Metabolite T₂ Relaxation Times of Coupled ¹H Spin Systems in Human Brain at 7T

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Introduction

MR spectroscopy (MRS) benefits from the higher sensitivity and increased spectral resolution at 7T compared to lower B_0 fields (1,2). However, accurate metabolite quantification, especially from datasets acquired at moderate to longer echo times ($TE \ge 20$ ms) or based on specific editing methods, often requires knowledge of the T_2 relaxation times of metabolites. So far, in human brain at 7T only T_2 s of singlets, but not of coupled resonances have been reported (3). Thus, the aim of this study was to determine the apparent T_2 relaxation times for 1H human brain metabolites including coupled spin systems at 7T using the spin echo full intensity acquired localized (SPECIAL) MRS technique (4).

Methods

Scans were performed on a 7T head only system (Siemens Medical Solutions, Erlangen, Germany) using a shielded quadrature transmit/receive surface RF coil. First- and second-order shims were adjusted using FAST(EST)MAP (5). ¹H single volume spectra were acquired for N = 6 volunteers using the SPECIAL technique with the following scan parameters: VOI = 23x23x23 mm³, TR =

4000 ms, $T_{acq} = 512$ ms, number of averages = 64, and TE = 6, 20, 40, 60, 80, 110, 130, 150, 170, 200, and

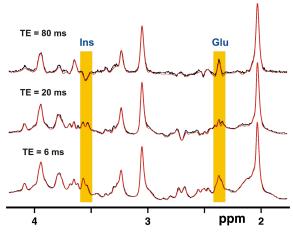


Fig. 1. ¹H spectra from the occipital lobe of a human volunteer acquired with the SPECIAL sequence (black lines) together with their corresponding fits from LCModel (overlayed in red) at three different TEs. J-Modulation of selected coupled spin resonances is highlighted. Note the very good agreement between the in vivo data and the respective fits.

ms. Metabolite concentrations were determined using LCModel (6) with simulated TE-specific basis sets, and resulting T₂ fits were realized in Matlab.

Results

Localized shimming resulted in water linewidths of 12.6 ± 0.9 Hz, and metabolite linewidths were estimated as 9.7 ± 1.7 Hz. Excellent mono-exponential T₂ fits were obtained for several metabolites due to the high quality of the acquired spectra. In addition, spectral modulations in the in vivo data were well described by the simulated basis sets (Fig. 1). The resulting T_2 values in compounds showing singlet resonances were in the range of 73 to 183 ms, while the T₂s of coupled metabolites

ranged from 23 to 227 ms (Table 1). The T_2 of macromolecules was found to be 26 ± 0.3 ms ($R^2 = 0.990$).

Discussion

The high signal-to-noise ratio (SNR) of the optimized acquisition methodology and the adequate modeling of J-modulation effects using simulated basis sets allowed the determination of apparent T₂ relaxation times for cerebral metabolites at 7T. T₂ values for singlets obtained with SPECIAL agreed very well with those found in previous reports (3) using another Hahn spin-echo based sequence. To the best of our knowledge, T₂s of

coupled resonances at this field strength are reported for the first time in this study. It is concluded that determination of T_2 s for coupled metabolites is feasible paving the way to improved quantification in MRS studies at 7T and to investigate physiological and pathological processes, since the T_2 of metabolites is sensitive to the cell microenvironment.

References and Acknowledgements (1) R. Mekle et al., MRM, 61(6), 1279-85, 2009; (2) I. Tkac et al., MRM, 62(4), 868-79, 2009; (3) S. Michaeli et al., MRM, 47(4), 629-633, 2002; (4) V. Mlynarik et al., MRM, 56(5), 965-970, 2006; (5) R. Gruetter, MRM, 43(2), 319-323. 2000; (6) S.W. Provencher et al., MRM, 30(6), 672-679, 1993.

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Table 1. Mean values plus standard deviations for metabolite T_2 relaxation times in human brain at 7T together with the mean determination coefficient (R^2) values of the corresponding fits for N = 6. CH_3 , CH_2 , and CH refer to the different groups of a compound.

Metabolite	T_2	\mathbb{R}^2
	(ms)	
Cr+PCr(CH ₃)	112 ± 16	0.997
Cr+PCr(CH ₂)	85 ± 13	0.994
PCr(CH ₂)	122 ± 44	0.937
Cr(CH ₂)	73 ± 14	0.988
NAA(CH ₃)	183 ± 30	0.993
NAA(CH,CH ₂)	68 ± 18	0.947
NAAG	66 ± 24	0.897
NAA+NAAG	161 ± 38	0.994
GPC+PCho	227 ± 112	0.827
Ins	86 ± 19	0.976
Asp	33 ± 3	0.909
Glu	64 ± 2	0.854
GSH	152 ± 36	0.867
GPC	23 ± 11	0.853
Ins+Gly	117 ± 27	0.963
Glu+Gln	57 ± 4	0.912