Characterisation of brain tumors with bolus tracking data: T1-weighted MRI versus CT

S. Sourbron[1], M. Dujardin[1], R. Luypaert[1], P. Van Schuerbeek[1], S. Makkat[1], F. De Ridder[1], C. Chaskis[1], T. Stadnik[1]

[1]Vrije Universiteit Brussel, Brussels, Belgium

PURPOSE

In a previous study [1] we demonstrated the feasibility of quantifying kinetic parameters in brain tumors using a deconvolution analysis of T1-weighted bolus tracking data. The aim of the present study is to investigate the correlation of these data and results with those obtained from dynamic contrast enhanced CT.

METHODS

So far our study includes 5 patients with confirmed neoplasms (4 grade IV glioma's and 1 metastasis), each of which underwent an MR examination followed by CT within 3 days. The MRI study was performed on a 1.5T Philips Intera scanner using the head coil. A bolus of 10ml Gd-DTPA was injected at 2ml/sec, after which a volume of 3 slices was measured every 0.9 sec for 3 minutes. We used a TURBO-FLASH sequence with TR 4.9 msec, TE 2.4 msec, flip angle 50°, TI 196 ms, 128x90 matrix reconstructed at 256x256, FOV 230x183 mm^2, slice thickness 6 mm, slice gap 1 mm. The CT study was performed on a four-row, multisection Siemens Volume Zoom. 40 ml of non-ionic contrast agent was injected at 4 ml/sec, after which a volume of 4 slices was acquired every 1.0 sec for 40 seconds. Imaging parameters were: 80kV, 209mAs, 512 matrix, 20cm FOV, slice thickness 6 mm. Post-processing was performed off-line using in-house built software written in IDL. Gd-DTPA concentration was calculated from the MRI signals assuming a linear relation with relaxation rate. For the CT data we assumed a linear relation with signal enhancement. Apart from this first step, CT and MRI post-processing were identical: first, an Arterial Input Function (AIF) was determined by manually selecting a region of interest (ROI) inside a large vessel. Second, the data were deconvolved using standard-form Tikhonov regularization and the L-curve criterion [2]. We made maps of Cerebral Blood Flow (CBF) as the maximum of the Impuls Response Function (IRF). The vascular peak of the IRF [1] was extracted by fitting it to a Gauss-function and was time-integrated to produce maps of Cerebral Blood Volume (CBV). Finally Mean Transit Time (MTT) was calculated as CBV/CBF. For comparison of quantitative values, a radiologist (MD) drew ROI's covering the tumor edge on the CBF map, avoiding areas of necrosis and large blood vessels.

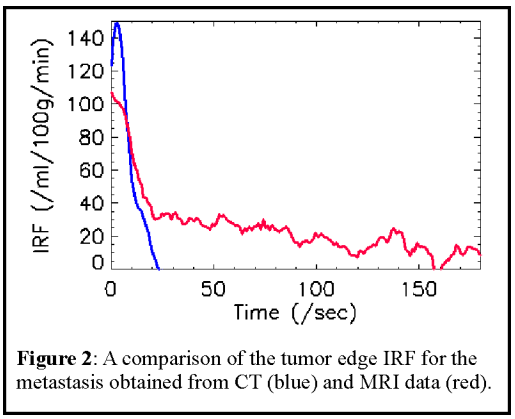

Figure 2: A comparison of the tumor edge IRF for the metastasis obtained from CT (blue) and MRI data (red).

RESULTS

Figure 1 illustrates that the higher spatial resolution of the CT maps allows to identify small structures within the tumor which are averaged out in the MRI data. Alternatively, the longer time window in MRI leads to significant advantages over CT in characterising the IRF: fig. 2 illustrates that the CT time window is generally insufficient to resolve the extravasation of the contrast in the tissue. A comparison of quantitative values (fig. 3) exposes a consistent behaviour for the group of glioma's: MRI values for CBV and CBF are systematically underestimated with respect to CT, but MTT values are in good agreement. Such observations can be explained by the effect of inflow in MRI, which induces an overestimation of the AIF with a factor estimated in the range 1.0-1.25 [4]. The values for the metastasis are an exception to this behaviour. Comparison of the IRF for this tumour (fig. 2) indicates that this may be due to differences in ROI placement: the CT IRF peaks approximately 2 sec later than the IRF obtained with MRI, which suggests that the CT ROI containes a larger fraction of venous blood vessels.

CONCLUSION

The higher spatial resolution of CT data presents obvious advantages over T1-weighted MRI in terms of mapping the tumor's internal architecture. On the other hand, the limited time window in CT does not in general allow the quantification and/or imaging of parameters expressing endothelial permeability. This may present a serious drawback as several studies indicate [1,3,5] that such parameters are promising markers for the characterisation of tumor tissue. Quantitative values for CBF and CBV obtained with MRI are weakly underestimated compared to CT and require correction for inflow. Our findings further indicate that an objective method for ROI placement is required in order to obtain reproducible values.

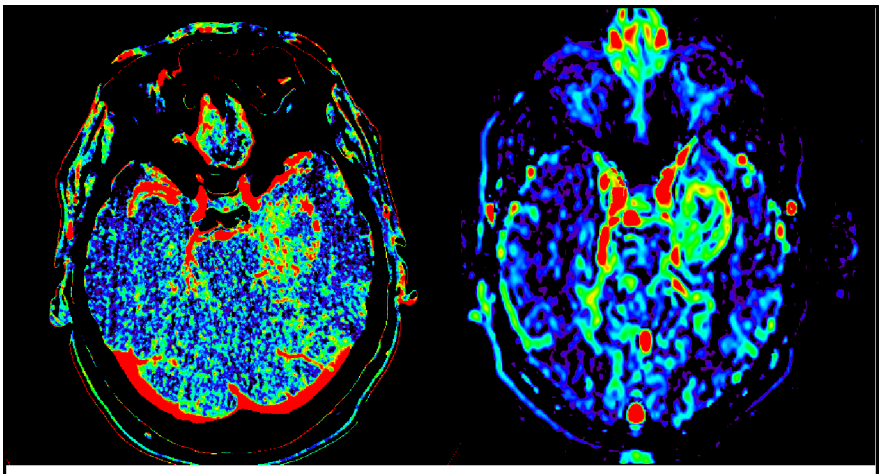

Figure 1: A typical example of a CBF map derived from CT data (left) and MRI (right). Both maps represent comparable (but not identical) cross sections of a patient with a grIV glioblastoma. The MRI image has been windowed and extrapolated to a 512 matrix size in order to facilitate comparison. Window settings are identical for both images: pixel values range between 0 (black) and 120 ml/100g/min (red).

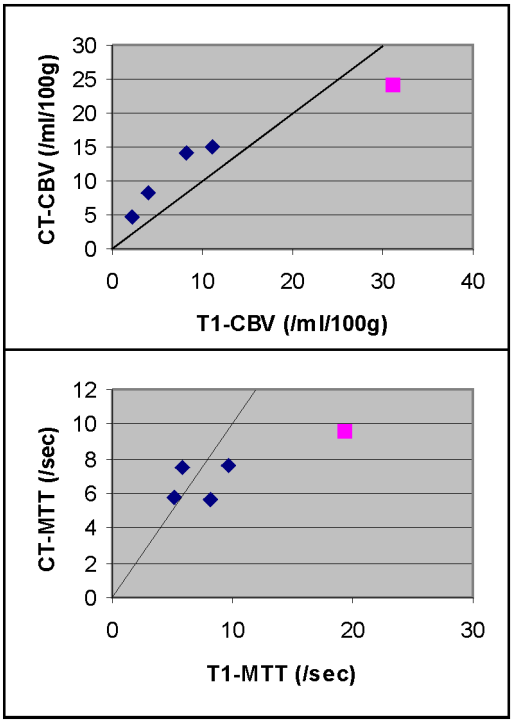

Figure 3: Summary of the ROI values for CBV (top) and MTT (bottom) for all glioma's (◊) and the metastasis (□). Superposed is the identity for comparison.

REFERENCES

[1] Sourbron et al. (2004) Proc. ESMRMB p188
[2] Sourbron et al. (2004) PMB 49:3307-24
[3] Cenic et al. (2000) AJNR 21:462-70
[4] Nazarpoor (2004) Proc. ESMRMB p527
[5] Benjaminsen et al. (2004) MRM 52:269-76