Whole Cerebrum Myelin Water Imaging In Less Than 15 Minutes

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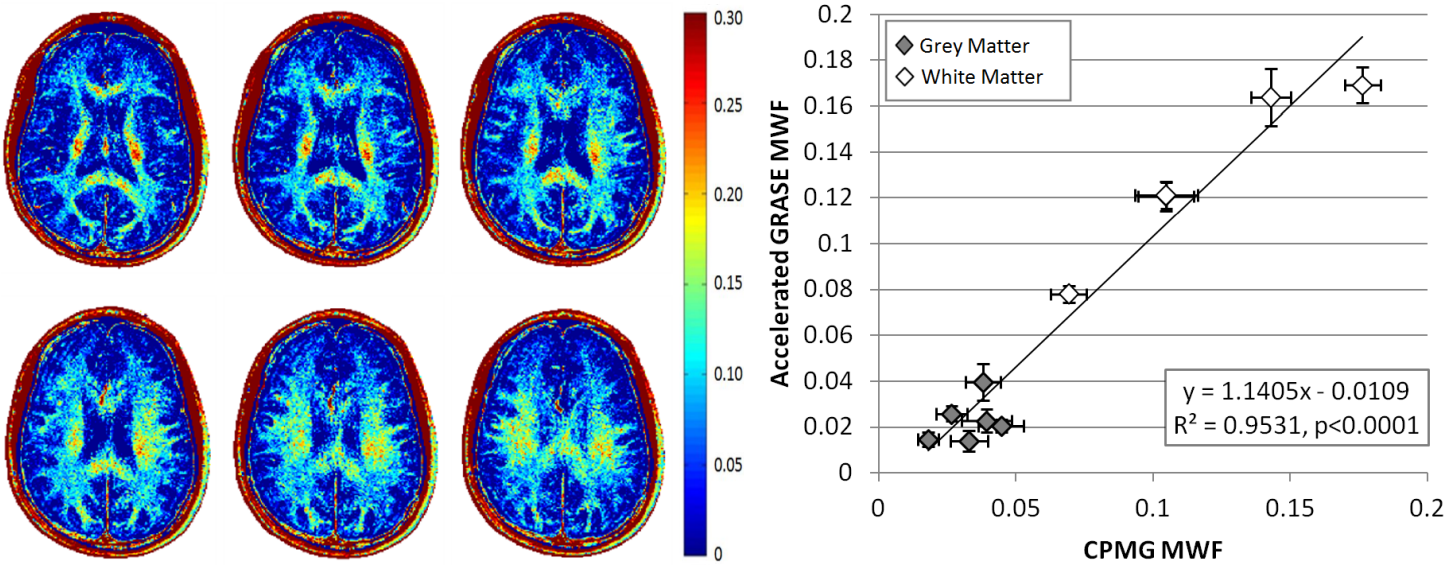
Introduction: Myelin water imaging (MWI), a magnetic resonance imaging technique capable of resolving the fraction of water molecules which are trapped between the myelin bilayers surrounding neurons, is an invaluable tool for investigating both normal and pathological brain structure *in vivo*. The majority of MWI analysis is performed via multi-component T_2 analysis. That is, decay curves from multi-echo spin echo images exhibiting T_2 contrast are decomposed into discrete T_2 components to create a T_2 distribution[1,2]. This technique has been validated against histopathology[3] and is currently regarded as the most specific surrogate MRI marker for myelin. The main limitation of this technique has been the long data acquisition times of about 20 minutes for one slice. For more brain coverage, these images must be acquired in 3D in order to prevent magnetization transfer effects from exciting multiple slices, resulting in prohibitively long data acquisition times. For MWI to be performed in a clinical setting, whole brain data at reasonable spatial resolution must be acquired within feasible scan durations. Here we present a method for the acquisition of myelin water fraction maps of the whole cerebrum within less than 15 minutes using a 32 echo 3D GRASE sequence.

Material and Methods: All measurements were performed on a Achieva 3.0T scanner, (Philips Medical Systems) using an eight-element eight-channel phased-array head coil for reception and an internal quadrature bird-cage coil for transmission. A three-fold acceleration of the data acquisition was achieved with the GRASE approach alone[4]. Further acceleration by a factor of 2 was achieved with partial parallel imaging (SENSE), and a further factor of 1.5 was provided by slice-undersampling followed by zero-filling. Taken together, 9-fold acceleration was achieved, allowing for coverage of the whole cerebrum within 14.4 minutes. Other imaging parameters were: TR=1000 ms, TE=10, 20, 30,..., 320 ms, 40 reconstructed slices at 2.5 mm thickness, acquired voxel size=1x1x5 mm, 232x192 matrix, receiver bandwidth: spin echo=33 kHz, gradient echo=188 kHz. GRASE uses gradient echoes for the periphery of k-space which induces minor T_2* weighting. Therefore the GRASE approach was compared to a conventional 3D CPMG method (TR=1200 ms, echo times=10, 20, 30,…, 320 ms, 7 slices, slice thickness=5mm, in-plane voxel size=0.9x1.6 mm, 256x128 matrix, receiver bandwidth=111 kHz, acquisition time=19.8 minutes)[5]. For both sequences myelin water fraction maps were computed off-line using a Non-Negative Least Squares (NNLS) approach[6] with a correction for stimulated echoes[7].

Results: 6 representative MWF maps from a 40 slice GRASE data set are shown in the left figure. The figure on the right demonstrates that myelin water fraction values in 9 normal volunteers from 11 regions of interest correlated extremely well between GRASE and CPMG (R^2=0.95, p<0.0001). However, as can be observed from the slope of the fit, there is a small bias. As mean MWF increased, GRASE tended to overestimate the MWF as compared to CPMG. However, the magnitude of this over-estimation reached only 0.017 as the mean MWF reached 0.2. Since we rarely see MWF values above 0.2, this bias is considered tolerable.



Discussion: We have shown that MWI is possible with an accelerated GRASE sequence. Results obtained with this approach are in good agreement with those attained from current standard sequences. Further, the myelin water fraction maps acquired using GRASE are of higher quality (higher spatial resolution, decreased flow artefact) than those of its predecessor, the standard CPMG sequence. Since we used a 3D technique, the loss in signal to noise ratio due to k-space undersampling is compensated by the significant increase in brain coverage. Routine MWI could be extremely useful in the diagnosis and treatment of neurodegenerative diseases such as multiple sclerosis. We believe that time efficient MWI will have a significant impact on the management of diseases and also the ability to address other questions in neuroscience.

References: **[1]** Mackay, A. et al., Magn Reson Med, 31, 673-677 (1994). **[2]** Whittall, K.P. et al., Magn Reson Med, 37, 34-43 (1997). **[3]** Laule, C. et al., Neuroimage, 40, 1575-80 (2008). **[4]** Mädler, B. and MacKay, A.L., in Proc of the 15th ISMRM, Berlin 2007, p1723. **[5]** Mädler, B. and MacKay, A.L., in Proc of the 14th ISMRM, Seattle 2006, p2112. **[6]** Whittall, K. and MacKay, A., JMR, 84, 134-152 (1989). **[7]** Prasloski, T. et al., Magn Reson Med, doi: 10.1002/mrm.23157 (2011).