Quantification of Parenchymal T1 in the Activated Visual Cortex in Grey Matter Nulled and VASO fMRI Images

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Introduction

Grey matter nulled (GMN) [1] and vascular space occupancy (VASO) [2] methods are recently developed fMRI techniques that detect changes in cerebral blood volume (CBV) associated with brain activation. Both GMN and VASO fMRI methods use inversion recovery (IR) approach. GMN targets to null the grey matter (GM) and VASO the blood signal. With different compartments being nulled in the two methods, one expects the parenchymal origins of signal changes with these fMRI methods to be complimentary. Here, we studied spatial and tissue type characteristics of activated voxels obtained with these two fMRI methods. We investigated spatial overlap and quantified baseline T_1 in the activated voxels obtained with both fMRI methods.

Materials and Methods

Six healthy male volunteers (aged between 24 and 52) were recruited, each providing with a signed informed consent before taking part in the study. A Philips Achieva 3.0T MR system (Philips Medical Systems, Best, The Netherlands) was used for MRI. A single oblique axial slice along the calcarine sulcus was manually selected. The fMRI scanning parameters were as follows: single shot GRE-EPI, TR = 3000 ms, FA = 90°, FOV = 224x224 mm, matrix = 112x112, SENSE factor = 2, slice thickness = 5 mm, TE = 10 ms, and TI = 703 ms for GMN and 889 ms for VASO. Visual stimulation consisted of 30 s OFF and 30 s ON in five cycles with B/W checkerboard flashing at 8 Hz. 110 dynamic images were acquired for each fMRI scan within a period of 330 s. Activation maps were obtained using FEAT (FMRI Expert Analysis Tool), part of FSL package (http://www.fmrib.ox.ac.uk/fsl). An inversion recovery sequence was used for T_1 measurements with inversion times (TI) = 200, 400, 600, 800, 1000, 2000, 3000 and 4000 ms. Data for T_1 measurements were acquired from the same slice without visual stimulation as above with TE = 10 ms and TR = 10 s at the same spatial resolution as for fMRI. Four repeats were averaged for T_1 measurements to improve signal to noise ratio. T_1 values at each activated voxel were determined by fitting the signal intensities from eight images with different TI to a three-parameter model defined as $S = abs(A\cdot[1-B\cdot\exp(-TI/T_1)])$. Routines under IDL 6.0 (Research Systems Inc., Boulder, CO) were used to compute signal amplitudes, overlap of activated voxels in both fMRI methods and T_1 values.

Results

Figure 1 shows both GMN (in yellow) and VASO (in blue) activation maps to visual stimulation for a typical subject overlaid on a GMN raw image. The activated areas appear to be different for GMN and VASO fMRI with only slight overlap. The overlap of the activated GMN and VASO voxels measured from 6 subjects was found to be 10.3 ± 4.9% (mean ± SD), confirming that the respective fMRI signals originate largely from different parenchymal areas. The numbers of activated voxels for GMN and VASO fMRI scans were 166 ± 41 and 194 ± 84, respectively. The corresponding signal changes in GMN and VASO fMRI scans were 6.0 ± 1.2% and -2.2 ± 0.3%, respectively. The collective T_1 distribution histograms averaged from the entire subject cohort for GMN and VASO fMRI activated voxels are shown in Fig. 2. It is evident that the distribution of T_1 values for GMN and VASO fMRI scans were different with the majority of VASO T_1 values being lower than those for GMN. 68.4% of activated voxels for GMN fMRI scans have T_1 values higher than 1300 ms, while for VASO fMRI scans 65.3% of active voxels have T_1 values lower than 1300 ms. The average T_1 values from all activated voxels were 1608 ± 283 ms and 1247 ± 214 ms for GMN and VASO fMRI, respectively (t-test, $p < 0.0001$). Interestingly, these values are close to typical T_1 values at 3T for blood (1627 ms) [3] and GM (1283 ms) [4], respectively.

Conclusions

The current results demonstrate that the activated voxels from GMN and VASO fMRI scans overlap only by 10%. Baseline T_1 values in the activated GMN and VASO fMRI voxels indicate that the GMN signal may originate from parenchyma dominated by blood, whereas VASO signal comes mainly from GM. This claim is supported by the match of the current T_1 values with the blood and GM T_1 values at 3T, respectively. Our observations suggest that the inversion recovery – based fMRI techniques under study can be used to probe a particular parenchymal compartment (blood or GM) for functional imaging studies, thereby offering wider options for brain activation studies than obtained by BOLD. Furthermore, when assessing blood volume change upon brain activation, GMN is useful; yet when imaging the entire activated parecnhymal area undergoing CBV change, both GMN and VASO fMRI methods should be used.

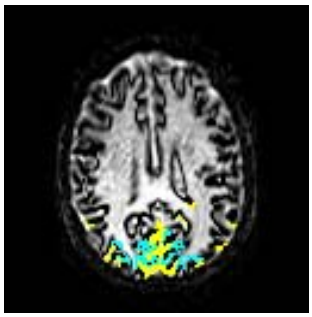

Figure 1. GMN (yellow) and VASO (blue) activation maps overlaid on a GMN baseline image for a subject.

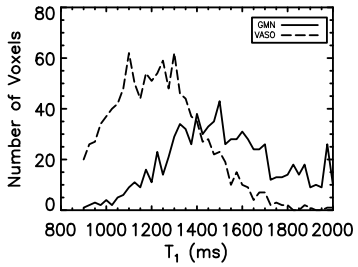

Figure 2. T_1 value distribution for GMN and VASO fMRI scans from all activated voxels of 6 subjects.

Reference:

[1] Shen Y, et al; J Cereb Blood Flow Metab 2008 (in press).
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