Radiomic Analysis of 3D MR Fingerprinting in Adult Brain Tumors



Louisa Onyewadume BA; Ozden Kilinc; Satyam Ghodasara; Debra McGivney; Sara Dastmalchian; Dan Ma; Jeffery Sunshine MD; Lisa R. Rogers DO; Marta Couce; Mark Griswold; Vikas Gulani; Jill Barnholtz-Sloan; Chaitra Badve; Andrew E. Sloan MD FACS

Introduction

Current MRI techniques have long scan times and generate qualitative images with limited diagnostic power, necessitating biopsy for final diagnosis. Magnetic Resonance Fingerprinting (MRF) simultaneously quantifies multiple tissue properties including T1 and T2 relaxation times.1 Based on our previous work with 2D single-slice MRF2, we now assess utility of 3D MRF to differentiate brain tumors subtypes.

Methods

In this ongoing study, 3D-MRF was performed in 27 patients with 14 glioblastomas (GBM), 2 anaplastic astrocytomas (AA), 17 metastases, and 4 lower grade gliomas (LGGs) on a 3T scanner. Volumetric MRF acquisitions were appended to clinical scans.2 MRF T1, T2 maps were generated (Fig.1) and volumetric ROIs manually drawn on ST (Solid Tumor) and PW (Peri-tumoral White Matter) regions as previously described.2 Mean T1, T2 values of (a) GBMs, (b) High Grade Gliomas (HGG=GBM+AA), (c) All gliomas (GBM+AA+LGG), and (d) Metastases were compared. 19 second-order texture features were computed using 3D gray level cooccurrence matrices (GLCM),3,4 and compared across tumor groups. AUC and ROC analyses were performed.

Learning Objectives

By the conclusion of this session, participants will be introduced to the concept of MR fingerprinting and application of 3D-MRF for quantitative tumor analysis. Participants will be made aware of the potential of 3D MRF to differentiate between various tumor types based on distinct tumor regions.

Results

Mean ST T1 values of gliomas (1668.5 \pm 142.4ms) trended higher than metastases $(1571.2 \pm 231.4 \text{ms}, \text{p}=0.08)$. Of all the statistically different texture results, sum variance and the information measure of correlation (IMC 1)-both functions of entropy-were most significant. Specifically, ST IMC1 values were higher in GBM than metastases, (T1: p=0.021, AUC=0.84 and T2: p=0.001, AUC=0.86; see Fig.2, 3). PW comparison between GBM and metastases revealed significant differences for cluster shade, contrast, and sum variance (p=0.010, AUC=0.87; p=0.013, AUC=0.86; and p=0.003, AUC=0.92, respectively) on T2 maps (See Fig.4). Combining T2 map variables of ST IMC1 and PW Sum variance gives best separation between GBM and metastases (See Fig.5).





