Distribution of arterial transit times investigated by MATISSE

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Introduction

The knowledge of the arterial transit time δ_a from the labeling plane into the brain is essential for blood-flow quantification and could also be of importance for the characterization of vascular diseases. Several continuous arterial spin labeling (CASL) techniques were applied in the past (1,2). In dynamic ASL (2), a time-varying periodic degree of arterial spin labeling (the labeling function, LF) was introduced. Several short labeling periods were placed within a single LF cycle, and the dynamic tissue response was measured. In previous work (3), the concept of the LF was used differently by quasi-sinusoidal modulation of the inversion efficiency. The time shift between the amplitude-modulated shape of the LF in a reference region and a region of interest was shown to be equal to their difference in δ_a. For short sampling intervals and 90° excitation pulses, the signal is predominantly of intravascular origin (3). This approach, which is subsequently referred to as 'Mapping of Arterial Transit times by Intravascular Signal SElection (MATISSE)', was improved to obtain whole-brain δ_a maps from a variety of subjects, and to validate the results by comparison with human vascular territories.

Method

All experiments were performed using a 3-T whole-body scanner (MedSpec 30/100, *Bruker BioSpin, Ettlingen, Germany*). For image acquisition, a microstrip helmet resonator of 23-cm inner diameter and 18-cm length was used (4). Simultaneous CASL of the left and right common carotid artery was achieved using a labeling coil which consisted of the perpendicular combination of two circular coil loops (6-cm diameter each) placed over the neck of the subject. MATISSE data were obtained from 10 healthy volunteers (5 male, 5 female, age 23-29 years). A gradient-echo EPI sequence was employed with an echo time of 17 ms, an acquisition matrix of 64×64, an acquisition bandwidth of 150 kHz, and a voxel size of 3×3×4 mm^3. The labeling gradient strength was 2 mT m^{-1}. A variable labeling frequency offset was added to the center labeling RF frequency for each repetition. The labeling RF pulse was applied during the first 400 ms of each TR interval (500 ms), and two slices were acquired without further delay during the last 100 ms. Four hundred and twenty repetitions were performed within one scan, during which the frequency offset of the labeling RF was cycled in 21 steps over a range of ± 4.5 kHz. The temporal relationship between the perfusion-weighted time series in different voxels was analyzed by the spectral-analysis method which was described in detail in Ref. (5).

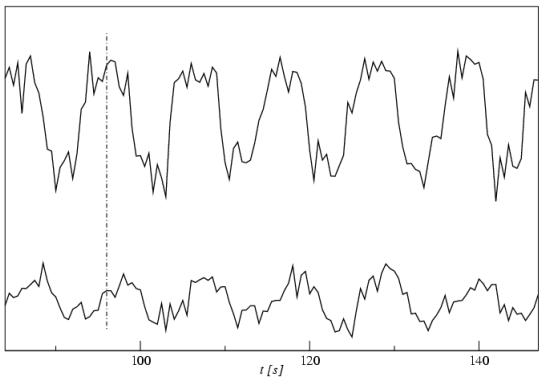

Fig. 1. Perfusion-weighted time series within 6 MATISSE modulation cycles obtained in a single subject. Each modulation cycle consists of 21 repetitions with *TR* = 500 ms.

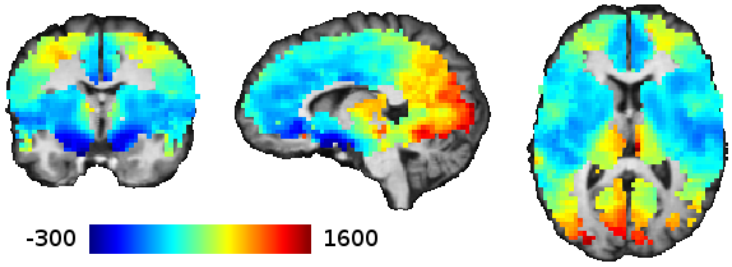

Fig 2. Averaged $\Delta\delta_a$ map of all 10 subjects overlaid onto a normalized brain in coronal, sagittal, and axial slices. Color-coded values are given in milliseconds relative to the reference region in the anterior insula.

Results

For a theoretical description of MATISSE, perfusion-weighted time series were simulated on the basis of a two-compartment model (6). Afterwards, the time shift between pairs of simulated time series was determined using the spectral-analysis tool (5) as applied to the in-vivo data. Comparison of the obtained time shift to $\Delta\delta_a$ assumed in the simulation yielded the systematic error of MATISSE. The accuracy of MATISSE was found to depend on *TR*, the length of the acquired time series, and the imaging gap interrupting the quasi-continuous labeling period. Another observation of the simulations was that exchange of labeled blood water with the tissue can be neglected.

Single-subject perfusion-weighted time series of two voxels in the left anterior insula (top, $\Delta\delta_a = -107$ ms) and in the left occipital brain (bottom, $\Delta\delta_a = 1320$ ms) are shown in Fig. 1. The shift between the two time series can easily be seen, as indicated by the vertical line. A $\Delta\delta_a$ map averaged over all subjects is shown in Fig. 2. The averaged perfusion-weighted time series within the left and right anterior insula were used as separate reference time series for the evaluation of $\Delta\delta_a$ in the left and right hemisphere, respectively. In the horizontal plane on basal-ganglia level, a large triangular-shaped area is readily distinguished in each hemisphere which corresponds with expected features of the territory of the medial cerebral artery (MCA). In the sagittal plane, short values for $\Delta\delta_a$ are found in an area around the dorsal aspect of the anterior corpus callosum, which corresponds well to the main trunk of the anterior cerebral artery (ACA). Zones of elevated $\Delta\delta_a$ were found between the main territories of MCA and ACA. Structures fed by the posterior cerebral artery (PCA) show $\Delta\delta_a$ values which are indicative of late arrival or even below threshold.

References

1. J. Wang et al., Magn Reson Med 2003;50:599-607.
2. E.L. Barbier et al., Magn Reson Med 1999;41:299-308.
3. T. Mildner et al., Proc. ISMRM 2006; 2686.
4. W. Driesel et al., Proc. ISMRM 2005; 948.
5. K. Müller et al., Neuroimage 2001;14:347-356.
6. J. Wang et al., Magn Reson Med 2002;48:242-254.