QUANTITATIVE MAGNETIZATION TRANSFER WITH FAT COMPONENT IN HUMAN MUSCLES

Ke Li[1,2], Richard D Dortch[1,2], Daniel F Gochberg[1,2], Seth A Smith[1,2], Bruce Damon[1,2], and Jane H Park[1,3]

[1]*Institute of Imaging Science, Vanderbilt University, Nashville, TN, United States,* [2]*Department of Radiology, Vanderbilt University, Nashville, TN, United States,* [3]*Department of Molecular Physiology and Biophysics, Vanderbilt University, Nashville, TN, United States*

Introduction:

Quantitative magnetization transfer (qMT) parameters describe the interactions between free and macromolecular protons in biophysical environments. These parameters include the ratio of macromolecular (m) to free (f) proton pool sizes (p_m/p_f) and the magnetization transfer rate (k_{mf}). The selective inversion recovery (SIR) technique [1] allows for determination of qMT parameters, by fitting the signals observed at very short through very long inversion recovery times to a bi-exponential model. This method has been successfully implemented in isolated muscles [2] and human brain [3]. In human muscles, particularly those affected by neuromuscular disease, the estimation of parameters based upon a bi-exponential model may be biased due to the existence of infiltrating fat. This is because fat is only partially inverted and exhibits a T_1 that is much shorter than muscle water (i.e, a bi-exponential model does not fully describe the data). In this work, the effects of fat on fitted qMT parameters were systematically evaluated. It is predicted that the two key parameters of interest (p_m/p_f and k_{mf}) are biased by the presence of fat. This assumption was validated with synthesized phantom data and *in vivo* human muscle data.

Methods:

Data were collected on a Philips 3.0T Achieva magnet, using a 16-channel torso coil for signal reception and body coil for excitation. The phantom consisted of a series of bovine serum albumin (BSA) samples (10%, 15%, and 20%) and a separate container filled with $MnCl_2$-doped water with a layer of vegetable oil on the top. *In vivo* data were obtained in an axial slice at the middle of right thigh of a healthy human subject. Imaging parameters were: FOV = 256 × 256 mm^2, matrix size =128 × 128, slice thickness = 7 mm, 16 inversion recovery time (t_i) points (logarithmically spaced between 10 ms and 10s), pre-delay (t_d) = 2.5 ms, SENSE acceleration factor = 2, FSE echo train length = 24, signal averages = 2 [3]. *In vivo* data were acquired with and without application of a gradient reversal method [4] for fat suppression. No fat suppression was applied for the phantom data. For simulations, the experimentally determined parameters for BSA and vegetable oil data were used. The synthesized signal was then generated by adding the fat signal to the BSA signal, and by varying the relative fat fraction sizes between 0 and 0.1, stepped by 0.01. Gaussian noise at signal-to-noise ratio (SNR) = 300 was then added to the generated signal data, and the resulting noisy data were fitted to the bi-exponential model [1]. *In vivo* data analyses were performed by fitting the observed signal recovery to a bi-exponential model.

Results and Discussion:

Simulations of synthesized phantom data are shown in Figure 1. For the 10%, 15% and 20% BSA samples, estimated p_m/p_f values were slightly lower than the true values at small fat fractions and elevated abruptly above their true values at fat fractions of 0.05, 0.08, 0.1 (especially for lower BSA concentations); while estimated k_{mf} values were consistently elevated for any fat contribution. It can be seen that pool size ratio estimates with higher macromolecular fractions are less sensitive to bias introduced from fat. Figure 2 shows the *in vivo* fitted p_m/p_f maps with and without fat suppression. The scan with fat suppression yielded p_m/p_f maps with slightly lower values and uncertainties, although fat signals were not fully suppressed. Particularly, the p_m/p_f of the vastus lateralis (VL) and rectus femoris (RF) muscles with and without fat suppression were determined [VL: 0.077 ± 0.011 (fat suppressed), 0.104 ± 0.075 (non-fat suppressed), and RF: 0.076 ± 0.014 (fat suppressed) and 0.101 ± 0.041 (non-fat suppressed)]. Note that for the simulations, a three-pool model may be used to fit the synthesized data and extract the qMT and fat parameters (not shown). However, the three-pool model fitting was found inapplicable to *in vivo* data, due to low SNR and model stability, which will be investigated in more details.

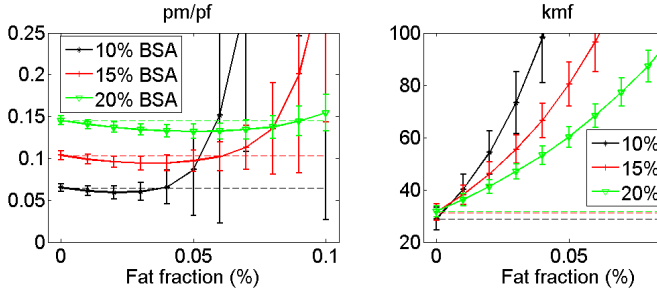

Figure 1. Fitted p_m/p_f and k_{mf} values of synthesized phantom data vs. fat fraction.

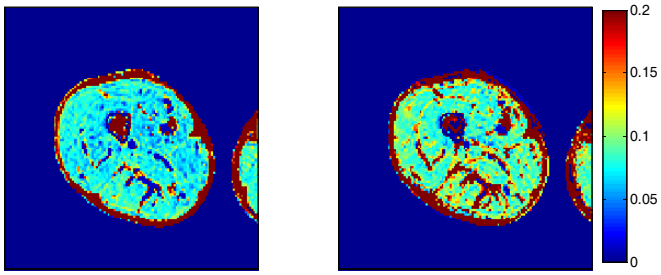

Figure 2. Fitted p_m/p_f maps for in vivo SIR data with (left) and without (right) fat suppressions.

Conclusion:

In this work, the effect of fat component on fitted qMT parameters was investigated. It was shown that the two parameters of most interest (p_m/p_f and k_{mf}) are biased when fat concentration is high relative to the macromolecular fraction. Analyses of human muscle data verified the effect of fat on fitted qMT parameters. It is hypothesized that at higher SNR the effect of fat contamination may be removed resulting in more robust estimates of qMT parameters in tissues with high natural fat abundance.

References:

[1] Gochberg, MRM 2007(57):437. [2] Louie MRM 2009(61):560. [3] Dortch, MRM 2011(66):1346. [4] Nagy, MRM 2008(60): 1256.

Acknowledgments:

NIH/NIAMS/ NIBIB R01 AR057091, K01 EB009120, and R01 EB000461.