Proton T2 measurement and quantitation of coupled-spin metabolites in Human Brain by PRESS at 3T in vivo

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INTRODUCTION

Relaxation times are important for quantitation of metabolite concentrations, especially in long-TE MRS methods [1]. While the signal from uncoupled spins is governed by the relaxation only, the spectral pattern and signal intensity of coupled resonances are also determined by the scalar coupling effects. Therefore, the J evolution effects have to be accounted for in measuring the transverse relaxation times of coupled resonances. Here, we report measurement of coupled-spin metabolites by point-resolved spectroscopy (PRESS) using optimized echo times. Preliminary *in vivo* results from the human brain are presented.

METHODS

A PRESS sequence was employed to measure the apparent transverse relaxation times (T_2') of brain metabolites at 3T. The first and second subecho times were optimized, with computer simulations, for glutamate (Glu) and glutamine (Gln) separation. Four pairs of subecho times were selected; (TE_1, TE_2) = (32, 22), (32, 80), (32, 214), and (36, 338) ms. The (32, 22) ms pair was the shortest possible echo times for given RF and gradient pulses. *In vivo* experiments were conducted on a whole-body 3T scanner (Philips Medical Systems). A body coil was used for RF transmission and an 8-channel phased-array coil for reception. Data were acquired in the steady-state conditions (TR = 3 – 3.4 s). Number of averages was 16, 32, 64, and 128 for the four TEs, respectively. LCModel software [2] was employed to analyze the *in vivo* data, using numerically calculated model spectra as basis functions.

RESULTS AND DISCUSSION

Figure 1 shows simulated spectra of Glu, Gln, GSH (glutathione), NAA, and Cr (creatine) at the four selected TE_1-TE_2 pairs. The C4-proton multiplets of Glu and Gln are well preserved at the echo times. Figure 2 presents *in vivo* spectra from the human occipital cortex, obtained with adjusted TR to maintain constant initial longitudinal magnetization prior to the 90° excitation RF pulse for various echo times and with TR = 8 s to obtain fully-recovered signal strengths (at TE = TE_1+TE_2 = 112 ms). The spectra are well reproduced by the fits. The spectral pattern in 2 – 3 ppm is in good agreement with Fig. 1. Myo-inositol (m-Ins) is well differentiated from neighboring resonances in the spectra at TE = 112 and 246. The lactate (Lac) 1.31 ppm resonance appears inverted at TE = 112 ms, but positive at TE = 246 ms. In T_2 fitting with a monoexponential function, the data at TE = 54 ms were excluded because of uncertainty of the fits due to the effects of macromolecule signals. Figure 3 presents T_2 values of metabolites included in spectral fitting. The T_2's of Glu, Gln and m-Ins were estimated to be ~160 ms, in agreement with a prior study [3]. The estimated T_2's of Cr, NAA, and GPCPC agree with published values [4]. The metabolite concentrations were estimated such a way that the fully-recovered signals at TE = 112 ms, obtained with TR = 8 s, were extrapolated to zero TE using the T_2 values from the fitting, as shown in Fig. 4. The concentration ratio with respect to Cr was estimated to be 8.2±1.3, 4.6±0.6, 9.5±0.8, and 1.1±0.1 (mean±SD, N = 5) for Glu, m-Ins, NAA, and GPC+PC, respectively.

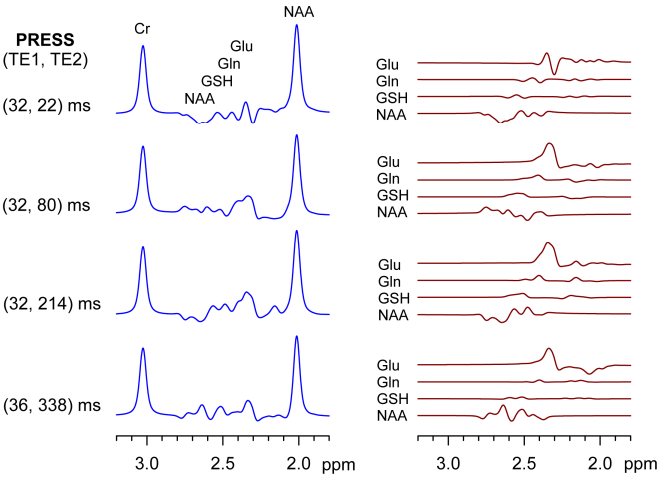

FIG. 1. Simulated spectra at four pairs of PRESS subecho times, at 3T, for Glu, Gln, GSH, NAA, and Cr at a concentration ratio of 10:3:2:10:8. Sum spectra are shown on the left and individual components on the right. Spectra are broadened to 6 Hz.

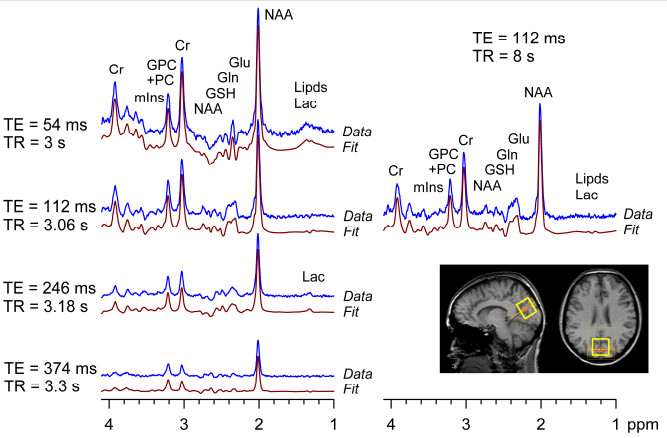

FIG. 2. *In vivo* spectra at 4 TEs, obtained with adjusted TR (left) and a spectrum at TE = 112 following a full recovery (TR = 8 s) (right) are shown together with LCModel fits. The voxel size was 25x30x30 mm^3.

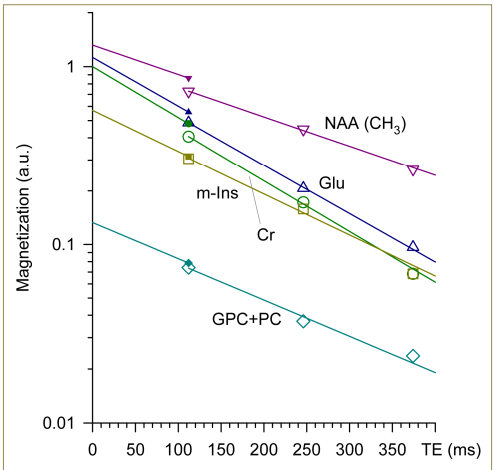

FIG. 4. Monoexponential regression for T_2 evaluation. With the resulting T_2 values, the magnetization values from the spectrum obtained with TR = 8 s (filled symbols) are extrapolated to zero TE, giving metabolite concentrations.

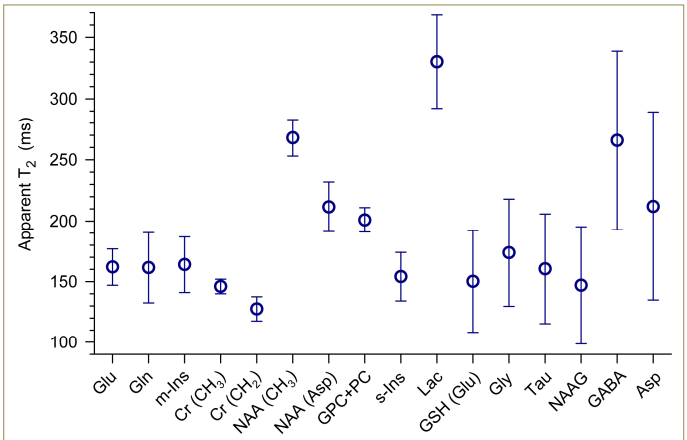

FIG. 3. Mean apparent T_2 of brain metabolites measured from the occipital cortex. Error bars represent standard deviation (N = 5).

REFERENCES

1. Schubert F et al. Neuroimage 2004;21:1762–1771. **2.** Provencher SW. Magn Reson Med 1993;30:672-679. **3.** Choi C. *et al*. ISMRM 2006. p. 3064. **4.** Mlynarik V *et al*. NMR Biomed 2001;14:325-331.