Echo time dependence of laminar BOLD activation at 7 Tesla

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Introduction

We present a multi-echo fMRI study at 7 T with 0.75 mm isotropic voxels and TEs ranging from 4.8 to 56 ms. This makes it possible to determine T_2^* at an unprecedented spatial scale making it possible to assess the local influence of myelinisation and vascularisation. As expected [1], the signal superficial to the cortex decays non-mono-exponentially because of a mixed compartment of venous blood (short T_2/T_2^*, complex decay pattern) and CSF (long T_2/T_2^*). Simultaneously the echo-time dependence of the functional activation in different layers is investigated, where the expectation is that activation in the pial veins will peak at an earlier TE than within GM due to the short T_2 of blood at high field strengths [2,3]. It is not to be expected however that after this initial peak the activation will completely disappear because the pial veins are surrounded by CSF and hence there will be a significant extravascular contribution at later TEs.

Methods

Five subjects were scanned after informed consent was given according to the guidelines of the local ethics committee. Functional scans were acquired on a 7 T whole body scanner (Siemens Medical, Germany) with a multi-echo 3D FLASH sequence. To improve signal-to-noise near the region of interest (visual cortex) a custom-built 7 channel surface coil receive array was inserted in a commercial 8 channel T/R headcoil. MR parameters were: voxel size 0.75x0.75x0.75 mm^3, matrix 256x256, 20 slices, FA 15°, BW 240 Hz/pixel, GRAPPA [4] was used for 4-fold acceleration along the primary phase encode direction (L-R). Ten equidistant echoes were acquired ranging from 4.8 to 56.1 ms, TR was 66 ms. Visual stimulation consisted of a 7.5 Hz flashing checkerboard, a black screen was used as a rest condition. Both conditions included a color changing fixation cross to which subjects responded using a button box. 19 volumes (91s each) were acquired, 10 were in the rest condition. All experiments were accompanied by a T1-weighted MP-RAGE acquisition of 80 slices which had the same orientation, voxel size and FOV as the functional runs. Retinotopy data [5] was acquired as well to determine the location of each subject's V1. The structural data were processed in FreeSurfer [6-7] to obtain the location of the WM-GM and the GM-CSF interfaces. These were used to plot profiles in the functional data perpendicular to the cortex. To correct for small errors in e.g. coregistration of the structural and functional datasets, the profiles were automatically realigned with respect to one another before averaging along the sulcus.

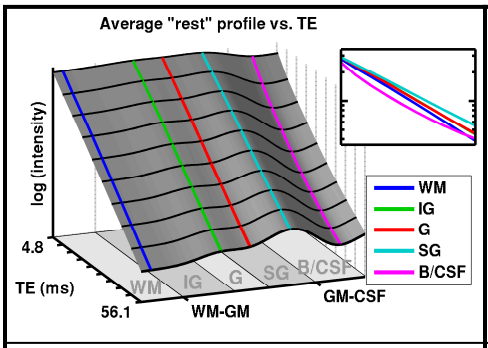

***Figure 1**: Signal intensity vs. TE vs. cortical depth. The blood/CSF compartment does not show mono-exponential signal decay [1]*

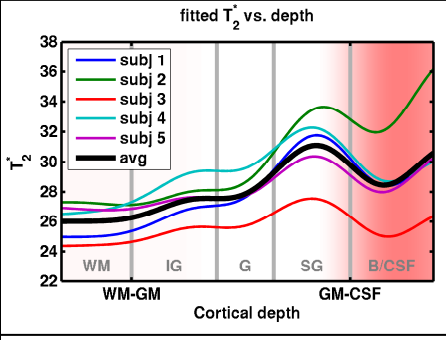

***Figure 2**: Fitted T_2^* values vs. cortical depth. The red shading depicts "goodness-of-fit".*

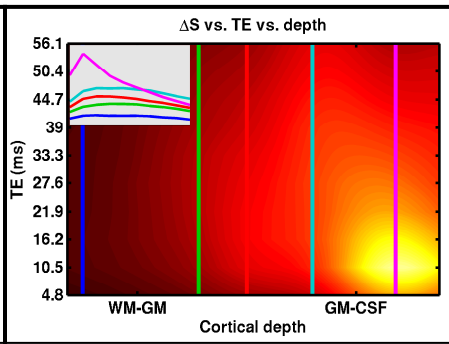

***Figure 3**: Functional signal change vs. TE vs. depth. The blood/CSF compartment clearly peaks earlier than the GM compartments (also see inset)*

Results

Fig. 1 shows the average intensity of the profiles on a logarithmic scale with respect to TE and cortical depth. The coloured lines are placed on the local minima/maxima of the through-cortical profile and are considered the centres of different laminar bins (WM, InfraGranular, Granular, SupraGranular and Blood/CSF). These lines are also displayed in the inset (as log(intensity) vs. TE) where the blood/CSF compartment clearly does not show mono-exponential behaviour having a steep beginning (blood) and a relatively flat ending (CSF).

Fig. 2 shows fitted T_2^* values versus cortical depth, the gray lines show the edges of the laminar bins as depicted in fig. 1. The background shading shows the sum-of-squares of the residual error after fitting as a measure of "goodness-of-fit" averaged over all subjects. As expected, the error is high for the blood/CSF compartment because it can not be described with mono-exponential decay and hence its fitted T_2^* value can not be trusted. Intersubject differences can be seen in terms of absolute value found; the shapes of the curves however are highly similar. We explain the shape to be the result of two effects. WM has a lower T_2 (and hence a lower T_2^*) than GM. The white matter fibers have to penetrate GM and will terminate at different layers depending on the target location of the fiber in question. Through the cortex, this would lead to a negative gradient of "WM" density when approaching the cortical surface. This yields low T_2^* values on the white matter side and higher T_2^* values on the pial surface side. On top of this gradient, a T_2^* modulation is present due to varying blood volume. As has been shown in [8-9] the capillary density is highest in the granular layer and its close surroundings. This could cause a local reduction in T_2^*. Both effects combined would yield a T_2^* profile as depicted in fig. 2.

Fig. 3 shows the signal change (checkerboard minus rest) with respect to cortical depth and TE averaged over subjects. The coloured lines (also shown in the inset as ΔS vs. TE) correspond to the same cortical depths as shown in fig 1. Clearly, in the blood/CSF compartment, the activation peaks at early TE corresponding very well to the reported blood T_2 of 7-13 ms at 7 T [3]. The cortical layers peak around 22-28 ms and the signal change remains highest for the supragranular layer due to the higher T_2^* value found there. Averaged over echo-time (data not shown) the cortical activation profile looks very similar to single-echo profiles reported at 3 T [10].

Discussion

Layer dependent T_2^* values have been reported for human V1 at 7 T showing a gradient from lower T_2^* near white matter and higher near the cortical surface with a superimposed dip in the granular layer. This dip could be caused by the high density of myelin and blood in this layer. We show that the GE intravascular contribution to BOLD at 7 Tesla is dominated by the pial compartment and that laminar GE-BOLD activation profiles are TE dependent. This could provide a method to potentially eliminate the intravascular contribution. The optimal TE to detect BOLD changes in parenchyma is about 28 ms considerably longer than previously thought as previous estimates have included venous blood.

References

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