Comparison of quantitative blood flow values from DCE- and DSC-based perfusion in glioblastoma multiforme and cerebral tissue.

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Purpose: Relative perfusion values measured with DSC-MRI are frequently used in the initial clinical work-up and the follow up of brain tumors [1-3]. However, absolute quantification may not be feasible due to the unknown difference in relaxivity between artery and tissue [4]. In this study, we compare the cerebral blood flow (CBF) values in glioblastoma multiforme, contralateral white as well as grey matter from T1-DCE-based [CBF_{T1}] and T2*-DSC-based [CBF_{T2}*] perfusion, as well as the lesion-to-normal-white matter CBF ratios from both techniques.

Methods:

All experiments were approved by the local ethical board. 9 measurements were performed in 5 anatomopathologically proven recurrent glioblastma multiforme patients in the supine position at 1.5T using the quadrature head coil (patient 2 to 5 had a baseline and a follow up scan after antiangiogenic therapy; average time between the two scans in the same patient was 29 days).

An IR-prepared-FLASH sequence acquiring 3 slices per second (TR 2.4 ms/ TE 2 ms/ TI 190 ms/ FA 50°/ matrix 146*256/ FOV 219-270 mm/ dynamics 250, temporal resolution 0.3s per slice, slice thickness 5 mm) was performed during the injection of 15 ml of a Gd-DTPA solution (Magnevist®) at 2ml/sec. Ten minutes later, a second measurement using T2*-weighted GE EPI perfusion with three slices at the same imaging position as the DCE-based perfusion (12 slices, slice thickness 5 mm, TR 1590ms, TE 52ms, 50 dynamics, temporal resolution 1.43s per 12 slices) was performed with a second bolus of 20 ml Gd-DTPA solution injected at 4ml/sec. Post-processing was performed offline on a personal computer using the software PMI 0.2 written in-house in IDL (Research Systems, Boulder, CO)[5]. Signals were transformed into concentrations by using a test tube containing 2mM Gadolinium in saline solution placed in the FOV during the measurement. Tracer concentrations were deconvolved with an AIF obtained close to the tumor. In each patient the same AIF region was chosen for DCE- and DSC-MRI. A simple inflow correction was applied to the DCE data.

Parametric maps of CBF from T1-DCE-based [CBF_{T1}] and T2*-DSC-based perfusion [CBF_{T2*}] were calculated as the maximum of the impulse response function. In each patient similar regions of interest were manually drawn by a radiologist (MD) on the CBF_{T1} and CBF_{T2*} maps. CBF_{T1} and CBF_{T2*} values were calculated for tumor, contralateral white and grey matter. These average CBF values were compared, as well as lesion-to-normal CBF ratio for DCE-based ($CBF_{LTN,T1}$) and DSC-based ($CBF_{LTN,T2*}$) perfusion.

Results:

Figure 1 illustrates a parametric map of CBF_{T1} (top) and CBF_{T2*} (bottom) at the same tumor location. Figure 2 shows a scatter plot of CBF_{T1} and CBF_{T2*} values for tumor as well as for grey and white matter and a scatter plot of $CBF_{LTN,T1}$ and $CBF_{LTN,T2*}$. No significant correlation was found between CBF_{T1} and CBF_{T2*} in tumor (R= -0.6, p=0.07), in white (R= -0.07, p=0.9) and grey matter (R= -0.5, p=0.2). However, $CBF_{LTN,T1}$ and $CBF_{LTN,T2*}$ showed a significant correlation (R=0.8, p=0.008).

Conclusion:

The CBF measures from DSC-based perfusion were systematically higher compared to the CBF from DCE-based perfusion and CBF measures from both techniques did not show any correlation. Overestimation of DSC-MRI values was reported earlier [6]. The observation is consistent with the overestimation expected by the difference in relaxivity between artery and tissue [4]. In view of the observed correlations between the relative values, DSC-MRI CBF values may be reliable when normalized to a reference tissue type. However, since values of CBF_{T1} are more in line with the findings for grey and white matter CBF from PET[7], DCE-based perfusion measures of CBF seem to be preferable in tumor perfusion work-up and follow up.

References:

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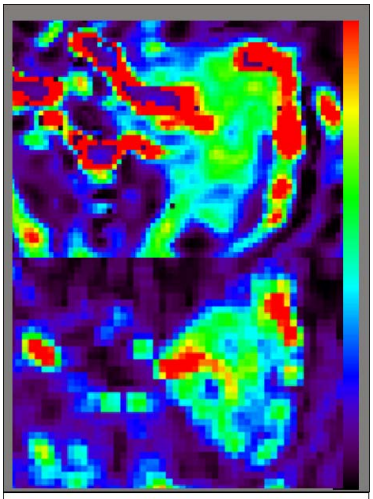

Figure 1: parametric image of CBF T1 (top, scale from 0 [black] to 240 ml/min/100ml [red]) and CBF T2* (bottom, scale ranging ten times higher, from 0 [black] to 2400 ml/min/100ml [red]) at the same slice position in a patient with glioblastoma multiforme near the left ACM.

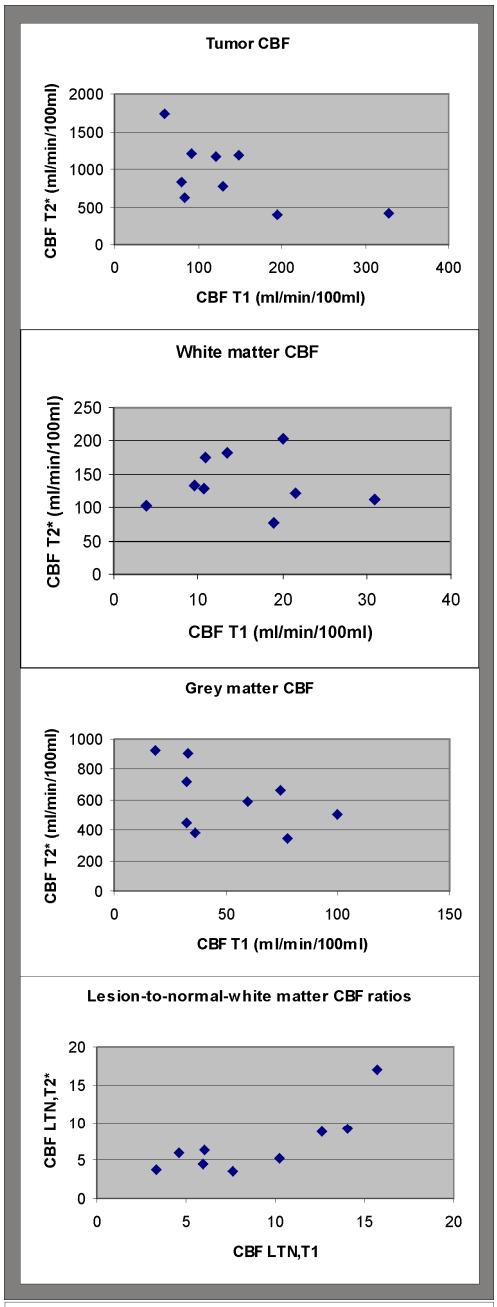

Figure 2: scatter plot of CBF values from T1 and T2* perfusion measurements in tumor, white and grey matter, as well as lesion-to-normal-white matter CBF ratios from both techniques.