SLIM Reconstruction of 1H MRS of Calf Muscles: A Feasibility Study

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Introduction

SLIM (Spectral Localization by Imaging) was originally proposed by Hu et al [1] as a technique to allow simultaneous acquisition of regional spectra from several arbitrarily shaped compartments. Accurate detection of muscle lipids is of importance because intramyocellular lipids [IMCL] content is known to be negatively correlated with insulin sensitivity, which is a strong predictor of the clinical onset of type 2 diabetic mellitus. Keys to accurate measurement of IMCL are: 1) better resolution of extramyocellular lipids [EMCL] from IMCL, and 2) reduction of the contaminations from bone marrow and subcutaneous fat. High resolution CSI with FT reconstruction can be efficient in removing those obstacles. However, it requires a long acquisition time to acquire all *k*-space encodings. Therefore, the goal of this study is to test whether non-Fourier SLIM reconstruction method with selective *k*-space phase encodings can generate ^{1}H MR spectra of well resolved IMCL and EMCL in calf muscle, which will eventually allow to acquire less *k*-space phase encodings.

Methods

Experimental: All data were acquired from healthy human legs with a TEM ^{1}H coil on a 4T Varian Inova MR system. MRI was performed using a gradient echo sequence with the following parameters: Slice thickness: 3 mm, FOV: 16x16 cm^2, In-plane spatial resolution: 128x128, TR/TE: 0.5 s/50 ms. Water suppressed CSI was measured on the same slice using semi-selective excitation spin echo pulse sequence with the following parameters: TR/TE: 2 s/24 ms, PE: 32x32, SW: 1600 Hz, NP: 1024 complex points, NA =1 [2].

SLIM: The theory and algorithm of SLIM were given in [1][3]. In vivo spectroscopic MR data are often originated from several compartments that possess homogeneous MR spectra and whose boundaries can be defined with the help of MR images. The phase encoded compartmental signals and the intrinsic compartmental signals are related by a so-called geometry matrix that can be calculated from the phase encoding gradients and the configurations of the compartments [1]. The intrinsic compartmental signals can then be recovered from the measured signals and the geometry matrix.

Post-processing: Image segmentation was performed manually in the scout image for 8 spatially homogeneous compartments as shown in Fig. 1, which were then digitized for the calculation of the geometry matrix. The boundaries of the selected compartments were sufficiently away from the fat deposits or the interfaces of bones, muscle groups and vessels to avoid possible signal contamination. A set of 15-by-15 phase encoded signals was chosen from the central part of the *k*-space of the conventional CSI data set for the SLIM reconstruction. The resultant time domain compartmental signals were processed. All the softwares were written in Matlab® (Matworks, Inc. Natick, MA, USA).

Results and Discussions

Figure 2 shows the SLIM reconstructed signals from the compartments 1 and 5 (bone marrow and soleus muscle). The signal intensities of the spectra are directly related to the average concentrations of the corresponding metabolites in the compartments. Spectrum from bone marrow (Fig 2a) exhibits a high lipid signal with about 30 times greater EMCL intensity compared to soleus muscle (Fig. 2b). In Fig 2(b), a spectrum from soleus shows well resolved IMCL and EMCL peaks.

Theoretically the signal contamination of SLIM is much less than that with the Fourier method [3]. However, we found that a smaller region within a muscle needs to be segmented to improve spectral quality (e.g. compartment 5 is only about 1/10 of the whole soleus muscle).

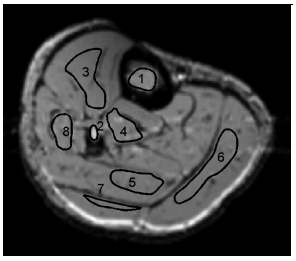

Figure 1: Proton MR image of a healthy human lower leg overlaid with the selected compartments in 2 bone morrows and 6 muscle groups.

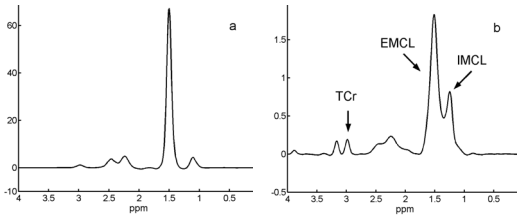

Figure 2 Examples of SLIM reconstructed compartmental signals from bone marrow (a, 1 in Fig. 1) and soleus (b, 5 in Fig. 1).

Conclusion

SLIM reconstruction resulted in a well resolved ^{1}H MRS in soleus using only about 20 % of entire CSI *k*-space encodings. This method can potentially be utilized to quantitatively measure the fat content in muscle groups using bone marrow or muscle water signals as internal references with less acquisition time [2]. Potentially with the combination of optimized phase encodings, the method will contribute to further improved localization and sensitivity, i.e. less contaminations from unwanted fat signals and increased SNR per time in measurement of IMCL content [4].

References

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