Quantitative analysis and mapping of myelin water frequency-shift using T_2* relaxation signals at 3T

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Introduction: Multi-echo gradient echo (MGRE) MRI provides an effective method to obtain quantitative measurements of myelin water fraction (MWF). Unlike using T_2 decay from Carr-Purcell-Meiboom-Gill (CPMG) sequence with a 180-degree pulse between each echo, MGRE has much lower specific absorption rate (SAR), much shorter first echo time (TE_1) and echo space (ESP), and shorter scan time for multi-slice imaging as it does not require refocusing pulses.[1] Data fitting with three-pool model of white matter (WM) can effectively assess the MR signal from myelin water, myelinated axonal water, and mixed water.[1] However, it is assumed in this model that there is no frequency-shift among these compartments in WM. A recent study shows the presence of phase shift in myelin water in anisotropic magnetic susceptibility map[2]. Another recent study showed non-exponential decay of white matter, reporting an observation of small frequency offset of myelin water about 19Hz at 3T and about 36Hz at 7T in splenium of corpus callosum[3]. Robust mapping of frequency shift of myelin water can lead to more accurate modeling of MGRE signals for improved quantification of MWF. This study demonstrates the preliminary results of mapping of frequency shift in the MGRE data collected from an *in vitro* postmortem human brain at 3T.

Materials & Methods

Data Acquisition: A postmortem brain of an old woman with long-standing chronic inactive MS was scanned. The MGRE sequence was applied on a GE 3T MRI scanner to obtain the T_2* decay data. The total number of echoes was 126, with TE_1 of 2.1ms and echo space of 1.1ms. The other scanning parameters were: matrix size=256×256, field of view (FOV)=20cm, repetition time (TR)=2s, slice thickness=5mm with 1mm gap. Five slices were acquired.

Data Analysis: The whole fitting process consists of two steps. In the first step, the original three-pool model was used to fit the measured decay signals as in Eq. (1):

$$S(t) = \left\| A_{my} e^{-t/T^*_{2,my}} + A_{ma} e^{-t/T^*_{2,ma}} + A_{mx} e^{-t/T^*_{2,mx}} + A_{Baseline} \right\| \quad (1)$$

where $S(t)$ is the T_2* decay signal, and A_{my}, A_{ma}, A_{mx} and $A_{Baseline}$ represent signal intensities from myelin water, axonal water, mix pool water and residual baseline noise, respectively. In the second step, a modified three-pool model, which includes the frequency-shift f_{my} of myelin water, was introduced to fit the measured decay signals. In this modified model, the first term in Eq. (1) is replaced by: $A_{my} e^{-t/T^*_{2,my} - j2\pi f_{my} t}$. The quasi-Newton algorithm was used for data fitting. The T_2* ranges of signal intensities of three components of WM were: 3-16ms for myelin water, 16-36ms for axonal water, and 36-160ms for mix pool water. After the fitting parameters were determined from the first step using the original three-pool model, those fitted parameters were used as the initial values of the second step fitting with the modified three-pool model. A mask for WM segmentation was also obtained from the result of the first step fitting.

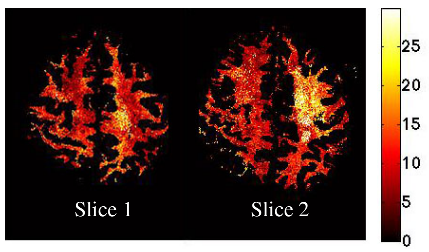

Fig. 1 Frequency-shift maps of myelin water (Hz)

Results and Discussion: Fig. 1 shows the maps of myelin frequency-shift for two slices (only WM regions are shown). The frequency-shift of myelin component is mostly centered in the range of 7 – 18 Hz for slice 1, shows in the histogram of Fig. 2. These results agree well with the data presented in a previous literature in splenium of corpus callosum.[3] Error maps of both steps of fitting shows that the average fitting error within WM area was reduced by 2.01% and 2.57% by using the modified three-pool model containing myelin frequency-shift for slice 1 and 2, respectively. The difference of root-mean-square fitting errors (RMSE) between the original and the modified three-pool models for the echoes in TE < 60ms are plotted in Fig. 3, with red and blue lines for both slices. In this figure, RMSE1 is the error in the first step with the original model, and RMSE2 is the error in the second step with the modified model, and these differences are represented in percentage. The results at TEs < 60ms were shown because most signal is in absence beyond this range. Fig. 3 shows that RMSE was reduced at almost all the TEs in both slices with the modified three-pool model. The averaged relative reduction of fitting error was 1.9% for TEs < 18ms and 1.6% for TEs < 60ms in these slices. Fig. 4 is the MWF map of slice 1 after second step fitting, which also agrees well with the results in previous literature.[1, 3]

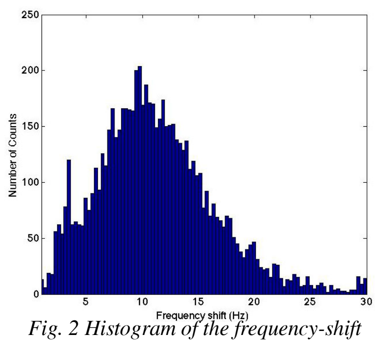

Fig. 2 Histogram of the frequency-shift in myelin water

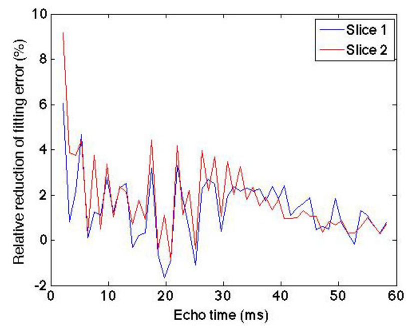

Fig. 3 Relative reduction of error for TE < 60ms, represented by (RMSE1 - RMSE2) / RMSE1 for two slices in Fig. 1, in percentage

Conclusion: A modified three-pool model with a frequency-shift in the myelin water component was proposed in this study. A two-step fitting procedure for the quantitation of myelin content was also proposed using this modified model. The frequency-shift obtained in the WM area in *in vitro* data agreed well with previous reported values. The data fitting error was reduced by employing the proposed three-pool model. Further validation of this proposed model with *in vivo* MGRE data is necessary.

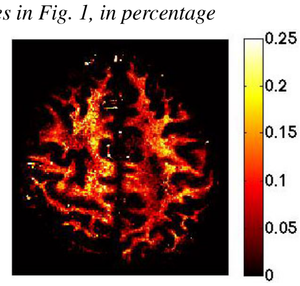

Fig. 4 MWF map after second step fitting

Reference

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