T_1 Measurements for Cortical Grey Matter, White Matter and Sub-Cortical Grey Matter at 7T

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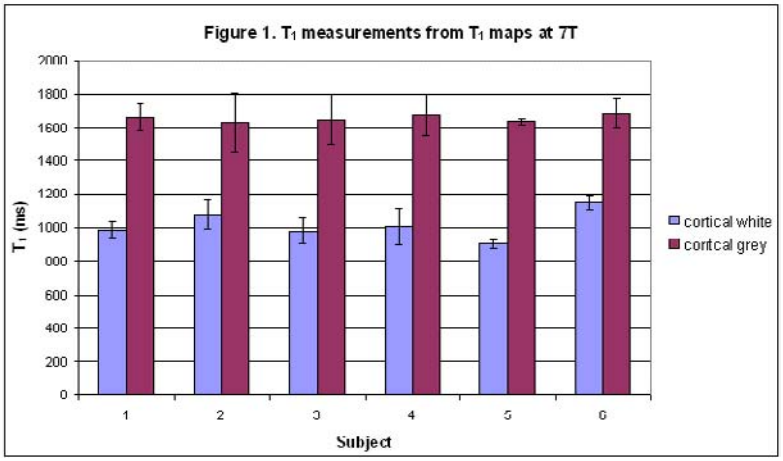
INTRODUCTION

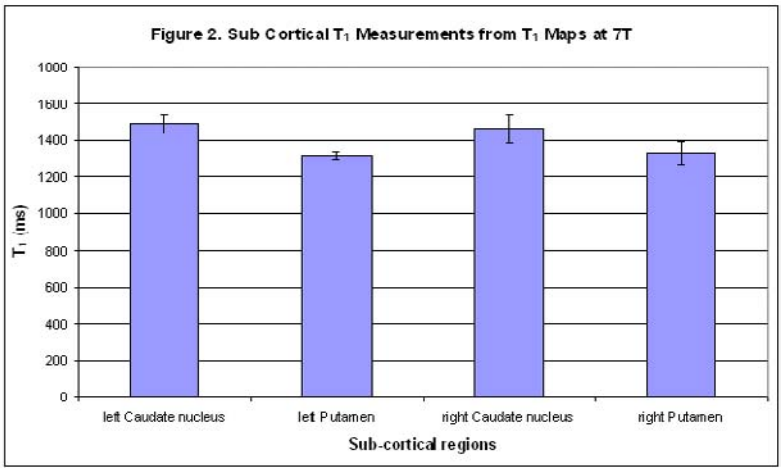
Knowledge of the relaxation times in tissue is important for optimization of image contrast and for choosing optimal sequence parameters for quantitative measurements, such as those used in measuring perfusion. The aim of this study was to measure the longitudinal relaxation time (T_1) at 7T, at high spatial resolution, in the cortical grey matter, white matter and sub-cortical grey matter nuclei, specifically the putamen and caudate nucleus.

METHOD

Image acquisition: 6 subjects age 26 ± 7.9 (mean ± standard deviation) years were scanned on a Philips Intera Achieva 7T MR scanner using an inversion recovery, turbo spin echo sequence with TSE factor of 10, TR of 5000ms and TE of 10 ms. Images were acquired for inversion times of 120, 200, 400, 600, 800, 1000, 1500, 1700 and 2000ms in a non-sequential order, in 26 minutes. An acquisition matrix of 256 x 256 and voxel size 0.78x0.78x3mm^3 was used and two stacks each comprising 5 contiguous transaxial slices with 1mm slice separation were acquired. The first stack sampled cortical grey matter data near the top of the head, while the second stack was placed over the sub-cortical, grey matter nuclei. Finally a high resolution 0.3x0.3x1.5 mm^3 anatomical image was acquired from 5 slices with this sequence using a TI of 120 ms, a TR of 3.5 s in 5 minutes 22 seconds (14 averages). **Pre-processing:** Masks were produced in Analyze using the volume acquired at TI= 2000ms and motion correction was performed using medx®. Because of the varying contrast in the IR set, images with neighbouring inversion times were registered to each other so that the data was progressively registered to the third volume (TI=400 ms). **Fitting:** It was expected that a full inversion would not be achieved in all regions of the head, requiring that the degree of inversion would have to be fitted for. Simulations [1] showed that for these sequence timings, and T_1<2s the signal behaviour in this sequence could be adequately fitted for T_1 using a three parameter fit for TI, S_o and F to $S(TI) = S_o(1-Fexp(-TI/T_1))$, using Powell's algorithm [2]. **Measurement of T_1:** For each subject, T_1 was measured from the T_1 maps in 3 regions of cortical grey matter in each of the stacks and in 3 and 4 regions in cortical white matter for stack 1 and 2 respectively. T_1 was also measured from ROI's that were drawn around the left and right putamen and caudate nucleus of each subject.

RESULTS





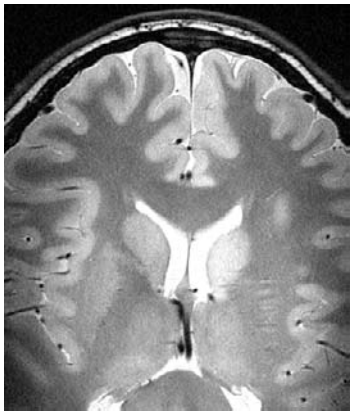


Figure 3.

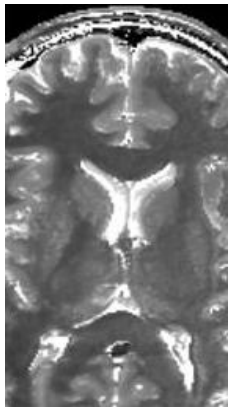


Figure 4.

Figure 1 shows the T_1 measurements for cortical grey matter and white matter for each subject. The mean ± standard deviation over subjects for white matter was 1017 ± 86ms and for grey matter was 1654 ± 21ms. *Figure 2* shows T_1 measurements for the sub-cortical grey matter regions investigated, averaged over all subjects. *Figure 3* shows the high resolution anatomical data set and *Figure 4* shows a corresponding T_1 map, apparently showing some partial volume errors at the interface between grey and white matter. It should be noted that the images displayed a drop-off in signal intensity in the temporal lobes, apparently due to RF field inhomogeneity.

DISCUSSION AND CONCLUSION

The cortical grey and white matter T_1 is longer than at 3T as expected, but still shows considerable dispersion between brain tissues. These results are consistent with those previously reported on a cadaver at 8T [2]. Sub-cortical regions show a lower T_1 value compared to the cortical grey matter. This is probably related to the higher iron content of these areas, which is also known to reduce their T_2 relaxation times [4]. This preliminary data will be used to optimise sequence timings to allow measurements to be made with shorter repetition times, and hence at higher spatial resolution with less sensitivity to partial volume effects.

REFERENCES

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[3] Mitchell et al, Proc. Intl. Soc. Mag. Reson. Med., 11, 1089, 2003. [4] Haacke et al, Magn. Reson. Imag. 23, 1, 2005.