BRAIN METABOLITES B1-CORRECTED PROTON T1 MAPPING IN THE RHESUS MACAQUE AT 3T

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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_1 weighting on the accuracy of metabolic quantification, we measured the B_1-corrected T_1s of NAA, Cho and Cr in several brain regions of five rhesus macaques at 3T with 3D MRSI at 180uL spatial resolution using a novel three-point protocol optimized for precision of T_1 per unit time.

Methods: Five healthy macaques were studied. All experiments were done in a 3T scanner (Siemens, Erlangen, Germany) using a transmit-receive knee coil. 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 three-point scheme that optimizes B_1 and T_1 precision by manipulating the number of averages: N_1, N_2, N_3 and nominal flip angles: α_1, α_2, α_3, at TR_1, TR_2 and TR_3 was used. This led to the following three-point protocol: TR_1=600 ms, α_1=85º, N_1=8; TR_2=1280 ms; α_2=40º, N_2=1; and TR_3=3600 ms, α_3=115º, N_3=2.

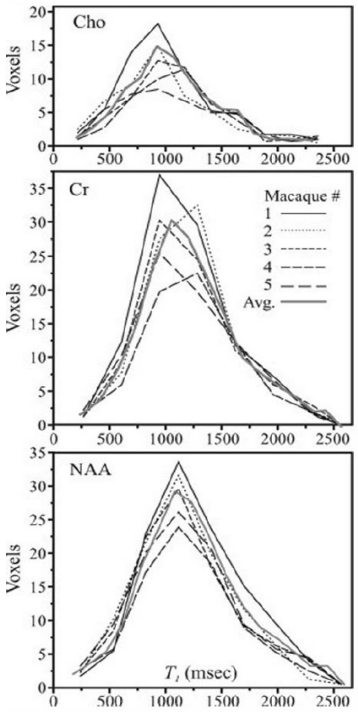

Fig 1. Cho, Cr and NAA B_1-corrected T_1s histograms from all 140 voxels in the VOI of each macaque (black lines), as well a normalized histogram for each metabolite formed from the 700 voxels in all the animals (thick solid gray line). Note the inter-animal histogram similarity reflected by the peak position and FWHM for each metabolite and proximity to the "global" histogram from all, suggesting that these distributions are characteristic

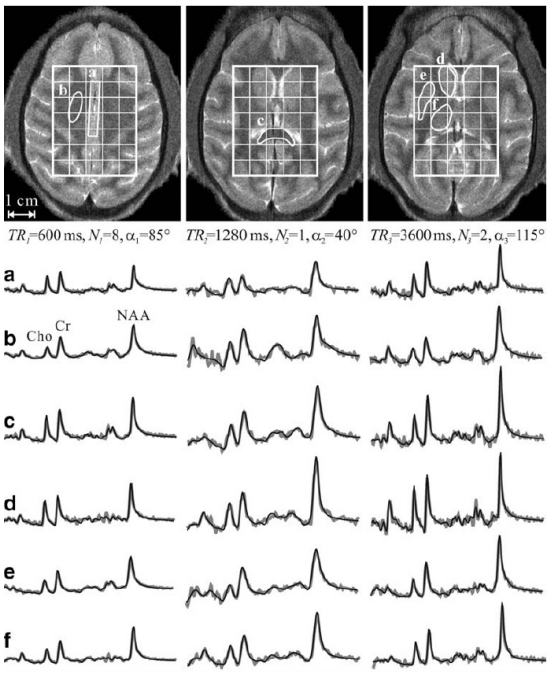

Fig 2. Top: Axial MRI showing the 3×4.2 cm^2 VOI (thick white frame), CSI grid (thin white lines) and the brain regions where the voxels' T_1 were averaged: a-cingulate gyrus, d-caudate head, e-lentiform nucleus, f-thalamus in the GM; and b-centrum semiovale and c-splenium of the corpus callosum in WM. Bottom: Real part of the average spectra from each region and time point (black lines) overlaid with the model lineshapes (gray lines).

Metabolite	SNR			Inter-animal T_1 CV
	TR1	TR2	TR3	
NAA	31.7±10.1	21.7±7.0	26.4±8.8	3.5%
Cr	22.7±9.3	14.9±5.6	23.7±8.9	1.9%
Cho	14.1±6.8	13.8±6.8	20.9±9.7	4.4%

Table 1. The SNR of 700 voxels (mean±sd) of NAA, Cr and Cho at the 3 different TRs, and the inter-animal CV of the 3 metabolites.

		T_1 (ms)		
		NAA	**Cr**	**Cho**
GM	Caudate head	1376±61	1370±75	1072±121
	Thalamus	1330±78	1272±30	1099±106
	Lentiform nucleus	1212±70	1293±40	1198±42
	Cingulate gyrus	1413±89	1123±99	1154±75
	Mean±SEM	**1335±25**	**1263±22**	**1147±68**
WM	Splenium of the CC	1222±33	1176±55	1132±27
	Centrum semiovale	1154±51	1224±49	1032±76
	Mean±SEM	**1166±19**	**1214±41**	**1047±44**

Table 2. Mean±SEM values of proton T_1 relaxation of the NAA, Cr and Cho in the various GM and WM brain regions and structures of the rhesus macaque brain shown in Fig. 2.

Results: The SNRs from the 700 voxels and the inter-animal coefficient of variation in the five macaques are compiled in Table 1. The B_1-corrected T_1 histograms for each metabolite in the 140 voxels from every monkey together with a normalized histogram for each metabolite from the 700 voxels in all the animals, are shown in Fig. 1. Their distributions exhibit a gratifying similarity in: (a) peak position, also reflected by less than 5% inter-animal CV (see Table 1); and (b) width, characterize by the CV of histograms FWHM: NAA=11%, Cr=16% and Cho=19%. The mean±standard error (SEM) of the 140 T_1s in each of the 5 animals were: NAA=1232±44, Cr=1238±23 and Cho=1107±56 ms. Regional T_1s were estimated in the six gray and white matter brain regions shown in Fig. 2 with their average spectra at each TR overlaid with the SITools-FITT model functions. Each was outlined on the axial MRI and our software averaged the T_1s in all voxels that fell entirely or partially within. The regional values compiled in Table 2 show GM T_1s to be 5 - 10% longer than WM, although this difference was statistically significant only for the NAA.

Conclusion: Combining 3D ^{1}H-MRS with an optimized acquisition protocol makes for efficient use of four hours to map regional brain metabolites' T_1s. The results reveal that these T_1s are sufficiently reproducible and that their variations among WM and GM structures in healthy rhesus macaques are small enough that use of a global average T_1 for each metabolite is justifiable for metabolic quantification. The overlap of the T_1 histograms of these metabolites indicates that they are probably characteristic to within very few percent making individual measurements unnecessary.

References

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