Measurement of Transverse Relaxation Times in Brain Tumors

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INTRODUCTION It is known that many neurological diseases change the inter/intra-cellular environment which affects the transverse relaxation times (T_2) of cellular metabolites [1]. Short T_2 may indicate increased restriction of molecular movement or increased amounts of paramagnetic species due to intratumoral microscopic hemorrhage whereas long T_2 may indicate that the molecules can move freely [1]. Thus these changes in T_2 may be a diagnostic marker for tumors. The present paper reports the T_2 of N-acetylaspartate + N-acetylaspartylglutamate (tNAA), creatine + phosphocreatine (tCr), glycerophosphorylcholine + phosphorylcholine (tCho) and water in tumors and in normal brain.

METHODS *In vivo* T_2 was measured in 9 glioma (low grade) patients using single voxel point resolved spectroscopy. All experiments were carried out on a 3T scanner (Philips Medical Systems Inc) using a body coil for RF transmission and an 8-channel phased-array coil for reception. Water-suppressed and unsuppressed water data was acquired from a FLAIR enhancing region and a normal appearing contralateral brain region at 8 echo times (TE = 58, 88, 118, 148, 178, 208, 238, 268 ms) from a 20x20x20 mm^3 voxel, using TR = 2 s, sweep width = 2500 Hz, number of sampling points = 2048 and number of averages = 16 for each TE. Water signal was suppressed using a four-pulse scheme. The total scan time for T_2 measurement was 5 minutes for each location. Residual water signal was removed using the HL-SVD filter of JMRUI [2]. Data was apodized with a 2-Hz exponential filter. Eddy current compensation and frequency drift corrections were performed using in-house Matlab programs. Metabolite signal estimates were calculated using LCModel software [3]. Spectral fitting was done using basis sets of 32 metabolites calculated using published chemical shift and J coupling constants [4] with volume localization RF and gradient pulses. The metabolite signal estimates were used to calculate the T_2 values using monoexponential nonlinear fitting. A two tailed unpaired t-test was performed to determine the differences between the estimated T_2 values in tumor and normal brain. Written informed consent was obtained prior to *in vivo* scans.

RESULTS AND DISCUSSION Figure 1 (**a**) and (**b**) show *in vivo* spectra, LCModel fits and residuals obtained from a FLAIR enhancing region and a contralateral normal brain region. The mean of the residuals for tumor and the normal brain spectra were close to zero (mean < 10^{-7}) and there is no variation across the ppm range. The spectra obtained from the tumor location shows elevated tCho and reduced tNAA, characteristic of tumors [5]. Figure 2 (**a**) and (**b**) show the monoexponential fittings for tNAA, tCr and tCho for the spectra in Figure 1. The T_2 of tNAA, tCr and tCho for the tumor location were 234 ms, 158 ms and 308 ms, respectively, whereas, for the contralateral normal brain location were 235 ms, 148 ms and 237 ms respectively. Signal decay vs TE were well represented by monoexponential fits, giving coefficients of determination (R^2) close to unity. The estimated T_2 values (mean ± SD) for the tumor location in the 9 glioma patients were tNAA = 295 ± 33 ms (mean R^2 = 0.89), tCr = 171 ± 19 ms (mean R^2 = 0.98), tCho 297 ± 50 ms (mean R^2 = 0.91) and water 135 ± 18 ms (mean R^2 = 0.99). In contralateral normal brain regions the estimated T_2 values were 294 ± 36 ms for tNAA (mean R^2 = 0.95), 152 ± 13 ms for tCr (mean R^2 = 0.97), 244 ± 22 ms for tCho (mean R^2 = 0.93) and 81 ± 7 ms for water (mean R^2 = 0.99) (Figure 3). The data with R^2 value < 0.7 were excluded from further analysis. The T_2 values of the metabolites in the normal brain are in agreement with previously published values [6]. Previous study at 1.5T reports T_2 of tNAA to be significantly different in tumors, whereas tCr and tCho were not significantly different [1]. In the present study we observed that the T_2 of tCr, tCho and water were significantly different between tumor and normal brain (p = 0.03, 0.015 and < 0.0001, respectively), however tNAA showed no significant difference (p = 0.97). These changes in T_2 may be potential diagnostic markers for tumors. In future studies the changes in T_2 for tCr, tCho and water should be considered during absolute quantification to avoid overestimation of these metabolites.

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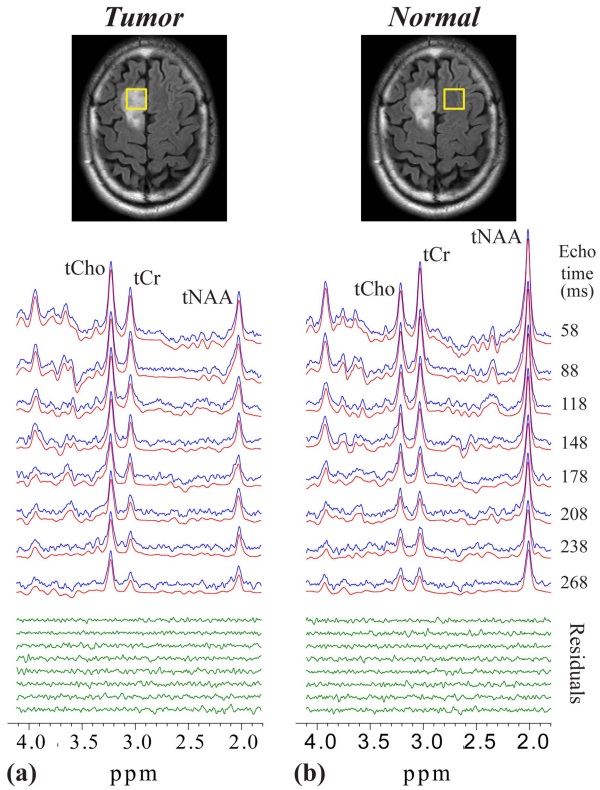

Fig. **1**: *Invivo* spectra (blue), LCModel fits (red) and residuals (green) at TE = 58, 88, 118, 148, 178, 208, 238, 268 ms from (**a**) a FLAIR enhancing region (tumor) and (**b**) the contralateral normal brain region of a glioma patient.

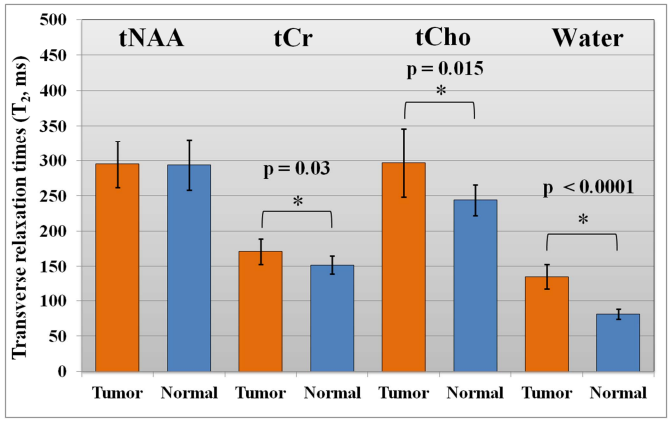

Fig. **3**: Relaxation times (T_2) of tNAA, tCr, tCho and water from tumor and contralateral normal brain regions in nine subjects with gliomas. tCr, tCho and water show significant difference in T_2 estimates. Error bars are the standard deviation.

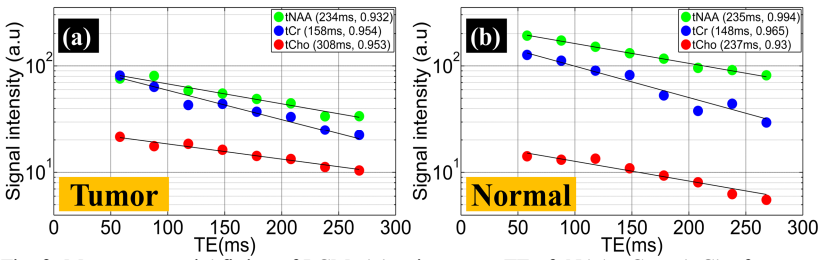

Fig. **2**: Monoexponential fitting of LCModel estimates vs TE of tNAA, tCr and tCho for tumor (**a**) and contralateral normal brain region (**b**) spectra from figure 1. The T_2 values and the coefficient of determination (R^2) are shown in the legend.