Metabolite T_1 Differs Within and Between Regions of Normal Human Brain

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Introduction

As MRS is conducted at shorter TRs, the T_1 weighting of the spectrum increases. Previous relaxation studies have not found metabolite T_1 differences within or between tissues when fitting recovery curves composed of signal from 2 TRs (Kreis) or 3 TRs (Frahm). In this study, by contrast, we collected signal at 7 TRs. Our goals are:

1. To assess the precision of T_1 estimates from saturation recovery curves comprised on varying number of TR points.
2. To accurately measure metabolite T_1 in occipital gray, parietal white and frontal white matter.
3. To determine whether metabolite T_1 times vary regionally.
4. To determine whether metabolite T_1 times in the same region are different from each other.
5. To compare metabolite T_1 times in solution and *in vivo*.

Methods and Analysis

Twenty-six healthy volunteers underwent MRS exams using a GE Signa Horizon Echospeed (1.5T). After axial and sagittal PD localizing scans, a 19.3*19.3*20 mm^3 voxel was positioned in occipital grey (n=10), parietal white (n=10) or frontal white (n=10). Seven spectra were acquired using the STEAM sequence with TE = 30ms, TM = 13.7ms and the following parameters:

TR (s)	0.547	0.734	1.200	1.500	2.500	3.500	5.000
NPTS	512	1024	2048	2048	2048	2048	2048
NAV	512	512	256	256	128	128	96

Table 1: STEAM parameters used in collecting data. NPTS is number of complex points, NAV is number of averages.

All spectra were analysed with LCModel (Provencher) using the TE30/TM13.7/TR5000 STEAM basis template collected previously on the same scanner. Peak areas were measured for choline (Cho), N-acetyl-aspartate (NAA), glutamine+glutamate (Glx), myo-inositol (Ins) and the CH_2 (Cr) and CH_3 (Cre) peaks of creatine. (Note Glx is measured since glutamine and glutamate are indistinguishable.) A monoexponential T_1 was fit to the peak areas at each TR for each metabolite:

$$S(TR) = S_o \cdot (1 - e^{-TR/T1}) \cdot e^{-TM/T1},$$

where *S(TR)* is the signal area at TR and S_o is the T_1 corrected signal area.

The T_1 mean and standard deviation for each metabolite was calculated in each tissue. The paired Student's t test was used to determine if the T_1 times for each metabolite were different from the other metabolites in each tissue. The non-paired t test was used to calculate whether the T_1 value differed between tissues for a given metabolite.

Phantoms of each chemical were scanned at 37°C and pH 7.2. Parameters were the same as listed in Table 1 with one quarter of the averages. The T_1 of each chemical was calculated.

To determine the percentage of pure white or gray matter in each tissue, a histogram analysis was performed on the axial PD images of the voxel.

Simulations were conducted to determine the variance of T_1 for saturation recovery curves with two TRs (1.5s and 5s), three TRs (1.5s, 3.0s, 6.0s) and seven TRs (Table 1). A synthetic saturation recovery curve with T_1=1.0s was corrupted with 5, 10, 15 and 20% noise. For each noise level, 1000 saturation recovery curves were T_1 fitted and the mean and standard deviation of the T_1 was calculated.

Results

The mean T_1 and standard errors are listed in Table 2 for each tissue and phantoms. The percentage written under the tissue name records the average purity of the tissue.

In each tissue the T_1 times ascend in the following order: Ins < Cho < NAA < Cre. Paired t tests verify that ranking between the metabolites are statistically significant. For example, in occipital gray matter, Ins was significantly lower than NAA and Cre ($p<0.004$ in both cases) and Cho was lower than NAA and Cre ($p<0.002$ and $p<0.0002$, respectively).

Between tissues, T_1 ascended from occipital gray to parietal white to frontal white. For example, unequal variance t tests determined that the T_1 of choline was lower in occipital than parietal ($p<0.003$), lower in parietal compared to frontal ($p<0.01$) and lower in occipital compared to frontal ($p<0.00005$).

The metabolites T_1 times in phantoms were longer than those *in vivo*. As well, within phantoms the ascending order of T_1 was: Ins < NAA < Cre < Cho.

	Occipital 78 ± 10 %	Parietal 96 ± 2 %	Frontal 87 ± 2 %	Phantom
Ins	0.86 (0.11)	1.12 (0.19)		1.47
Cho	1.01 (0.05)	1.23 (0.04)	1.42 (0.07)	2.71
NAA	1.27 (0.07)	1.31 (0.05)	1.55 (0.11)	1.57
Cre	1.39 (0.05)	1.51 (0.06)	1.77 (0.08)	2.25
Cr	0.84 (0.09)	1.20 (0.15)		1.58
Glx	0.86 (0.09)	1.25 (0.10)		1.62

Table 2: T_1 times in seconds for each metabolite in each tissue and phantoms. The percentage under the tissue name indicates the purity.

Simulations demonstrated that the standard deviation of the T_1 estimate doubles with each additional 5% of noise. Furthermore, the standard deviation of the 3TR data was roughly double that of the 7TR data, and the 2TR was larger still.

Discussion

The T_1 trend seen in phantoms is consistent with a simple physical model where T_1 is proportional to 1/molecular weight (Fig. 1).

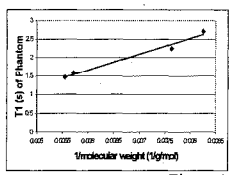

Figure 1

Figure 2 shows the consequence of omitting T_1 corrections within and between brain regions. T_1 weighted signal area ratios for each metabolite to Cre in occipital gray are plotted for metabolites in each tissue assuming TR=1s and unit concentration for all metabolites. The bars in the graph (for each region) are in the following order: Cre, NAA, Cho, Ins. Within each tissue, metabolite ratios are overestimated compared to Cre. Between regions, metabolite ratios are underestimated compared to occipital gray.

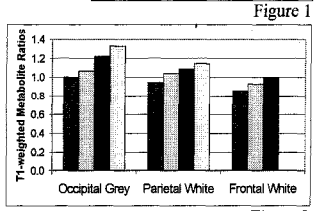

Figure 2

References

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