METABOLITE T2 MAPPING IN THE HEALTHY RHESUS MACAQUE BRAIN AT 3 T

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Introduction: The biochemical, morphological, and functional similarity between human brain and its rhesus macaque counterpart has lead to extensive use of the latter as an advanced model for neurological disease and treatment studies. To facilitate correction for the adverse effect of T_2 weighting on the accuracy of metabolic quantification, we measured the T_2s of NAA, Cho and Cr in several brain regions of four rhesus macaques at 3T with 3D MRSI at 180uL spatial resolution using a two-point protocol optimized for precision per unit time.

Methods: Four healthy macaques were studied. All experiments were done in a 3T scanner (Siemens, Erlangen, Germany) using a transmit-receive knee coil. Axial and sagittal MRI were acquired. A 30_{LR} mm × 42_{AP} mm × 20_{IS} mm VOI was graphically prescribed in a 96_{LR} mm × 96_{AP} mm × 20_{IS} mm FOV, and aligned along the splenium-genu axis of the corpus callosum. The VOI was excited using PRESS and the FOV was partitioned into 16_{LR}×16_{AP} 2D CSI and 4th order 1D Hadamard spectroscopic imaging along the inferior-superior direction. A two-point scheme that optimizes not just the usual two TEs, but also the number of averages, N_1 and N_2, at each, for the best T_2 estimate/unit time was used. Using the literature human Cr T_2≈180 ms, as the initial value for the sought after T_2s, has led to TE_1=30 ms (minimum for our setup), N_1=4 and TE_2=260 ms (TE_1+1.25×T_2), N_2=12. All experiments share the same TR=1800ms.

Results: Sample regional spectra at the short and long echo times are show in Fig 1. They demonstrate the SNR and spectral resolution obtained from 180ul voxels at these TEs. The regional and global T_2 values obtained are compiled in Table 1 as means ± standard error of the mean (SEM). Note that the T_2s of NAA, Cr and Cho are very similar in both GM and WM structures. The T_2 histograms for the NAA, Cr and Cho from all voxels in the VOIs in each of the four animals studied are shown in Fig. 2. Note the overall histogram shape for each of the three metabolites is very similar. The results reveal that these T_2s are in excellent agreement with the corresponding T_2s obtained in the human brain.

Conclusion: Combining 3D ^{1}H-MRS with an optimized two-point acquisition protocol makes for the most efficient use of time to map the T_2 distribution of ^{1}H-MRS observable neuro-metabolites in rhesus macaques. These regional T_2 values are (i) similar among animals indicating that they may be characteristic; and (ii) in excellent agreement with reported values in humans at that B_0, as expected from a model-system. The T_2s and their variations between WM and GM structures indicate that for the purpose of ^{1}H-MRS quantification at 3 T the use of one T_2 value for each metabolite is sufficient for intermediate or long TE across both humans and macaques.

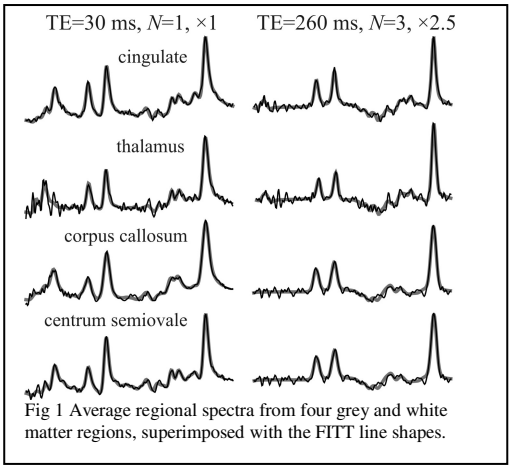

Fig 1 Average regional spectra from four grey and white matter regions, superimposed with the FITT line shapes.

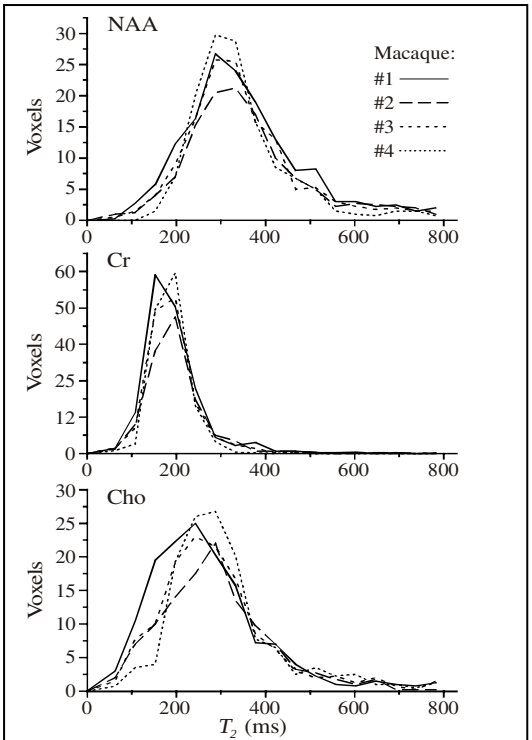

Fig 2 Histograms of the NAA, Cr and Cho T_2s from all voxels in the VOI for the 4 macaques.

		NAA T_2 (ms)	Cr T_2 (ms)	Cho T_2 (ms)
Gray matter (GM) structures:	Caudate	323±18	178±8	261±13
	Thalamus	337±5	175±10	289±8
	Putamen	338±16	179±5	283±13
	Cingulate gyrus	304±7	178±8	264±15
	GM structures Average	**325±8**	**178±2**	**274±7**
White matter (WM) structures:	Splenium of CC	308±6	181±1	248±7
	Centrum semiovale	316±7	182±4	263±9
	WM structures Average	**311±4**	**181±1**	**255±8**
Global WM+GM average		**316±7**	**177±3**	**264±9**

Table 1 Mean±SEM T2 relaxation times (ms) at 3 T of the N-acetylaspartate (NAA), creatine (Cr) and choline (Cho) in the various GM and WM brain regions.

References

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