inhomogeneity correction, and image co-registration. Measurements included volumes and surface areas of enhancing, nonenhancing, and necrotic tumor. At least 3 neuroradiologists independently reviewed MRI scans of 75 glioblastoma patients in the TCGA database on the basis of 26 imaging features (VASARI,

https://wiki.nci.nih.gov/display/CIP/VASARI). Tumors were classified as Proneural, Neural, Classic, or Mesenchymal subtypes based on gene expression. Proneural subtype is associated with improved outcome. Genomic data were obtained from TCGA's publicly available information, including mutation status (e.g. TP53 gene). Subgroups were identified based on copy number data (e.g. CDKN2A homozygous deletions).

RESULTS

Proneural tumors had smaller volume of necrosis by computer-aided measurements (p=0.04). A suggestion that Proneural tumors have smaller enhancing tumor volume (p=0.06) supports an association between minimal enhancing tumor (\leq 5% proportion of the overall tumor) and Proneural classification (p=0.0006), as qualitatively assessed by neuroradiologists. Mesenchymal tumors were also associated with higher necrosis volume (p=0.05). A suggested association between larger necrosis volume and CDKN2A homozygous deletion (p=0.07) was noted. Morphology may also be an important feature, since Classic glioblastomas had greater surface area to volume ratio of enhancing tumor (p=0.002).

CONCLUSION

Quantitative computer-aided measurements and qualitative visual assessment of glioblastomas are associated with certain genomic features. In particular, Proneural classification is associated with decreased necrosis, and possibly with smaller enhancing tumor volume.

CLINICAL RELEVANCE/APPLICATION

A combination of quantitative computer-aided measurements and radiologist qualitative assessment of glioblastomas may be potentially helpful in predicting genomic features and clinical outcome. A combi

FIGURE (OPTIONAL)

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