Rapid whole brain T1 rho mapping

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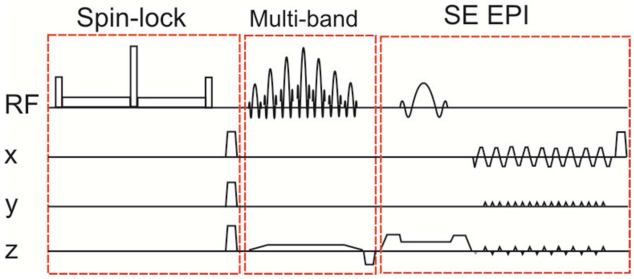
Purpose To acquire whole brain T1-rho map under 5 minutes using single-shot acquisition and multi-band imaging.

Introduction T1-rho reflects the spin-lattice relaxation in the rotation frame, it can be manipulated via the adjustment of the spin-lock time (TSL) and spin-lock field to provide varying contrast. T1 rho weighted images have shown superior contrast to conventional T1 and T2 in various applications such as cartilage, cardiac and tumor. In addition, T1 rho mapping has been shown to be a viable bio-marker for detecting neurodegenerative diseases [1], which generally show little morphological changes. However, T1 rho acquisition is often constrained to single slice due to the long TSL needed, which makes the cross-examination with other measurements such as resting state fMRI difficult. In this work, we develop a rapid T1-rho mapping method that utilizes single-shot EPI acquisition and multi-band excitation that completes a 2mm isotropic whole brain T1 rho mapping within 5 minutes, which allows this acquisition to be added in a Parkinson disease related clinical study.



Method **Fig.1** shows the pulse sequence used in this study. A B0-B1 insensitive spin-lock module that uses a 180 refocus and a phase cycling scheme is used for the T1 rho preparation [2], followed by crusher gradients on three axes. The non-selective nature of the spin lock module allows multiple slices to be simultaneously acquired with a multiband excitation RF. A single shot spin echo EPI acquisition along with Z-axis gradient blipping scheme was used to introduce additional phase shift in k-space to generate a shifted-FOV aliasing pattern [3].

Figure 1 Slice multiplexing T1 rho weighted acquisition

Experiment This method is used to be used in a Parkinson diseases studies and healthy volunteers were first scanned for verification. A total of 70 slices were needed to achieve whole brain coverage and an isotropic 2mm resolution. A slice multiplexing factor of 2 leads to 35 acquisitions in total. The acquisition matrix used was 128x128 with a TE of 24ms and a TR of 2000ms, and this gives an acquisition time of 1:10 per volume. Four TSL times of 20ms, 40ms, 60ms and 80ms were acquired at a spin-locking field of 400Hz for deriving the T1 rho map. Hence the overall acquisition time was 4:40 minutes. To investigate the effects of multiplexing of the T1rho map, multi-band acquisition and single band acquisition were compared.

Results **Fig.2a** shows the resulting slice-multiplexed acquisition where the top half volume is shifted and overlapped with the bottom half volume. **Fig.2b** shows cross sections of the reconstructed T1 rho map obtained, and the numerical values agree with those published [1]. **Fig.3c** compares the T1-rho values of selected deep nuclei, WM and GM regions obtained from normal and slice-multiplexing acquisition, it shows that almost identical values were obtained although the acquisition time was halved.

Discussion and conclusion In this work, single-shot EPI with slice-multiplexing was used to acquire whole brain T1 rho map within an acceptable time for clinical studies, which has great potential for further exploiting the values of T1-rho measurements in neurodegenerative diseases. There are two potential factors that may affect the quality of the slice multiplexing T1-rho map compared to conventional acquisitions: increased noise level attributed to *g*-factor and differing N/2 Nyquist ghosting correction for EPI. The former has been shown to have minimal effects due the favorable aliasing pattern received: actually only a small portion of the brain overlapped due to the geometry of human head (**Fig2.a**). The latter is related to the fact that the effects of eddy-current on different slices may be slightly different, for which the correction is generally performed on a per-slice basis. Currently it is performed based on the multiplexed slice, which could be sub-optimal. However no obvious residual ghost was observed thus far; and this may be improved by acquiring separate calibration data at different slice locations.

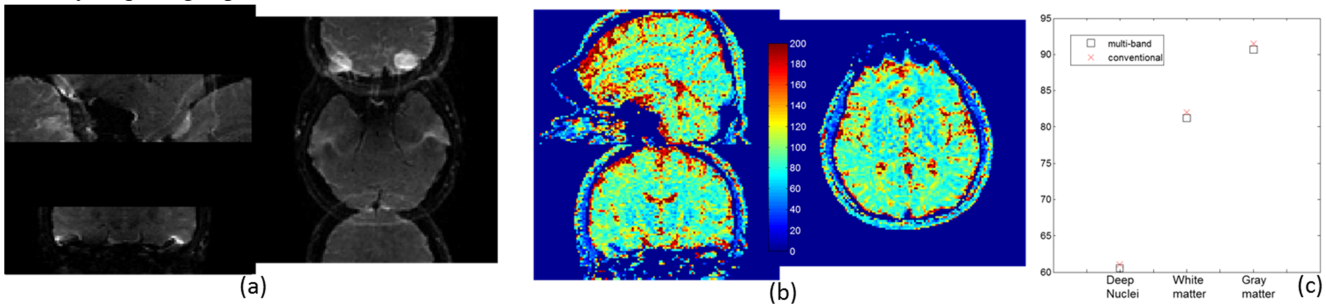


Figure 3 (a) Slice Multiplexed whole brain acquisition (b) cross sections of the whole-brain T1 rho maps (c) comparison of calculated T1 rho values

Reference [1] A. Borthakur, et al, Neuroimage, 2008; [2] W. Witschey II, et al. JMRI, 2007; [3] K. Setsmpop, et al MRM, 2012