Effects of SPREAD on Proton MRSI Spectra of Human Calf Muscle

Zhengchao Dong[1,2], Feng Liu[1,2], Yunsuo Duan[1,2], Alayar Kangarlu[1,2], and Yudong Zhang[3]

[1]*Columbia University, New York, NY, United States,* [2]*New York State Psychiatric Institute, New York, NY, United States,* [3]*Nanjing Normal University, Jiangsu, China*

TARGET AUDIENCE

MR scientists and biomedical scientists interested in metabolism, diabetes and psychiatry.

PURPOSE

Proton MRSI has been applied for almost twenty years to the in vivo measurement of intramyocellular lipids (IMCL) in muscle. This has been made possible by the "bulk magnetic susceptibility" (BMS) of extramyocellular lipids (EMCL) that shifts its resonance line by as much as 0.21 ppm from IMCL. However, the inhomogeneities of B_0 produce broadening of spectral lines and distortion of lineshape in MR spectra, which can easily obscure the small difference in the resonance frequencies of IMCL and EMCL generated by BMS. Despite many efforts to resolve IMCL and EMCL signals, adequate spectral resolution in the proton MR spectra of calf muscle is still not assured routinely[1,2]. In the present study, we showed that the SPREAD (Spectral Resolution Amelioration by Deconvolution)[3] technique can improve the spectral resolution of proton MRSI data and we conducted Monte Carlo simulations to assess the effects of SPREAD on the accuracy of spectral fitting.

METHODS

Data Acquisition: We acquired MR data from calf muscle on a whole-body 3T scanner (Signa GE Healthcare) using a dedicated bird-cage extremity coil built in house. The protocol was approved by the local Institutional Review Board. The volunteers were positioned in the supine, foot-first position in the bore of the scanner, with their right calves positioned in the coil along the direction of the main magnetic field. Upon completion of the prescan, the system frequency was shifted by -448 Hz, centered on the resonance of lipid signal. MRSI data were acquired using a multi-planar spectroscopic imaging sequence[4] with parameters: FOV = 20x20 cm^2; Number of slices = 2; Slice thickness = 9 mm; Spacing = 3 mm; Number of phase encoding steps = 804, located in a circle inscribed within a square of 32 x 32 in *k*-space; Repetition time = 1200 ms; Echo time = 144 ms; Spectral width = 2000 Hz. Partial echoes of 512 points were acquired with the echo falling at the 128th point. Water suppression was realized by shifting the frequency of the RF pulses for WS to 448 Hz. Following the MRSI scan, high resolution MR images for field mapping were acquired by SPGR sequence. The location of the SPGR image volume was copied from that of the MRSI scan. The TEs of the two sets of MR images were 2.3 and 5.8 ms, respectively.

***Data Processing*:** We reconstructed complex MR images from *k*-space datasets using fast Fourier transform. We unwrapped the phase images, from which we produced raw field maps and reconstructed 3D lineshape signals for each MRSI slice within the muscles. The reconstructed lineshape signals had the same in-plane resolution and point spread function, and the same spectral resolution and data points, as those of the MRSI signals. The reconstructed lineshapes were used to de-convolve the measured MRSI spectra as described previously[3]. We performed Monte Carlo (MC) simulations to assess the effects of SPREAD on the accuracy of spectral fitting. To this end, we added complex noise with a Gaussian distribution to both the spectra before and after SPREAD, and then measured the parameters of the peaks (areas, frequencies, etc) after spectral fitting. The level of the added Gaussian noise is twofold of that in the original signal. We repeated these procedures with 200 noise realizations for each dataset and compared the relative standard deviations ("rSD", defined as the ratio of standard deviation to mean) of the measured parameters of the peaks in the spectra.

RESULTS

The measured MRSI spectra typically exhibit severe overlap of EMCL and IMCL, making accurate spectral fitting and IMCL measurement difficult. After the SPREAD procedure, the spectra are better resolved (Fig. 1), potentially allowing improved IMCL measurement. The results of the MC experiment show that the rSDs of the areas of the IMCL peak measured by spectral fitting reduced by 20% to 90% (Table 1) for the voxels shown in Fig. 1.

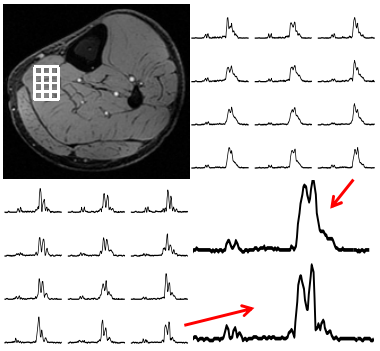

Fig. 1. Original spectra (upper right) and SPREAD processed spectra (lower left) from voxels overlaid on the MR image (upper left), and blow-ups (lower right).

DISCUSSIONS & CONCLUSION

The results presented in previous section show that the SPREAD method improves the resolution of the EMCL and IMCL peaks. As the spectral resolution of ^{1}H MRSI spectra of the calf muscle is poor compared with ^{1}H MRSI spectra of the brain, the application of SPREAD to muscle MRSI is more desirable than to brain MRSI. The results of MC experiment proved our hypothesis that the rSDs of the measured IMCL peak areas are smaller than those of measured on the original spectra. This is because (1) the improved spectral resolution limited the uncertainty of the fitting peaks and (2) the SPREAD method corrected the lineshape distortions. We note, however, that the present MC experiment is only an indirect test of the effect of SPREAD on the accurate measurement of IMCL. Future work should evaluate the reproducibility of the method and assess the effects of the method on the absolute quantification of the IMCL in human calf muscle.

Table 1. Results of the Monte Carlo experiment: rSDs (in%) of IMCL peak areas of the original spectra and SPREAD processed spectra (in red). The cells in the table correspond to the voxels in Fig. 1.

13.88/11.15	19.85/4.709	9.318/5.657
38.78/6.756	50.50/4.731	6.879/5.395
27.93/8.438	21.03/12.81	18.36/9.235
42.75/23.57	23.65/16.72	19.01/8.052

REFERENCES

1. Newcomer BR, Lawrence JC, Buchthal S, et. al. High-resolution chemical shift imaging for the assessment of intramuscular lipids. Magn Reson Med 2007;57(5):848-858.
2. Dong Z, Hwang JH. Lipid signal extraction by SLIM: application to 1H MR spectroscopic imaging of human calf muscles. Magn Reson Med 2006;55(6):1447-1453.
3. Dong Z, Peterson BS. Spectral resolution amelioration by deconvolution (SPREAD) in MR spectroscopic imaging. Journal of Magn Reson Imaging 2009;29(6):1395-1405.
4. Duyn JH, Gillen J, Sobering G, et. al. Multisection proton MR spectroscopic imaging of the brain. Radiology 1993;188(1):277-282.