REGIONAL METABOLITE T2 IN THE HEALTHY RHESUS MACAQUE BRAIN AT 7 T

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Introduction: The brain of the rhesus macaque is biochemically, morphologically, and functionally similar to its humans counterpart. Consequently, macaques are increasingly used as advanced models for 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 7T with 3D MRSI at 64uL 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 7 Tesla scanner (Siemens, Erlangen, Germany) using a transmit-receive head coil. A 32_{LR} mm × 40_{AP} mm × 16_{IS} mm VOI was graphically prescribed in a 64_{LR} mm × 64_{AP} mm × 16_{IS} mm FOV. The VOI was excited using PRESS and the FOV was partitioned into $16_{LR}\times16_{AP}$ 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, N1 and N2, at each, for the best T^2 estimate/unit time was used. Using the literature human T_2=100 ms, as the initial value for the sought after T_2s, has led to TE1=39 ms (minimum for our setup), N1=4 and TE2=165 ms (TE1+1.25×T_2), N2=12. All experiments share the same TR=1600ms.

Methods: Sample spectra at the short and long echo times are shown in Figs. 1. They demonstrate the SNR and spectral resolution obtained at 7T from 64uL voxels at these TEs. The average metabolite SNRs, for the short TE were 9.8±1.0, 10.0±1.0 and 8.9±1.2 for NAA, Cr and Cho. The regional 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, as expected, nearly half the 180 – 250 ms reported for these metabolites at 3T in the human brain in vivo. Comparing with single-voxel T_2s reported at 7T by Michaeli et al. shows that human Cr and NAA values are in agreement with the Macaque's, 109 versus 114ms and 158 versus 169ms (Cho T_2 was not reported).

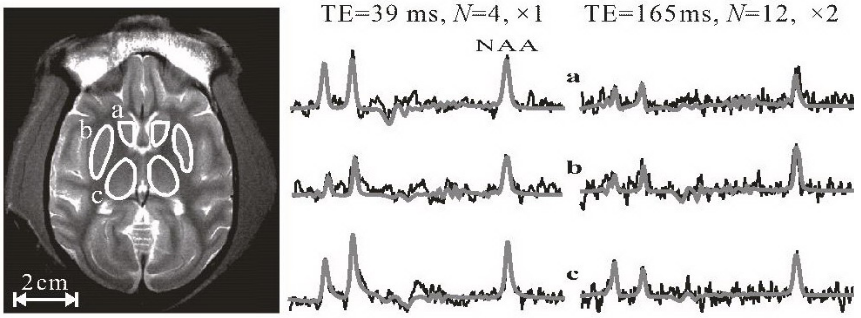

Fig 1. Left: Axial images showing the ROI where the voxels' T_2 were averaged: (**a**) caudate nucleus, (**b**) putamen, (**c**) thalamus. Right: Spectra at the two *TE*s from one 64 μL voxel within the each of the corresponding ROIs, superimposed with the FITT lineshapes used for T_2 estimation(grey lines).

		NAA T_2 (ms)	Cr T_2 (ms)	Cho T_2 (ms)
Gray matter (GM) structures:	Caudate	173±13	109±13	132±16
	Thalamus	183±14	118±4	131±8
	Putamen	174±12	116±6	122±10
	Cingulate gyrus	169±6	126±4	133±3
	GM structures Average	175±3	118±4	129±3
White matter (WM) structures:	Splenium of CC	180±3	112±4	133±8
	Centrum semiovale	167±4	119±6	122±5
	WM structures Average	173±6	116±4	127±6
Global WM+GM average		169±2.3	114±1.9	128±2.4

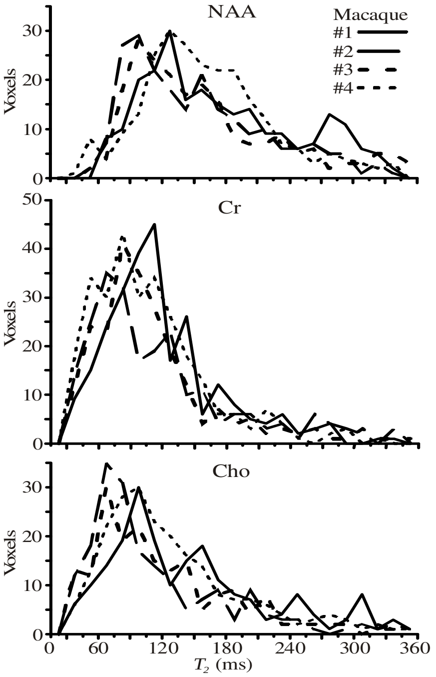

Fig 2 Histograms of the NAA, Cr and Cho T_2s from all voxels in the VOI for the 4 macaques.

Conclusion: Combining 3D 1H-MRSI with an optimized two-point acquisition protocol makes the most efficient use of ~4 hours to estimate regional brain-metabolites T_2 in the Rhesus macaque at spatial resolution proportional to analogous structures in the human counterpart. The study provides these regional T_2 values, in line with the inverse relationship with field strength and in good agreement with human in vivo values. These values and their variations between several WM and GM structures indicate that for the purposes of metabolic quantification use of one T_2 value for each metabolite is sufficient for T_2 weighting corrections for intermediate TE sequences at 7T.

References

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