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Relaxation Times of Skeletal Muscle Metabolites at 7T

Ligong Wang, PhD^{1,*}, Nouha Salibi, PhD², Yan Wu, PhD¹, Mark E. Schweitzer, MD¹, and Ravinder R. Regatte, PhD¹

¹Center for Biomedical Imaging, Department of Radiology, New York University Langone Medical Center, New York, NY, USA

²Siemens Medical Solutions, Malvern, PA, USA

Abstract

Purpose—To demonstrate the feasibility of quantitatively evaluating and measuring T_1 and T_2 relaxation times of human tibialis anterior (TA) muscles metabolites *in vivo* at 7T and to compare these results with those of 3T.

Materials and Methods—A model lipid phantom (corn oil) and healthy volunteers ($n = 4$, mean $\pm$ SD age 35.6 ± 5.6 years) were scanned on 3T and 7T whole body MR scanners. A voxel of $10 \times 10 \times 10 \text{ mm}^3$ was positioned on the lipid phantom and right calf TA muscles using the single-voxel stimulated echo acquisition mode (STEAM) pulse sequence. All magnetic resonance spectroscopy (MRS) data were processed with Java-based Magnetic Resonance User Interface (JMRUI) using Hankel Lanczos Singular Value Decomposition (HLSVD) filtering to remove the residual water signal.

Results— T_1 shows a steady increase while T_2 shows a slight decrease with B_0 and the spectra show larger spectral resolution at 7T than at 3T in the lipid phantom. T_1 values of all the metabolites are higher while T_2 values are slightly lower at 7T than those of 3T compared to reported results in TA. The maximum percentage of increase in T_1 is about ~488%, the maximum percentage of decrease in T_2 is about ~65%.

Conclusion—The preliminary results can potentially be used for calculating relaxation correction factors required for absolute quantitation of skeletal muscle metabolite concentrations and for further protocol and sequence optimization.

Keywords

relaxation times; 7T; nuclear magnetic resonance spectroscopy; skeletal muscle

INTRODUCTION

Proton Magnetic Resonance spectroscopy (^1H -MRS) is a powerful noninvasive and nondestructive chemical assessment tool for the investigation of biochemistry in various tissues such as for studying the marrow of vertebral bodies (1), evaluating the metabolites in gliomas and the biochemical profiles of human brain tumors (2-4), and perhaps most importantly in the musculoskeletal system, investigating the lipid metabolism of human skeletal muscles (5-20). The trend in musculoskeletal MR, somewhat delayed when compared to neuroimaging, is to move beyond morphologic imaging into physiologic imaging, and MRS provides this type of information in terms of providing insight into the

* For correspondence: Center for Biomedical Imaging Department of Radiology New York University Langone Medical Center 660 1st Ave, 4th Floor, New York, NY 10016, USA Phone: (212) 263-4827 Fax: (212) 263-4830 Ligong.Wang@nyumc.org .

specifics of tissues' chemical composition. Depending on the evaluated nucleus, MRS allows the observation of high-energy phosphates (^{31}P MRS), muscular glycogen (^{13}C MRS), and intramyocellular lipids (^1H MRS) (7,11,17).

Previous work (6) has demonstrated good reproducibility of measurements for both single-voxel and multi-voxel ^1H MRS measurements of intramyocellular lipid (IMCL) when performed in human tibialis anterior (TA) muscle *in vivo*. Although the multi-voxel ^1H MRS measurement method was found to offer greater flexibility and reliability, and higher sensitivity to IMCL differences, single voxel proton magnetic resonance spectroscopy (SV- ^1H -MRS) had the advantages of shorter scan time, wider availability, and greater ease of implementation, making it an attractive alternative to investigate the chemical composition variation in human skeletal muscles. Furthermore, it is easier to accurately position and shim on a small single voxel compared to the larger volume of interest (VOI) needed for multi-voxel MRS. Other studies (7,21,22) have found that proton MR spectroscopic imaging of human muscles containing fibers parallel to the external static magnetic field showed more separation of the observed metabolite signals, which also scaled with the volume of the muscular tissue. Therefore, precise anatomical localization of the voxel is mandatory for ^1H -MRS of muscle, especially for the measurement of those orientation-dependent features of the muscle spectrum (7).

SV- ^1H -MRS of human skeletal muscle at ultra high fields (UHF) can provide accurate quantitation of muscular metabolite concentration due to improved spectral resolution and high signal to noise ratio (2). Quantitative evaluation of relaxation times is extremely important for accurately quantifying metabolite concentration, optimizing measurement protocols in MR spectroscopy, and in quantitative spectroscopic imaging (5).

Although previous studies have measured ^1H relaxation times of skeletal muscle metabolites mostly at clinical field strengths (5-9,18,19), to the best of our knowledge, there have been no quantitative measurements of T_1 and T_2 relaxation times of human skeletal muscle *in vivo* metabolites performed at UHF (7T) in the literature. Therefore, the objective of the present study was to demonstrate the feasibility of quantitatively measuring and evaluating T_1 and T_2 relaxation times of *in vivo* human tibialis anterior muscles metabolites at 7T.

MATERIALS AND METHODS

Model Lipid Phantom

The *in vitro* experiment used the corn oil as model lipid phantom.

Human Subjects

The *in vivo* experiment included healthy human subjects ($n = 4$, mean $\pm$ SD age 35.6 ± 5.6 years, three males and one female). Informed consent was obtained from all the subjects, and the local institutional review board (IRB) approved the MR imaging and the spectroscopy protocols.

Imaging Hardware

All the spectroscopy experiments were performed on 3.0T and 7.0T whole body MRI/MRS scanners (MAGNETOM Trio and MAGNETOM 7T, Siemens Medical Solutions, Erlangen, Germany) with multinuclear capabilities and actively shielded (3T) and un-shielded (7T) gradients (45 mT/m for z orientation; 40 mT/m for x, y orientations; maximum slew rate: 200 mT/m/ms). An 18-cm inner-diameter quadrature birdcage knee RF coil (In Vivo Corp., Gainesville, FL) was employed for all the imaging measurements.

MR Imaging and Spectroscopy

Model lipid phantom and tibialis anterior (TA) muscle of human subjects were scanned on both the 3T and 7T MR scanners. Subjects were positioned supine with the feet first inside the magnet bore. The right calf was placed inside the coil and immobilized with firm padding, with the long axis of the tibia aligned with the orientation of the B_0 field. The left leg was supported outside the coil. After localizer images were acquired in the axial, sagittal, and coronal planes, a voxel of $10 \times 10 \times 10 \text{ mm}^3$ was positioned in the oil phantom and right calf TA muscles (Fig.2) for T_1 and T_2 measurements using the single-voxel stimulated echo acquisition mode (STEAM) pulse sequence.

For a given T_1 and T_2 measurement a series of water-suppressed spectra were acquired after automated shimming, which was followed by manual optimization of the shims. At 3T, for T_1 measurement of the lipid phantom the following parameters were utilized: mixing time (TM) = 10 ms; Averages = 16; BW = 2000 Hz; TE = 20ms; TR = 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.5, 2 s; for T_2 measurements: TM = 20 ms; Averages = 16; BW = 2000 Hz; TR = 6 s; TE = 25, 50, 75, 100, 150, 200, 250, 300 ms.

At 7T, for T_1 measurement of lipid phantom the following parameters were utilized: TM = 10 ms; Averages = 4; BW = 4000 Hz; TE = 10 ms; TR = 0.5, 1, 2, 3, 4, 5, 6, 7, 8, 10 s; for T_2 measurement, TM = 10 ms; Averages = 4; BW = 4000 Hz; TR = 7 s; TE = 15, 25, 35, 45, 55, 75, 100, 150, 200 ms.

At 3T, for T_1 measurement of human TA muscles the following parameters were utilized: TM = 10 ms; Averages = 16; BW = 2000 Hz; TE = 20ms; TR = 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.5, 2 s; for T_2 measurement, TM = 10 ms; Averages = 16; BW = 2000 Hz; TR = 6 s; TE = 25, 50, 75, 100, 150, 200, 250, 300 ms.

At 7T, for T_1 measurement of human TA muscles the following parameters were utilized: TM = 10 ms; Averages = 16; BW = 6000 Hz; TE = 10 ms; TR = 0.5, 1, 2, 3, 4, 5, 6, 7 s; for T_2 measurement, TM = 10 ms; Averages = 16; BW = 6000 Hz; TR = 6 s; TE = 25, 35, 45, 55, 75, 100, 150, 200 ms.

Spectral Fitting and Data Processing

All MRS data were exported and processed on an offline computer using Java-based Magnetic Resonance User Interface (JMRUI) software package based on the Advanced Method for Accurate, Robust, and Efficient Spectral (AMARES) fitting algorithm (18,23,24). Hankel Lanczos Singular Value Decomposition (HLSVD) filtering was used to remove the residual water peak (25). For the AMARES fitting procedure, the data were zero-filled to 2048, six peaks including the methyl (CH_3), methylene protons (CH_2)_n, Creatine (Cr), and trimethylamines (TMA) from IMCL and EMCL were described with the assumption of Gaussian line shapes. These peaks were manually selected for T_1 and T_2 calculation. The related damping factor relationships were used based on the criteria previously set in ref. (25).

RESULTS

Representative stacked T_1 (variable TR), T_2 (variable TE) spectra recorded from the lipid phantom and the TA of a healthy male volunteer at 3T and 7T are depicted in Fig.1 and Fig. 2, respectively. Fig. 3 shows typical 3T and 7T localized 1D-MR ^1H spectra recorded from T_2 series of the TA muscle of a 37-year-old healthy subject (TE = 50 ms), and the MR spectra show the fitted peaks with JMRUI and residuals at 3T and 7T, respectively. The top, the middle, and the bottom row of Fig. 3 (a) and (b) show the traces of the residue, the individual components, and the actual acquired spectrum at 3T and 7T, respectively. In the

lipid phantom, the T_1 shows a steady increase while T_2 shows a relatively apparent decrease with the increase in B_0 (Table 1 and Table 2). The T_1 values at 3T are in the range between 271 ± 14 ms and 702 ± 20 ms with the highest value of $-\text{CH}_3$ at 0.9 ppm and the lowest value of $=\text{CH}-\text{CH}_2-\text{CH}=\text{}$ at 2.79 ppm. The T_1 values at 7T are in the range between 356 ± 40 ms and 1221 ± 80 ms with the highest value of $-\text{CH}_3$ at 0.9 ppm and the lowest value of $=\text{CH}-\text{CH}_2-\text{CH}=\text{}$ at 2.79 ppm (Table 1). The T_2 values at 3T are in the range between 46 ± 4 ms and 182 ± 21 ms with the highest value of $-\text{CH}_3$ at 0.9 ppm and the lowest value of $\text{CH}_2-\text{CH}=\text{CH}-\text{CH}_2$ at 2.2 ppm. In contrast, the T_2 values at 7T are in the range between 29 ± 2 ms and 92 ± 13 ms with the highest value of $-\text{CH}=\text{CH}-$ at 5.4 ppm and the lowest value of $\text{CH}_2-\text{CH}=\text{CH}-\text{CH}_2$ at 2.2 ppm (Table 2).

Other T_1 values are also higher at 7T than at 3T, while corresponding T_2 values are apparently lower at 7T than that of 3T. At 3T, the T_1 values of $-\text{CH}_3$, $(\text{CH}_2)_n$, $\text{CH}_2-\text{CH}=\text{CH}-\text{CH}_2$, $=\text{COO}-\text{CH}_2-\text{CH}_2$, $=\text{CH}-\text{CH}_2-\text{CH}=\text{}$, and $-\text{CH}=\text{CH}-$ for lipid phantom are 702 ± 20 ms, 356 ± 10 ms, 274 ± 11 ms, 440 ± 160 ms, 271 ± 14 ms, and 537 ± 14 ms, respectively, whereas the T_1 values of the corresponding metabolites at 7T are 1221 ± 80 ms, 896 ± 270 ms, 499 ± 20 ms, 514 ± 20 ms, 356 ± 40 ms, and 928 ± 140 ms, respectively (Table 1). At 3T, the T_2 values of $-\text{CH}_3$, $(\text{CH}_2)_n$, $\text{CH}_2-\text{CH}=\text{CH}-\text{CH}_2$, $=\text{COO}-\text{CH}_2-\text{CH}_2$, $=\text{CH}-\text{CH}_2-\text{CH}=\text{}$, and $-\text{CH}=\text{CH}-$ for lipid phantom are 182 ± 21 ms, 91 ± 6 ms, 46 ± 4 ms, 49 ± 8 ms, 56 ± 3 ms, and 119 ± 8 ms, respectively, whereas the T_2 values of the corresponding metabolites at 7T are 54 ± 7 ms, 55 ± 6 ms, 29 ± 2 ms, 36 ± 8 ms, 44 ± 4 ms, and 92 ± 13 ms, respectively (Table 2). The maximum rate of change for T_1 increase with the increase of B_0 is $\sim 152\%$, and the minimum rate of change for T_1 increase with the increase of B_0 is $\sim 17\%$ (Table 1). The maximum rate of change for T_2 decrease with the increase of B_0 is $\sim 70\%$, and the minimum rate of change for T_2 decrease with the increase of B_0 is $\sim 21\%$ (Table 2). The spectra from lipid phantom at 7T show larger spectral resolution than those at clinical fields (18) (Fig.1).

In human TA, the T_1 values at 3T are in the range between 372 ± 119 ms and 1095 ± 268 ms with the highest value of TMA at 3.2 ppm and the lowest value of EMCL- CH_2 at 1.5 ppm. The T_1 values at 7T are in the range between 1339 ± 40 ms and 2187 ± 1001 ms with the highest value of EMCL- CH_2 at 1.5 ppm and the lowest value of TMA at 3.2 ppm (Table 3). The T_2 values at 3T are in the range between 64 ± 16 ms and 131 ± 14 ms with the highest value of Cr- CH_3 at 3.03 ppm and the lowest value of EMCL- CH_3 at 1.1 ppm. The T_2 values at 7T are in the range between 28 ± 7 ms and 64 ± 7 ms with the highest value of EMCL- CH_2 at 1.5 ppm and the lowest value of $=\text{CH}-\text{CH}_2-(\text{CH}_2)_n$ at 2.24 ppm (Table 4). Similarly, the T_1 values are relatively higher at 7T than at 3T, whereas the T_2 values are slightly lower at 7T than that of 3T. At 3T, the T_1 values of TMA, Cr- CH_3 , IMCL- CH_2 , and EMCL- CH_2 for TA muscle are 1095 ± 268 ms, 900 ± 147 ms, 546 ± 115 ms, and 372 ± 119 ms, respectively, whereas the T_1 values of the corresponding metabolites at 7T are 1339 ± 40 ms, 1632 ± 164 ms, 1494 ± 158 ms, and 2187 ± 1001 ms, respectively (Table 3). At 3T, the T_2 values of TMA, Cr- CH_3 , IMCL- CH_2 , and EMCL- CH_2 for TA muscle are 110 ± 19 ms, 131 ± 14 ms, 75 ± 5 ms, and 81 ± 3 ms, respectively, whereas the T_2 values of the corresponding metabolites at 7T are 39 ± 3 ms, 53 ± 6 ms, 56 ± 4 ms, and 64 ± 7 ms, respectively (Table 4). The maximum rate of change for T_1 increase with the increase of B_0 is $\sim 488\%$, and the minimum rate of change for T_1 increase with the increase of B_0 is $\sim 22\%$ (Table 3). The maximum rate of change for T_2 decrease with the increase of B_0 is $\sim 65\%$, and the minimum rate of change for T_2 decrease with the increase of B_0 is $\sim 17\%$ (Table 4).

DISCUSSION

Theoretically, *in vivo* MRS of the human skeletal muscle at higher field strength should be superior because of improved sensitivity and chemical shift dispersion. However, certain factors such as relaxation time differences, line-broadening due to magnetic susceptibility

effects, and radiofrequency (RF) coil efficiency could potentially offset the expected improvement at higher field strengths (4). Single-voxel localized proton MR spectroscopy of human skeletal muscle has been performed at field strengths of 0.47T (21), 1.5T (1,4,6,7,12,14-16,17,22), 1.89T (9), 2.0T (16), 2.1T (10), 3.0T (5,8,18), and 4.0T (4). Although some work has been reported about proton MR spectroscopy of phantoms, animal models, and the human brain at 7T (3,19), there have been no related studies about proton MR spectroscopy of human skeletal muscle performed at ultra-high-field (UHF) strengths (7T and above) in vivo. With the increasing availability of ultra-high-field human MR scanners (7T), it is becoming important to quantitatively evaluate the T_1 and T_2 relaxation times of human skeletal muscle metabolites at UHF and to compare human skeletal muscle spectroscopy at UHF to spectroscopy performed at lower field strength. UHF MR scanners and multi-channel RF coils have the potential to provide higher signal-to-noise ratio (SNR) and better spectral resolution, which can be used to either shorten acquisition time or improve detection of human skeletal muscle metabolites (2).

To the best of our knowledge, this is the first study to quantitatively measure T_1 and T_2 proton relaxation times of human TA muscle metabolites at 7T. In the present work, we report the results of single-voxel localized proton spectroscopy of human TA muscle performed at both 3T and 7T in a lipid phantom and volunteers. Data at both field strengths were compared in terms of T_1 and T_2 relaxation times. For the lipid phantom, the T_1 and T_2 relaxation times were found to be in good agreement with the results of previous studies (5,16,22) performed at field strengths ranging from 1.5T to 4T. Generally, the T_1 relaxation times in human muscle at 3T were slightly higher than those at 1.5T or 2T. The T_1 values of human muscle for the peaks in the range of 1.0 ppm and 1.5 ppm at 1.5T or 2T are all in the proximity of 300 ± 30 ms, and the T_1 for the peak 3.2 ppm is about 1150 ± 115 ms. On the other hand, the T_2 relaxation times in human muscle at 3T showed no apparent variation from those at 1.5T or 2T. The T_2 values of human muscle for the peaks in the range of 1.0 ppm and 1.5 ppm at 1.5T or 2T are all in the proximity of 90 ± 9 ms, and the T_2 for the peak 3.2 ppm is about 110 ± 11 ms (16). Specifically, in the lipid phantom, T_1 demonstrated a steady increase whereas T_2 demonstrated a slight decrease with B_0 . Similarly, the calculated T_1 as well as T_2 relaxation times of human TA muscle evaluated show the same trends as those reported at lower field strengths (5) with T_1 values being higher and T_2 values being slightly lower at 7T compared to 3T.

In addition, all the series of TR and TE dependent spectra in the lipid phantom and human TA muscle are apparently better resolved and visualized at 7T compared to 3T (Fig. 1, Fig. 2), as was expected. In MRS of the lipid phantom, T_1 and T_2 of the small peak at 5.3 ppm can be measured at 7T but not at 3T (Table 1, Table 2). In MRS of human TA muscle, T_1 and T_2 of the peak at 2.24 ppm ($=\text{CH}-\text{CH}_2-(\text{CH}_2)_n$), 2.4 ppm ($-\text{CO}-\text{CH}_2-\text{CH}=\text{}$), and 5.4 ppm ($-\text{CH}=\text{CH}-$) can be measured at 7T but not at 3T (Table 3, Table 4). In the analysis for human skeletal muscle spectroscopy, T_1 and T_2 of the small peaks at 2.24 ppm and 2.4 ppm were measured at 7T but not at 3T. The overlapping Creatine (Cr) and Choline (Cho) peaks were fitted using restrictions on their relative frequency shift and on their linewidths. Likewise, the peak at 5.4 ppm did not give reliable quantification for T_1 and T_2 evaluation at 3T. Although T_1 and T_2 relaxations of all these small signals cannot be reliably measured at 3T, they are possible to evaluate at 7T because of the higher spectral resolution using the UHF MR scanner.

The T_1 and T_2 relaxation times fitting errors in this work were further evaluated in Tables (5, 6, 7, 8, and 9) and Figures (4 and 5). Table 5 showed the line widths of representative peaks with the spectral full width at half maximum (FWHM) values at 3T and 7T. Tables 6, 7, 8, and 9 listed the chi-squared values for T_1 and T_2 relaxation times fitting in corn oil and TA at 3T and 7T, respectively. The chi-squared values (r^2) for fitting TA muscle T_1 data

varied from 0.941 to 0.993 at 7T and from 0.583 to 0.823 at 3T. On the other hand, the chi-squared values (χ^2) for fitting TA muscle T_2 data varied from 0.767 to 0.993 at 7T and from 0.521 to 0.995 at 3T.

On the other hand, Fig. 4 showed representative examples of a mono-exponential TA muscle T_1 fit to the integral value M of the lipid peak as a function of TR and the corresponding fit to the logarithm of $(M_0 - M)$ (M_0 being the fully relaxed lipid signal) of the lipid signal with Fig. 4 (a) the TA muscle lipid peak at 1.3 ppm at 3T, Fig. 4 (b) the corresponding fit to the logarithm of $(M_0 - M)$ at 1.3 ppm at 3T, Fig. 4 (c) the TA muscle lipid peak 1.1 ppm at 7T, and Fig. 4 (d) the corresponding fit to the logarithm of $(M_0 - M)$ at 1.1 ppm at 7T, respectively.

Fig. 5 showed representative examples of a mono-exponential TA muscle T_2 fit to the integral value M of the lipid peak as a function of TR and the corresponding fit to the logarithm of $(M_0 - M)$ of the lipid signal with Fig. 5 (a) the TA muscle lipid peak at 1.5 ppm at 3T, Fig. 5 (b) the corresponding fit to the logarithm of $(M_0 - M)$ at 1.5 ppm at 3T, Fig. 5 (c) the TA muscle lipid peak at 1.5 ppm at 7T, and Fig. 5 (d) the corresponding fit to the logarithm of $(M_0 - M)$ at 1.5 ppm at 7T, respectively. All the above results demonstrated the excellent fitting of the T_1 and T_2 relaxation times at 3T and 7T.

It is assumed that all the fragments from the same lipid chain should have similar T_1 or T_2 values. However, on the contrary, our results showed that different parts of the lipid chain have different T_1 or T_2 values. This might be probably due to their different resonance response among the various chains of lipids. Another reason may be that partial residual dipolar coupling can also influence the relaxation times (18-20).

There are certain limitations in the current study that should be acknowledged. First, we scanned a small number of volunteers. This is not unusual in a proof of concept study. Second, we did not evaluate any diseased muscles as this would be a progression of this early work. Third, prior investigators (21,22) report that the orientation of muscle fibers is closely related to their function, and the structural information obtained from MRS data may be of extreme importance for muscular physiological studies, an aspect that we did not study. Future investigations could concentrate on the influence of human skeletal muscle fiber orientation and the results of MRS at UHF strengths as a means to gain insight into muscle function and physiology.

In summary, this study demonstrates the feasibility of quantitatively measuring and evaluating T_1 and T_2 relaxation times of human tibialis anterior muscle metabolites at 7T *in vivo*. The relaxation numbers can be utilized for the absolute quantification of skeletal muscle metabolite concentrations and the optimization of sequence parameters. To our best knowledge, this is the first study to report T_1 and T_2 relaxation times of several metabolites in human TA muscle under *in vivo* conditions at 7T. The preliminary results will be used for calculating the relaxation correction factors required for absolute quantitation of metabolite concentrations. The calculated relaxation times are also used for protocol and sequence optimization for follow-up investigations on human skeletal muscle.

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Fig.1.

Representative stacked T_1 (variable TR), T_2 (variable TE) spectra consisting of lipid chemicals recorded from lipid phantom (corn oil) using the STEAM pulse sequence at 3T and 7T are depicted, respectively. Spectral resolution is significantly better at 7T.

Fig.2.

Representative stacked T_1 (variable TR), T_2 (variable TE) spectra consisting of human TA muscle metabolites recorded from TA muscle of a healthy male volunteer using the STEAM pulse sequence at 3T and 7T are depicted, respectively. A voxel of $10 \times 10 \times 10 \text{ mm}^3$ was positioned and used for localized proton spectra in the healthy human volunteer (7T localizer image shown). Spectral resolution is significantly better at 7T.

Fig.3. Representative 3T and 7T localized 1D MR ^1H spectra recorded from T_2 series of the TA muscle of a 37-year-old healthy subject with $\text{TE} = 50$ ms. The MR spectra show the fitted peaks with JMRUI and residuals at 3T and 7T, respectively. The top, the middle, and the bottom row of Fig. 3 (a) and (b) show the traces of the residue, the individual components, and the actual acquired spectrum at 3T and 7T, respectively.

Fig.4.

Representative examples of a mono-exponential T_1 fit to the integral value M of the TA muscle lipid peak at 1.1 ppm as a function of TR and the corresponding fit to the logarithm of $(M_0 - M)$ at 3T and 7T. (a) mono-exponential fit of TA muscle lipid peak at 1.3 ppm at 3T, (b) the corresponding fit to the logarithm of $(M_0 - M)$ at 3T, (c) similarly, the mono-exponential fit of TA muscle lipid peak 1.1 ppm at 7T, (d) the corresponding fit to the logarithm of $(M_0 - M)$ at 7T.

Fig.5.

Representative examples of a mono-exponential T_2 fit to the integral value M of the TA muscle lipid peak at 1.5ppm as a function of TR and the corresponding fit to the logarithm of (M_0-M) at 3T and 7T. (a) mono-exponential fit of TA muscle lipid peak at 1.5 ppm at 3T, (b) the corresponding fit to the logarithm of (M_0-M) at 3T, (c) similarly, mono-exponential fit of TA muscle lipid peak at 1.5 ppm at 7T, (d) the corresponding fit to the logarithm of (M_0-M) at 7T.

Table 1Comparison of T_1 Relaxation Times in Corn Oil at 3T and 7T

Corn Oil	$-\text{CH}_3$ (0.9ppm)	$(\text{CH}_2)_n$ (1.3ppm)	CH_2 - $\text{CH}=\text{CH}-\text{CH}_2$ (2.2 ppm)	$-\text{COO}-\text{CH}_2$ - CH_2 (2.4 ppm)	$-\text{CH}-\text{CH}_2$ - $\text{CH}=\text{CH}-$ (2.79 ppm)	Glycerol (5.3 ppm)	$-\text{CH}=\text{CH}-$ (5.4ppm)
3T (ms)	702±20	356±10	274±11	440±160	271±14	NM *	537±14
7T (ms)	1221±80	896±270	499±20	514±20	356±40	506±60	928±140
Change (%)	74	152	82	17	31	NM	73

* NM = Not Measured

Table 2Comparison of T₂ Relaxation Times in Corn Oil at 3T and 7T

Corn Oil	-CH ₃ (0.9ppm)	(CH ₂) _n (1.3ppm)	CH ₂ - CH=CH- CH ₂ (2.2 ppm)	=COO- CH ₂ -CH ₂ (2.4 ppm)	=CH-CH ₂ - CH= (2.79 ppm)	Glycerol (5.3 ppm)	-CH=CH- (5.4ppm)
3T (ms)	182±21	91±6	46±4	49±8	56±3	NM [*]	119±8
7T (ms)	54±7	55±6	29±2	36±8	44±4	30±3	92±13
Change (%)	70	40	37	27	21	NM	23

^{*} NM = Not Measured

Table 3Comparison of T₁ Relaxation Times in Tibialis Muscle (TA) at 3T and 7T

TA	IMCL-CH ₃ (0.9ppm)	EMCL-CH ₃ (1.1ppm)	IMCL-CH ₂ (1.27ppm)	EMCL-CH ₂ (1.5ppm)	=CH-CH ₂ - (CH ₂) _n (2.24ppm)	-CO-CH ₂ - CH= (2.4ppm)	Cr- CH ₃ (3.03ppm)	TMA (3.2ppm)	-CH=CH- (5.4ppm)
3T (ms)	866±216	440±108	546±115	372±119	NM *	NM	900±147	1095±26 8	NM
7T (ms)	1946±606	1427±33 8	1494±15 8	2187±1001	1372±239	1971±235	1632±164	1339±40	2036±404
Change (%)	125	224	174	488	NM	NM	81	22	NM

* NM = Not Measured

Table 4Comparison of T₂ Relaxation Times in Tibialis Muscle (TA) at 3T and 7T

TA	IMCL- CH ₃ (0.9ppm)	EMCL- CH ₃ (1.1ppm)	IMCL-CH ₂ (1.27ppm)	EMCL- CH ₂ (1.5ppm)	=CH-CH ₂ - (CH ₂) _n (2.24ppm)	-CO-CH ₂ - CH= (2.4ppm)	Cr- CH ₃ (3.03ppm)	TMA (3.2ppm)	-CH=CH- (5.4ppm)
3T (ms)	68±6	64±16	75±5	81±3	NM [*]	NM	131±14	110±19	NM
7T (ms)	42±12	53±1	56±4	64±7	28±7	29±8	53±6	39±3	56±21
Change (%)	38	17	25	21	NM	NM	60	65	NM

^{*} NM = Not Measured

Table 5

Spectral Full Width at Half Maximum (FWHM) Values of TA Muscle at 3T and 7T

Peak Position (ppm)	FWHM (Hz) 3T	FWHM (Hz) 7T
1.1	21.04	19.74
1.3	9.26	15.82
1.5	11.78	28.93
3.0	27.40	39.70
3.2	26.0	39.30

Table 6

Chi-squared (r^2) Values for T_1 Relaxation Times Fitting in Corn Oil at 3T and 7T

Corn Oil	-CH ₃ (0.9ppm)	(CH ₂) _n (1.3ppm)	CH ₂ - CH=CH-CH ₂ (2.2 ppm)	=COO-CH ₂ - CH ₂ (2.4 ppm)	=CH-CH ₂ - CH= (2.79 ppm)	Glycerol (5.3 ppm)	-CH=CH- (5.4ppm)
r^2 (3T)	0.99	0.994	0.991	0.802	0.989	NM *	0.952
r^2 (7T)	0.974	0.784	0.994	0.997	0.97	0.973	0.894

* NM = Not Measured

Table 7Chi-squared (r^2) Values for T_2 Relaxation Times Fitting in Corn Oil at 3T and 7T

Corn Oil	-CH ₃ (0.9ppm)	(CH ₂) _n (1.3ppm)	CH ₂ - CH=CH- CH ₂ (2.2 ppm)	=COO- CH ₂ -CH ₂ (2.4 ppm)	=CH-CH ₂ - CH=CH- (2.79 ppm)	Glycerol (5.3 ppm)	-CH=CH- (5.4ppm)
r^2 (3T)	0.909	0.969	0.987	0.923	0.995	NM *	0.976
r^2 (7T)	0.913	0.928	0.973	0.809	0.964	0.979	0.947

* NM = Not Measured

Table 8Chi-squared (r^2) Values for T_1 Relaxation Times Fitting in Tibialis Muscle (TA) at 3T and 7T

TA	IMCL-CH ₃ (0.9ppm)	EMCL-CH ₃ (1.1ppm)	IMCL-CH ₂ (1.27ppm)	EMCL-CH ₂ (1.5ppm)	=CH-CH ₂ - (CH ₂) _n (2.24ppm)	-CO-CH ₂ - CH= (2.4ppm)	Cr- CH ₃ (3.03p pm)	TMA (3.2ppm)	-CH=CH- (5.4ppm)
r^2 (3T)	0.616	0.768	0.790	0.583	NM *	NM	0.823	0.736	NM
r^2 (7T)	0.189	0.93	0.962	0.791	0.951	0.944	0.732	0.75	0.916

* NM = Not Measured

Table 9

Chi-squared (r^2) Values for T_2 Relaxation Times Fitting in Tibialis Muscle (TA) at 3T and 7T

TA	IMCL- CH ₃ (0.9ppm)	EMCL- CH ₃ (1.1ppm)	IMCL-CH ₂ (1.27ppm)	EMCL- CH ₂ (1.5ppm)	=CH-CH ₂ - (CH ₂) _n (2.24ppm)	-CO-CH ₂ - CH= (2.4ppm)	Cr- CH ₃ (3.03ppm)	TMA (3.2ppm)	-CH=CH- (5.4ppm)
r^2 (3T)	0.974	0.760	0.975	0.995	NM *	NM	0.521	0.918	NM
r^2 (7T)	0.760	0.838	0.990	0.982	0.967	0.481	0.812	0.982	0.936

* NM = Not Measured