Lipid Signal Extraction in Proton MR Spectroscopic Imaging of Human Calf Muscles

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Introduction

Recently, muscle lipid measurement using MRS has drawn attention in diabetes research because intramyocellular lipids (IMCL) content is known to be negatively correlated with insulin sensitivity, which is a strong predictor for type 2 diabetic mellitus. However, IMCL quantification is often hampered by a severe spectral overlap between IMCL and extramyocellular lipids (EMCL), and by strong lipid contaminations from subcutaneous fat (SF) and bone marrow fat (BF). Since SF and BF signals are typically 1 to 2 orders of magnitude larger than muscle signals, they often cause artifacts or bleed into IMCL peak even if proper apodizations are applied. Several methods have been reported to eliminate these problems with post-acquisition processing [1, 2]. However, none of the methods offer a selective extraction of SF or BF signals. The SLIM method, previously proposed as a localization technique to reconstruct spectra from multiple arbitrarily shaped compartments [3, 4], is capable of locating signal sources of arbitrary shapes. Therefore, the goals of this study were to utilize the SLIM technique 1) to implement a new post-acquisition processing method to selectively extract SF and BF signals, and 2) to demonstrate the effectiveness of the method in ^{1}H MRSI of the human calf.

Methods

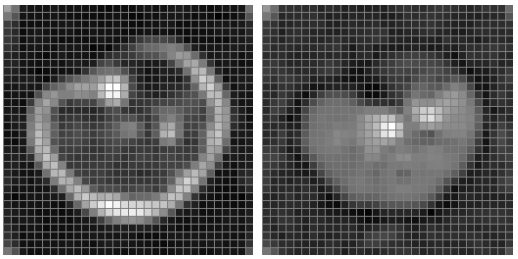
Experimental: Data were acquired from 4 healthy subjects with a TEM ^{1}H coil on a 4T Varian Inova MR system. Fat MRI and water MRI were performed using a gradient echo sequence, with and without an inversion recovery, respectively. Parameters were slice thickness = 3 mm; FOV = 16x16 cm^2; In-plane spatial resolution = 128x128 and TR/TE = 0.5 s/50 ms. Water suppressed MRSI was measured on the same slice using semi-selective excitation spin echo pulse sequence with the following parameters: TR/TE = 1 s/24 ms; PE = 32x32; SW = 1600 Hz; NP = 1024 complex points [5].

SLIM based LSE algorithm: The theory and algorithm of SLIM are given in [3, 4]. The human calf was first segmented into 3 fat and several muscle macro-compartments based on the high resolution fat MRI. These macro-compartments were auto-segmented to smaller compartments, which were ~ 0.06 and 2 cm^2 (in-plane size) for fats and muscles, respectively. SLIM was applied to obtain compartmental signals, from which fat signals were reconstructed by inverse SLIM. A fat-removed signal was obtained by subtracting fat signals from the raw signal.

Post-processing: The whole set of 32x32 MRSI data were used in the LSE and SI reconstruction. The resultant time domain muscle signals were processed by the conventional FFT procedure for the SI display, with Hanning or Kaiser windowing. The spectral processing included Gaussian linebroadening of 6 Hz, baseline correction and phase correction. For numerical evaluation of the performances of the proposed method, the voxel spectra before and after LSE were compared using the relative difference D_r, where $D_r = (I_b - I_a)/I_b$, and I_b and I_a are the signal intensities before and after LSE. All of the software was written in Matlab® (MathWorks, Inc. Natick, MA, USA).

Results and Discussions

Fig. 1 shows MRSIs of the calf (a) before and (b) after LSE processing. Selective removal of SF and BF signals is clearly illustrated in Fig. 1b. Fig. 2 shows the voxel spectra (a) within, (b) near and (c) far away from SF, before (upper traces) and after (lower traces) the LSE. As seen from the figures, the fat signal was reduced by an order of 3 to 4 (Fig. 2a). The lipid contamination was eliminated to such an extent that the voxel adjacent to the SF exhibits separated IMCL and EMCL peaks (Fig. 2b) comparable to a voxel distant from the SF, which retains similar spectra before and after LSE (Fig. 2c). The mean and standard deviation of the relative differences (D_r) of IMCL peaks in each muscle were less than 1% using voxels selected within muscles and far away from SF and BF. Therefore, the results show that the LSE method does not reduce the signal intensity of muscles, and only selectively removes the target fat signals. After fat signal removal, it is possible to apply moderate spatial filtering in the FFT SI reconstruction so as to improve the spatial/spectral resolutions [1, 2].



a **b**

Fig. 1. MRSIs before (a) and after LSE (b).

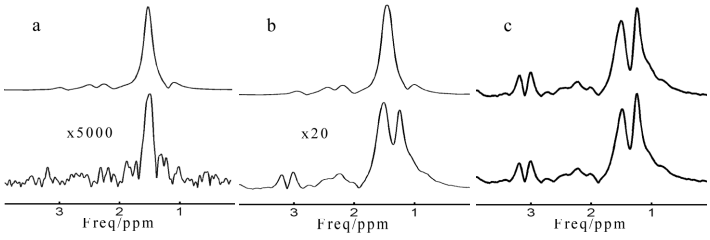


Fig. 2. Voxel magnitude spectra within (a), near (b) and far away from (c) fat regions.

In conclusion, the postprocessing method based on the SLIM technique can successfully eliminate selected lipid signals from the time domain proton MRSI data. The effectiveness of the method was demonstrated in vivo with experiments on the human calf. The advantages of the method are that the quality of spectra near SF regions can be improved as comparable to the ones within muscles and an improved spatial/spectral resolution can be obtained with a moderate spatial filtering in FFT SI reconstruction.

References

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