T1 and T2 Relaxation Time Measurements of Metabolites in Human Calf Muscle at 7 Tesla

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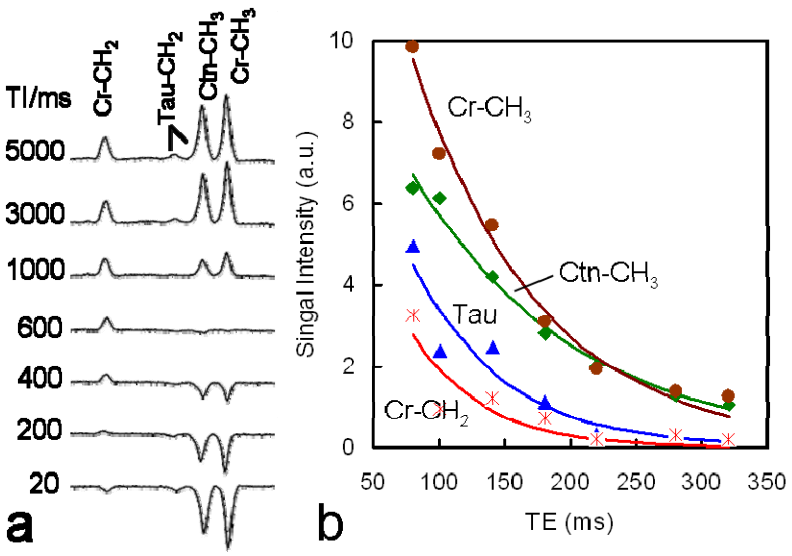
Introduction

High field ^{1}H MRS has the potential to become a valuable clinical tool for diagnosis of many metabolic diseases in muscle, brain, liver and other organs (1). Since metabolite concentrations are of interest and are typically determined by comparing signal intensities in spectra collected using a particular set of acquisition parameters, TR and TE, any attempt to quantitatively transform the NMR signal intensities into concentration requires the knowledge of T1 and T2 for the metabolites of interest. Accurate T1 and T2 values are not only necessary for optimizing sequence acquisition parameters (2), but also as fundamental NMR parameters in characterizing the tissue molecular environment of those metabolites (1,3). Though the T1 and T2 values can be found for common metabolites at low fields, very few data are available for metabolites at 7T. This study was designed to accurately measure T1 and T2 values for creatine, carnitine, taurine and water in skeletal muscle at 7 T.

Methods

Six healthy volunteers between the ages of 27-38 years participated in the study following guidelines established by our local IRB with informed written consent. To avoid possible exercise-associated physiological variations among the different subjects, all subjects rested 20 minutes prior to being placed in the magnet. Skeletal muscle MRS data were collected using a STEAM-based sequence and a customized 2-channel T/R coil on a Philips 7T MRI scanner (Achieva, Best, The Netherlands) with the leg positioned parallel to Bo. T_1 was measured by inversion-recovery using a TR of 8 s and TE of 120 ms, with a varying inversion delay time (TI) from 20 to 5000 ms. The apparent T_2 decay constant was evaluated using a constant TR of 10 s and TEs varying from 80 to 320 ms. Depending on signal intensity and scan time, 7 to 11 data points were typically collected for both T_1 and T_2. The signal decay (T_2) and recovery (T_1) curves for all resonances were fit to mono-exponential functions. A correction for the overlapping carnitine and the most upfield taurine CH_2 resonance was made by subtracting the lowfield taurine CH_2 resonance (3.41 ppm) from the carnitine signal (3.19 ppm) prior to curve fitting.



Results and Discussion

Figs. 1a and 1b show typical T_1 inversion-recovery plots for soleus muscle metabolite resonances in the 2.9 - 3.8 ppm region and representative T_2 decay curves for these same metabolites, respectively, collected at 7T using a STEAM sequence. The lines through the T_2 data reflect the mono-exponential fits. The apparent T_2 and T_1 values obtained for creatine (Cr), carnitine (Ctn), taurine (Tau) and water are summarized in Table 1. The T1 and T2 values for creatine represent total creatine (Cr and P-Cr). In comparison, a T_2 value of 114 ms was recently reported for Cr-CH_3 in the rhesus macaque brain as determined using PRESS and dual TE method at 7T (1) and 109 ms (PRESS) and 221 ms (CP-LASER) in human brain (4). The T_2 of brain water was reported to be 60 ms (PRESS, TE = 138.6 ms) and 88 ms (CP-LASER) at 7T (4). The shorter T2 values found here for muscle metabolites may reflect the larger anisotropy of muscle tissue.

Mol	δ/ppm	T1/s	T2/ms
Cr-CH_3	3.01	0.95 ± 0.05	91.6 ± 5.7
Cr-CH_2	3.91	0.76 ± 0.23	71.3 ± 3.4
Ctn	3.19	0.95 ± 0.04	95.6 ± 5.9
Tau	3.41	1.45 ± 0.16	72.0 ± 7.6
H_2O	4.67	1.44 ± 0.15	25.4 ± 3.1

Conclusions

T_1 and T_2 relaxation times were measured for several skeletal muscle metabolites in humans at 7T and compared with those available 7T data in brain (Cr-CH_3 and water). These data will be valuable as a reference for future comparisons under different physiological and disease conditions.

References

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