Measurements of T_2 Relaxation of *J*-coupled Metabolites in the Human Brain at 4 Tesla

D. K. Deelchand[1], M. Marjanska[1], K. Ugurbil[1], and P-G. Henry[1]

[1]Department of Radiology, Center for Magnetic Resonance Research, Minneapolis, MN, United States

Introduction: Quantification of ^{1}H spectra often requires knowledge of T_1 and T_2 relaxation times to correct for signal losses due to relaxation and saturation. While most measurements of T_2 of brain metabolites in humans have reported values for singlet resonances, there are few T_2 values available for *J*-coupled spin systems, e.g. glutamate. For T_2 measurements of *J*-coupled metabolites, the signal changes due to *J*-modulation can be taken into account by simulating the spectral patterns at each echo time. Moreover within the same molecule, the T_2 for non-similar protons can be different as was recently reported at 1.5 T [1]; this can be resolved by using separate basis spectrum for each resonance (e.g. two basis spectra for NAA: singlet and multiplet). This work demonstrates the use of LCModel analysis to quantify ^{1}H LASER [2] spectra in the human brain at 4 T using simulated basis set to determine the T_2 relaxation time of *J*-coupled metabolites.

Methods: Six healthy subjects were examined at 4 T. Localized ^{1}H NMR spectra were measured from a 27 ml VOI in the visual cortex using LASER sequence. The acquired spectra were analyzed using LCModel, whereby basis spectrum for each metabolite was simulated using home-written programs [3] based on product operator formalism and using measured or published values of chemical shifts and *J*-couplings [4]. For the analysis, two basis sets were utilized: a standard set and a set where the singlet and multiplet of NAA and the CH_2 and CH_3 groups of total creatine (tCr = Cr + PCr) were separated. For T_2 measurements, spectra were acquired at seven different echo-times (TE = 53, 75, 100, 150, 200, 300 and 400 ms). The data were fitted using a mono-exponential decaying function to determine the T_2 values.

Table 1: Measured T_2 (mean ± SD)

Metabolites	T_2/ms
NAA singlet	277 ± 8
NAA multiplet	194 ± 29
Glutamate	127 ± 26
Myo-Inositol	134 ± 31
tCr CH_3	170 ± 9
tCr CH_2	110 ± 7

Results: The simulated spectral pattern of NAA multiplet (CH_2 group) at different echo times is consistent with the measured *in vivo* spectra in the human brain (Fig. 1). Using the standard basis set for LCModel analysis, residues were found for tCr and NAA multiplet resonances (data not shown), and also there was an overestimate in NAAG peak at long TE (≥100 ms) that compensates for the discrepancy between NAA single and NAA multiplet. However using the basis set with separate spectra, a better fit was obtained with minimal signal present in the residuals, and the relative amplitudes of NAA and NAAG singlets were as expected based on literature values (not shown). The individual T_2 exponential fits for NAA multiplet and glutamate were nearly identical in all subjects (Fig. 2), and T_2 for NAA multiplet was 194 ± 29 ms (~30% shorter than the T_2 of NAA singlet). Smaller but similar T_2 was observed for glutamate and *myo*-inositol (Table 1). For total creatine, the protons in the CH_3 group had a longer T_2 compared to the CH_2 group.

Discussion and Conclusion: The T_2 of coupled spin systems was successfully measured in NAA, glutamate and *myo*-inositol since the relaxation mechanism in LASER minimizes J-evolution. Since T_1 and also T_2 relaxation times depend on the sequence utilized, the T_2 values for singlet reported in this study using LASER were different from published values measured at the same field strength [5-6]. To account for different relaxation times of protons within the same molecule, separate basis set can be utilized as demonstrated in this study or the prior knowledge about relaxation can be included when simulating the basis spectra. In conclusion, this work demonstrates the possibility to measure the T_2 of *J*-coupled metabolites (NAA multiplet, glutamate and *myo*-inositol) in the human visual cortex using a simulated basis set, thus making it possible to determine the correction factors for quantitation of these metabolites in the brain when using the LASER sequence.

References: [1] Soher et al. MRM, 2005. [2] Garwood et al. JMR, 2001. [3] Henry et al. MRM, 2006. [4] Govindaraju et al. NMRB, 2000. [5] Posse et al. MRM, 1994. [6] Hetherington et al. MRM, 1994.

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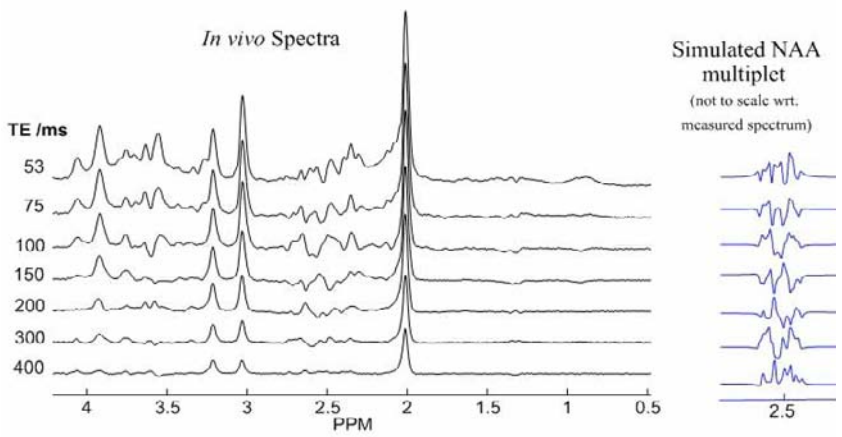

Fig. 1: ^{1}H LASER spectra acquired *in vivo* at different TEs from the human brain at 4 T and the simulated spectra of NAA multiplet.

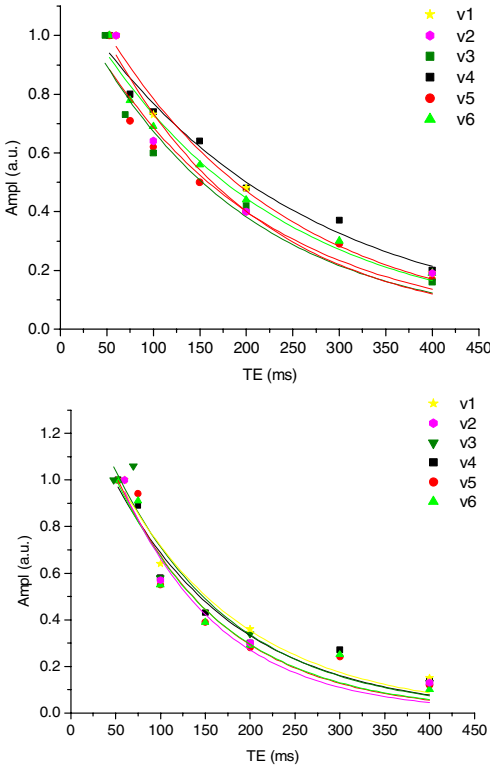

Fig. 2: Individual T_2 fits for NAA multiplet (*top*) and glutamate (*bottom*).