APPLICATION OF MULTI-TI ARTERIAL SPIN-LABELING MRI IN BRAIN TUMORS: COMPARISON WITH DYNAMIC SUSCEPTIBILITY CONTRAST

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Target audience: Radiologists, neurosurgeons, scientists and MRI researchers interested in brain perfusion imaging.

Introduction:

Perfusion imaging in brain tumors has important clinical and diagnostic implications. Compared to dynamic susceptibility contrast (DSC), arterial spin-labeling (ASL) is a noninvasive alternative magnetic resonance perfusion imaging method for visualizing and quantifying cerebral perfusion of brain tissue without exogenous contrast agents. Multi-TI arterial spin-labeling (mTI-ASL) MR sequences measure the perfusion with multiple transit time after labeling and can provide timing information such as bolus arrival time (BAT) and more accurately quantified regional cerebral blood flow (rCBF). This study aimed to present the feasibility of mTI-ASL for brain tumors in the clinical environment and compare it with dynamic-susceptibility contrast-enhanced perfusion imaging (DSC) to test the hypothesis whether mTI-ASL could substitute DSC in brain tumor cases.

Materials and method:

A total of 13 patients with histologically proven brain tumors (9 gliomas, 3 metastatic tumors and 1 lymphoma) underwent the mTI-ASL and DSC scan. All data were collected on a MAGNETOM Skyra 3T MR scanner (Siemens AG, Erlangen, Germany). The mTI-ASL images were acquired using a prototype 3D ASL sequence with the following parameters. mTI-ASL with: TR/TE 4600/22 ms, 20 slices, slice thickness 4 mm, 16 inversion time from 500 to 4000 ms, total acq. time 5 min including an M0 scan. The Buxton model with a non-linear fit to rCBF and BAT was used for quantification. DSC scans were acquired using a gradient-echo echo-planar imaging (EPI) sequence with an intravenous bolus injection of gadolinium contrast agent (0.1 ml/kg) with the following parameters: TR/TE 160/30 ms, FOV = 230×230mm^2, matrix size=128x128, slice thickness=4mm, gap 20%, 20 slices, measurements=60. The DSC data were then post-processed on a Siemens syngo.via workstation using MR perfusion evaluation tools. The rCBF maps obtained from mTI-ASL and DSC, respectively, were normalized by the values of the contralateral normal-appearing supraventricular white matter of frontal-parietal in each patient. Pearson correlation coefficients were calculated between normalized rCBF.

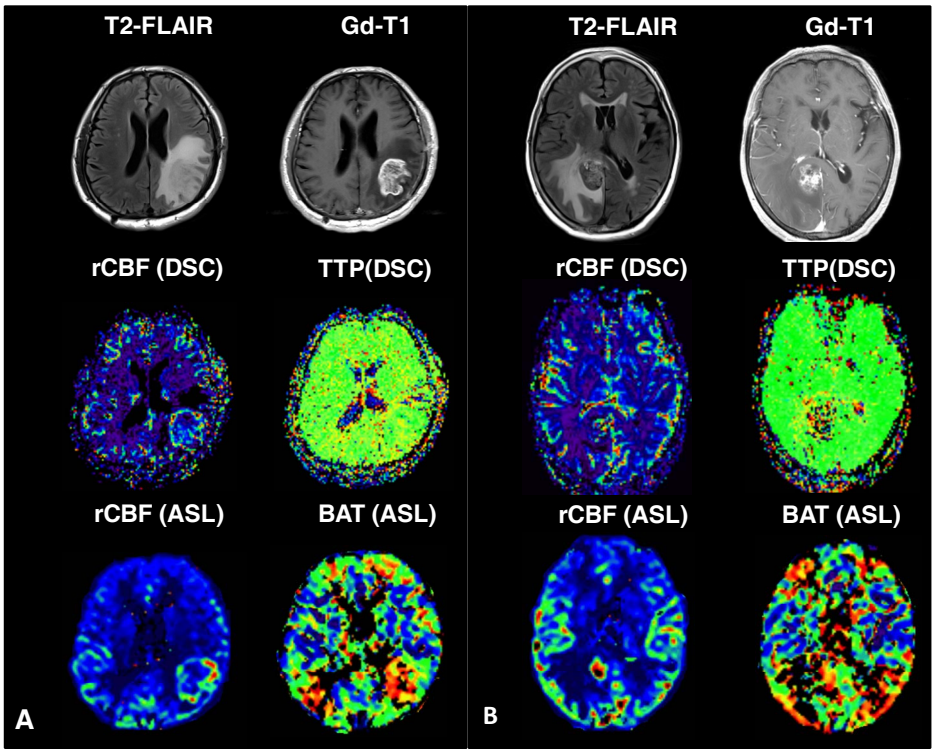

Figure 1. The images of T2-FAIR , Gd-T1 and the results obtained from mTI-ASL and DSC of two patients. (A) Patient with glioblastoma (WHO grade IV) in the left temporal-parietal lobe. (B) Patient with metastatic tumor in the right occipital lobe secondary to the lung cancer

Results:

Hyper-perfusion was detected in all the solid parts of tumors both in mTI-ASL and DSC. The rCBF value was significantly increased in tumors compared to the contralateral white matter in all patients. The bolus timing information included BAT, TTP and MTT, which all demonstrated prolongation in the tumor area in most cases. The results showed highly significant correlations between the rCBF measured by mTI-ASL and DSC (r=0.7901, p=0.0038). Due to the different temporal resolution of the BAT measured by mTI-ASL compared to the TTP obtained from DSC, computing the correlation coefficient value couldn't test the temporal information. Instead, we reviewed the consistency of prolongation or shortening of the perfusion timing in the lesion areas and found that in 77% (10/13) of cases, the prolongation of BAT agreed well with TTP.

Conclusions:

Incorporating a complete Buxton model fitting for rCBF and BAT calculation, mTI-ASL is able to significantly improve quantification and can provide additional bolus timing information. Its performances in measuring CBF and timing information of blood flow were consistent with DSC.