Quantitative CBF measurement by T1 weighted MRI is possible at 3 Tesla

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Introduction

Measurement of brain perfusion is important in vascular, degenerative and neoplastic diseases and when studying normal brain physiology. Using MRI, accurate determination of perfusion is difficult to obtain. Dynamic contrast enhanced (DCE) T_1 -weighted MRI is a well established method for estimating blood brain barrier deficiency (1). Here, we investigate whether this method enables to measure quantitative perfusion at 3 T. **Methods**

All MRI experiments were performed on a 3 T system (Philips Achieva, The Netherlands) with an eight-element SENSE head coil. A Gd contrast bolus (Omniscan, 0.1 ml/kg bodyweight to avoid full relaxation) was injected using an automatic contrast injector (Medrad). The bolus passage was imaged using a saturation recovery gradient recalled sequence with a 90 degrees non-selective preparation prepulse (TI = 120 ms), followed by gradient spoilers. Low TI has previously been shown to minimize the effect of water exchange (2). Image parameters were flip angle α =30 degrees, TR=3.82 ms, matrix size 96 (reconstructed to 256), scan percentage 80%, centric phase ordering, SENSE 2, FOV=240 mm, and 4 slices 8 mm thick, giving a spatial and temporal resolution of 2.5x3.1x8 mm³ and 1.0-1.1 s, respectively. 180 dynamic frames were obtained. The bolus (5 ml/s, 20 ml saline) was injected after the 10th dynamic. The most caudal slice was placed orthogonal to the internal carotid artery, in order to optimize the arterial input function. The MR signal as function of time s(t) is related to concentration c(t) by

[1] $s(t) = M_0 sin(\alpha) [1 - exp(-TI(R_1 + \Delta R_1(t)))], \Delta R_1(t) = r_1 c(t)$

The contrast relaxivity r1 of 4 s⁻¹mM⁻¹ was provided by the manufacturer for 3 T, and was assumed equal for tissue and blood vessels. We measured R_1 and M_0 before contrast injection using the same sequence as for monitoring the bolus passage, using 1 frame and a set of 11 TI values from 0.12 to 10 s. The signal equation for a saturation recovery (Eq. [1] with $\Delta R_1 = 0$, since centric phase encoding is used) was fitted to the data points in order to determine R_1 and M_0 maps. Then c(t) during the bolus passage is found from [1]. To ensure that MR signals are comparable between sequences, images were stored in the PAR/REC format provided by Philips, which contains full information about scaling. Scan time was 10 minutes for R_1 measurement and dynamic imaging.

Blood vessels were clearly visible during the bolus passage (Fig.1A). In Fig.1B an arterial input function (AIF) taken from 1 pixel in the MCA is shown along with a tissue curve from a GM ROI. We rescale the AIF by a vein curve, based on conservation of tracer, to avoid partial volume effects of the narrow arteries. Tissue curves are then deconvoluted using Tikhonovs approach (3); an example of a fit is shown in Fig.1C. Resulting perfusion maps for the 4 slices are shown in Fig.1D. Remark the clear delineation of WM, GM and basal ganglia. To evaluate perfusion values quantitatively we measured CBF in 6 GM and WM ROI's (no significant regional dependence was found) in 7 subjects, giving CBF(GM) = (42.5±8.0) ml/100g/min in agreement with PET values (typically in the range 40–60 ml/100g/min when using 15 H₂O (4,5,6)) and CBF(WM) = (13.6±3.8) ml/100g/min. Finally, on a single subject we repeated the CBF measurement during visual stimulation with a 8 Hz reversing checkerboard. The difference of the CBF maps is shown in Fig.1E, with a quantitative change of 28 ml/100g/min in a ROI in the visual area.



Figure 1. A. Most caudal slice, 25th dynamic shows signal enhancement as the bolus reaches the feeding arteries. B. Arterial input function (top) and signal curve from a GM ROI. C.Fit of tissue curve from B, converted to concentration. D. CBF maps, scale to the left is ml/100g/min. E. CBF change during visual stimulation.

Discussion

We demonstrate that T1-weighted DCE-MRI at 3 T can be used to calculate pixelwise brain perfusion (CBF) maps, with CBF values for grey and white matter in good agreement with PET studies. Compared to standard T2*-weighted DCE-MRI (7), T1-weighted DCE-MRI offers better image quality, straightforward determination of input function and good agreement with PET without need for normalization. Drawbacks are less coverage, longer scan time, and the relatively small MR signal changes necessitates high field strengths. Further studies are needed to confirm the potential of the present method. **References**

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