Enhancing Spectral Resolution in Proton MRSI of Human Calf Muscles Using SPREAD

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Introduction

The measurement of intramyocellular lipids (IMCL) in muscle is important for understanding lipid utilization and the pathophysiology of a variety of diseases, such as diabetes, obesity, and insulin resistance. The accurate measurement of IMCL using biopsy is hindered, however, by the difficulties of complete separation of IMCL and extramyocellular lipid (EMCL). In recent years, in vivo proton magnetic resonance spectroscopy (MRS) and spectroscopic imaging (MRSI) have been employed to assess EMCL and IMCL stores in humans and animals [1,2] based on the effect of "bulk magnetic susceptibility" (BMS) of EMCL. However, magnetic field inhomogeneities caused by spatial variations of the static magnetic field (B_0) produce spectral line broadening and lineshape distortion that will decrease spectral resolution and hamper the separation of IMCL and EMCL. We applied SPREAD (Spectral Resolution Amelioration by Deconvolution) [3] to improve the spectral resolution of proton MRSI data measured in human calf muscle at 3T.

Methods

Principles of SPREAD The MR spectrum from a volume of a sample being scanned can be regarded as a combination of many spectral lines originating from tiny sub-volumes of the volume. The magnetic field within each of the sub-volumes can be regarded as homogeneous. The spectral lines from the signals originating in these sub-volumes will have the same natural linewidth, but slightly differing frequencies that are created by small variations in the strengths of the local magnetic fields where the sub-volumes are located [4,5]. Mathematically, this combination of spectral lines from sub-volumes is described as a convolution of the natural linewidth and the profile of the lineshape of the signal originating from the overall volume. The lineshape can be derived from the field map. By deconvolving the measured spectrum from the lineshape function, one can remove the effect of field inhomogeneity and significantly reduce the linewidth of the spectrum, thereby enhancing the spectral resolution of MRSI data [6].

Experimental We acquired MR data on a human lower leg using a whole-body 3T scanner (Signa 3T HDx, GE Healthcare, Waukesha, WI), equipped with a home-built bird-cage coil for receiving radiofrequency signals. Axial slices of interest were prescribed for both MRSI and MRI. Prior to the MRSI scan, manual prescanning was performed to identify the resonance frequency of water signal and perform first-order field shimming. Upon finishing the prescan, the system frequency was shifted by -448 Hz, which at 3T was the resonance frequency of lipid signal at 1.3 ppm. MRSI data was acquired using a multiple 2D SI pulse sequence [7] with the following parameters: number of slices = 2; slice thickness 9mm, spacing 3 mm; FOV = 20 x 20 cm^2; nominal number of phase encoding steps = 32 x 32; TR/TE = 1200/144 ms; spectral width = 2000 Hz. Water suppression (WS) was realized by shifting the frequency of the RF pulses for WS to 448 Hz. No outer volume saturation was applied. Total scan time for MRSI acquisition was 15 min. Immediately following the MRSI scan, high resolution MR images for field mapping were acquired using a commercial 2D MRI sequence, with TEs of 3.3 and 4.6 ms, respectively. Each MRSI slice covers 3 high-resolution MRI slices. Total scan time was approximately 3.3 min. The signal-to-noise ratio of the MR images was approximately 80.

Data Processing We obtained phase images from the complex MR images reconstructed from k-space data using a 2D Fourier transform. We calculated the field maps from the unwrapped phase images and reconstructed the matrix of the lineshapes from the field map [5]. The lineshapes were employed in the deconvolution. Details of the data processing are found in [3].

Results

An MR image of the lower leg and a field map are shown in Fig. 1. Field inhomogeneity broadened the spectral lines of both IMCL and EMCL, causing them to overlap severely (Fig. 2). Furthermore, the accompanying peaks from the $-CH_3$ groups of IMCL and EMCL, respectively, are completely merged with the broadened dominant peaks of the $(CH_2)_n$ group. Thus, separation of IMCL and EMCL is exceedingly difficult. Following SPREAD, however, these peaks are better resolved, facilitating the more accurate measurement of IMCL.

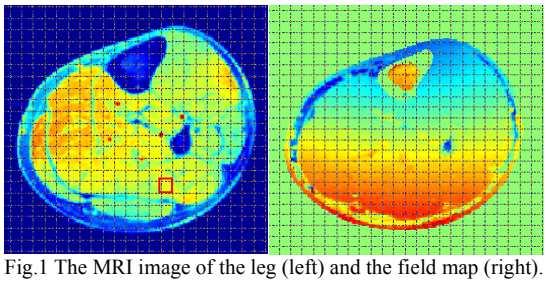

Fig.1 The MRI image of the leg (left) and the field map (right).

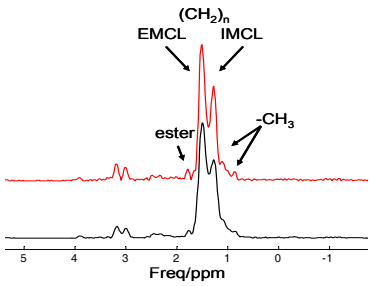

Fig. 2. MRS spectrum from the voxel shown in the red portion of the image in the left panel of Fig. 1 (black), and the spectrum after application of SPREAD (red).

Discussion

Our results show that SPREAD can improve the spectral resolution of proton MRSI from the lower leg of humans. The application of SPREAD to the proton MRSI of human calf muscle is easy and straightforward. Some technical modifications to the conventional pulse sequences are required to implement this technique, however. First, fat signals should be suppressed in acquiring MRI images for field mapping. Second, the system frequency for MRSI should be shifted by 3.5 ppm from water to the resonance of lipid at 1.3 ppm, so as to eliminate the mismatch of the spatial locations of the voxels in the measured MRSI and the reconstructed lineshapes that is caused by the effects of the differences in chemical shift of water and fat. Third, water suppression is still required, although the frequency of the RF pulse for WS should be shifted to high field by 3.5 ppm. This is a post-acquisition technique that is compatible with any experimental and post-processing procedures.

References

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