Myelin Water Fraction of the Whole Brain: 3D GRASE MWI vs. 3D ViSTa MWI

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INTRODUCTION Myelin water imaging (MWI) has been suggested as a potential biomarker that may provide specificity to demyelination in multiple sclerosis. In conventional MWI, the signal decays from multiple water compartments (myelin, axonal and interstitial water) are measured by multi-echo to estimate the short T_2 (myelin water) fraction (1). Methods have been developed to cover a 3D volume using spiral (2) or GRASE readout (3). However, the multi-exponential fitting is ill-conditioned and the resulting myelin water fraction (MWF) map is noisy (Fig. 1 left). Recently, a new MWI method, Direct Visualization of Short Transverse Relaxation Time Component (ViSTa (4) or background-suppressed MWI (5)) has been proposed. This method selectively acquires the myelin water signal by suppressing axonal and extracellular water signals based on the T_1 difference (4). Compared to conventional MWI, ViSTa generates a substantially improved myelin water image (Fig. 1, right), suggesting potential for clinical use. This method can cover a 3D volume and provide a quantitative MWF (see below). In this work, we compared a 3D ViSTa MWF map with a conventional 3D GRASE MWF map. The spatial distribution of the MWF over the whole brain was compared qualitatively and quantitatively. Additionally, intra-session reproducibility was tested using a test-retest scan.

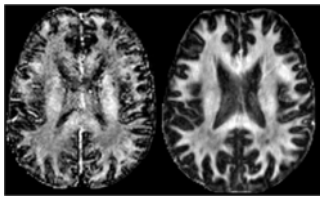

Figure 1. GRASE (left) vs. ViSTa (right) MWI

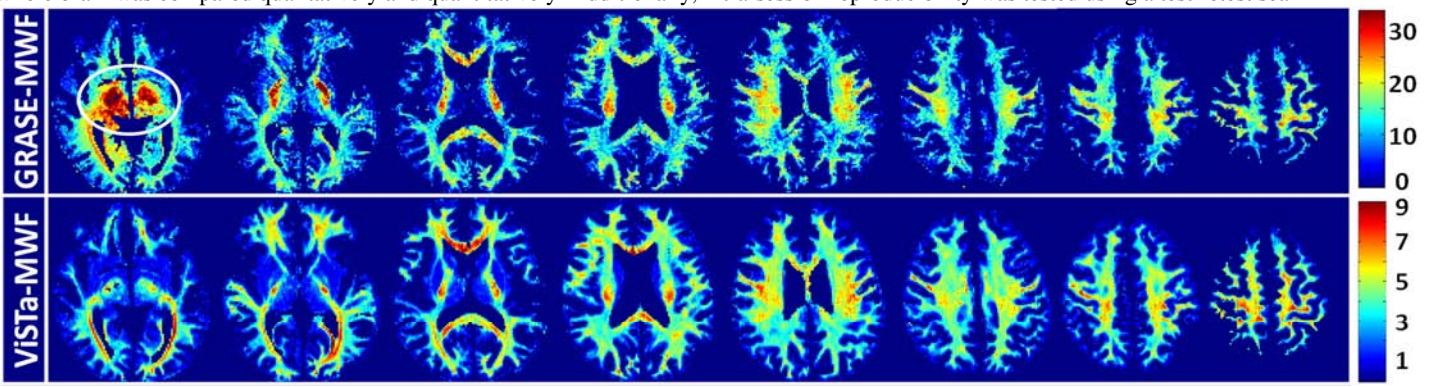

Figure 2. MWF maps from 3D GRASE (upper) and 3D ViSTa (lower)

METHODS For the comparison of the whole brain MWF, data were collected from five subjects at 3T (IRB-approved). ***3D GRASE:*** A 3D GRASE sequence was implemented as in (3). The scan parameters were as follows: 20 slices, resolution = 1.5 × 1.5 × 4 mm^3, TR = 1000 ms, TE = 10:10:320 ms, phase encoding lines per each segment = 3, partial k-space in slice = 6/8, and scan time = 13.33 min. To generate the MWF, the multi-echo data were processed using a regularized nonnegative least-square fitting method (1, 3). The stimulated echo was corrected (3, 6). ***3D ViSTa*:** A 3D volume was covered by replacing a 2D readout in (4) with a 3D segmented EPI readout while keeping the same sequence structure and timing. For the excitation pulse, a minimum phase SLR pulse (7) was used. Unwanted arterial and fat signals were suppressed by flow and fat saturation pulses. The scan parameters were as follows: 32 slices, resolution = 1.5 × 1.5 × 4 mm^3, TR/TE = 1160/6.5 ms, $TI_1/TI_2/TD$ = 560/220/380 ms, partial k-space in phase = 6/8, PE lines per segment = 11, number of segments = 11 and scan time = 6.53 min. In order to match the scan time with the 3D GRASE, the 3D ViSTa data were acquired twice and averaged. To quantify the MWF in ViSTa, a proton density-weighted GRE scan that had the same readout as 3D ViSTa was acquired using a TR of 75 ms and flip angle of 5° (0.5 min). The ViSTa MWF was calculated by dividing the ViSTa data by the GRE data, then multiplying by a scaling factor (*f*). This scaling factor compensates for T_1 and T_2^*-weighting in ViSTa and GRE scans using nominal values (see ref. 4 for details). ***Data analysis:*** After generating MWF maps from each method, a voxel-wise correlation of the two MWF maps was calculated in a white matter mask, which was generated from the 4th echo GRASE image segmented by SPM5. ***Reproducibility:*** To test intra-session reproducibility, the GRASE and ViSTa scans were acquired twice in a single session (three subjects). All of the parameters were the same as above, except the resolution (2 × 2 × 4 mm^3) to reduce the scan time.

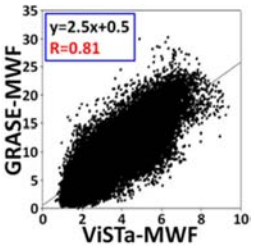

Figure 3. Voxel-wise correlation between ViSTa and GRASE

RESULTS Compared to 3D GRASE, 3D ViSTa can cover a larger volume in a shorter scan time. More importantly, ViSTa provides superior image quality with little or no speckle-like noise (Figs. 1 and 2). When compared (Fig. 2), the two maps reveal qualitatively similar MWF distributions across the slices, although the range of the MWF is different. This difference is due to the incomplete inclusion of certain factors such as cross relaxation, exchange, MT, and direct saturation effects in the scaling factor (*f*). In both maps, higher MWF is observed in genu, splenium, internal capsule, SLF, ILF, and the white matter near the primary motor/sensory cortices. In GRASE, a lower slice shows artifacts (circled) most likely from B_1 inhomogeneity in the slice profile. When the voxel-wise correlation was performed between ViSTa and GRASE MWF maps (Fig. 3), the mean correlation coefficient (cc) was 0.75 ± 0.04 (n = 5), suggesting a high similarity between the two maps. The reproducibility test results suggest that ViSTa is more reproducible (cc = 0.97 ± 0.01; n = 3) than GRASE (cc = 0.88 ± 0.03; n = 3).

CONCLUSION and DISCUSSION Compared to conventional 3D MWI, 3D ViSTa provides a high quality MWF map with wider coverage in a shorter scan time. The ViSTa MWF map shows a good correlation with that of GRASE, and demonstrates better reproducibility. The MWF differences may be adjusted by modifying the scaling factor (*f*) to match the two scans.

REFERENCES [1] Mackay, MRM, 1994, 31, 673 [2] Oh, MRI, 2006, 24, 33 [3] Prasloski, Neuroimage, 2013, 63, 533 [4] Oh, Neuroimage, 2013, 83, 485 [5] Oh, ISMRM, 2013, #867 [6] Prasloski, MRM, 2012, 67, 1803 [7] Pauly, IEEE, 1991, 10, 53

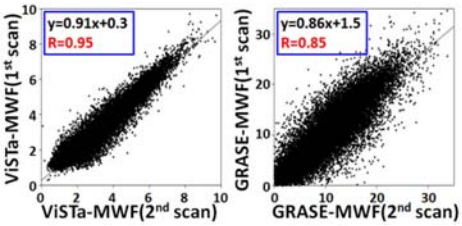

Figure 4. Reproducibility results