Accelerated Breath-Hold Multi-Echo FSE Pulse Sequence Using Compressed Sensing and Parallel Imaging for T2 Measurement in the Heart

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Introduction: Measurement of proton transverse relaxation time (T_2) can be used to detect pathological changes in tissue for a variety of clinical applications, including identification of edema and iron overload. The most widely used T_2 mapping pulse sequence is the Carr-Purcell-Meiboom-Gill (CPMG) sequence [1,2]. For body MRI, however, a CPMG pulse sequence is typically performed with navigator gating due to its low data acquisition efficiency. A new T_2 mapping pulse sequence [3] based on multi-echo fast spin-echo (ME-FSE) readout with a net acceleration rate (R) of 3.2 (parallel imaging [PI] with R = 1.6 + turbo factor = 2) has been proposed to perform breath-hold (BH) body MRI acquisition. This new T_2 mapping pulse sequence uses a reverse centric k-space reordering to sample the central half with more accurate even echoes and the outer half of k-space with less accurate odd echoes, and thereby provides even-echo CPMG accuracy. The new T_2 mapping pulse sequence has been reported to yield spatial resolution of 2.7 mm x 3.8 mm within a breath-hold duration on the order of 20s. While this spatial resolution may be adequate for liver imaging, it may be marginally acceptable for cardiac imaging where myocardial wall thickness is typically on the order of 10 mm. We propose to further accelerate this pulse sequence using a recently developed joint reconstruction algorithm that combines compressed sensing (CS)[4] and PI to exploit joint sparsity of randomly undersampled data acquired from different receiver coils, as previously described [5]. Cardiac ME-FSE imaging is a good candidate for this joint CS-PI approach, since spatial and temporal correlations in the image series result in sparse representations. The purposes of this study were to highly accelerate the T_2 mapping pulse sequence using the joint CS-PI technology and evaluate accuracy of the resulting T_2 measurements.

Methods: For convenience, ME-FSE with parallel imaging alone and ME-FSE with CS-PI are considered the standard and accelerated T_2 mapping pulse sequences, respectively. Both the standard and accelerated T_2 mapping pulse sequences were implemented on whole-body 3T MRI scanners (Siemens; Tim Trio; Verio) equipped with a 32-element cardiac coil array (Invivo). The relevant imaging parameters for both pulse sequences are: FOV = 300 mm x 300 mm, slice thickness = 8 mm, echo spacing= 5 ms, turbo factor =2, number of images=10, echo train duration = 103 ms, receiver bandwidth = 531 Hz/pixel, fat suppression and double-inversion, black-blood preparation pulses. The accelerated T_2 mapping pulse sequence used R = 6, acquisition matrix = 192 x 192, and BH duration = 17s. This acceleration factor was chosen based on a simulation experiment with a fully sampled ME-FSE data (not shown). The standard T_2 mapping pulse sequence used GRAPPA [6] parallel imaging with R = 1.8, acquisition matrix = 192 x 76, and BH duration = 21 s. Note that, in order to maintain a BH duration on the order of 20s, the spatial resolution in the phase-encoding direction in the standard sequence was set at only 40% of the resolution achieved in the accelerated sequence. For validation, we imaged a phantom consisting of five bottles containing different concentrations of manganese chloride ($MnCl_2$) in distilled water: 0.135, 0.270, 0.405, 0.540 and 0.675 mM. $MnCl_2$ was chosen because its T_1/T_2 is similar to that of biological tissues, and these concentrations were chosen to emulate clinically relevant T_2 values in tissues. Eight adult volunteers (5 males and 3 females; mean age = 27.4 ± 1.4 years) were imaged in a mid-ventricular short-axis plane at mid diastole, with electrocardiogram gating. GRAPPA image reconstruction was performed on-line using a commercially available reconstruction algorithm. Joint CS-PI reconstruction was performed off-line using customized software developed in Matlab (MathWorks, MA). For more details on the joint CS-PI reconstruction, please see reference 5.

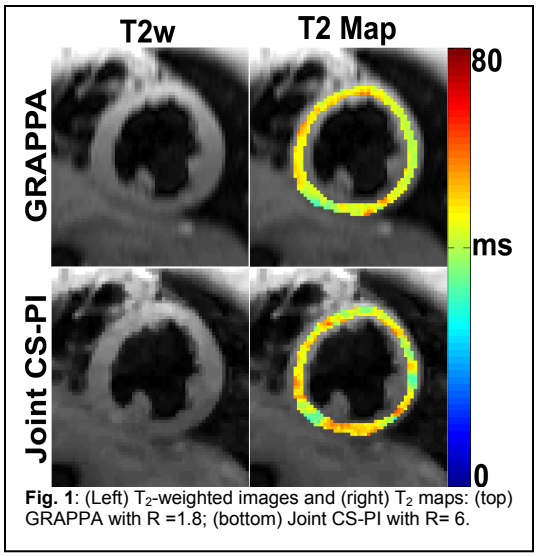

Fig. 1: (Left) T_2-weighted images and (right) T_2 maps: (top) GRAPPA with R =1.8; (bottom) Joint CS-PI with R= 6.

For the phantom data, five bottles were manually segmented to mask out the background. For in vivo data, myocardial contours were manually segmented using short-axis planes. The corresponding pixel-by-pixel T_2 maps were calculated by non-linear least square fitting for three parameters of the mono-exponential relaxation equation. The three unknown parameters were: initial signal amplitude, T_2, and background noise. The T_2 values were averaged over each region of interest (phantom or myocardium). The five mean R_2 ($1/T_2$) measurements of the $MnCl_2$ phantom were plotted as a function of $MnCl_2$ concentration, and the relaxivity of $MnCl_2$ was calculated using a linear regression analysis. Phantom and In vivo T_2 measurements were pooled, and a Bland-Altman analysis was performed to evaluate the accuracy of the accelerated T_2 mapping pulse sequence against the standard T_2 mapping pulse sequence.

Results: The standard and accelerated T_2 mapping pulse sequences in the phantom studies yielded $MnCl_2$ relaxivity of 93.9±1.8 and 93.8±2.9 s^{-1}/Mm, respectively. Figure 1 shows representative in vivo T_2-weighted (T_2w) images (first images in series) and the corresponding T_2 maps acquired using the standard and accelerated T_2 mapping pulse sequences. As expected, the accelerated T_2 mapping pulse sequence yielded higher spatial resolution in the phase-encoding direction. Accordingly to the Bland-Altman analysis, the T_2 measurements obtained with the two pulse sequences were in good agreement (mean difference =-0.2 ms; upper and lower 95% limits of agreement were 2.2 and –2.7 ms, respectively), suggesting that T_2 measurements by the two pulse sequences are quantitatively equivalent.

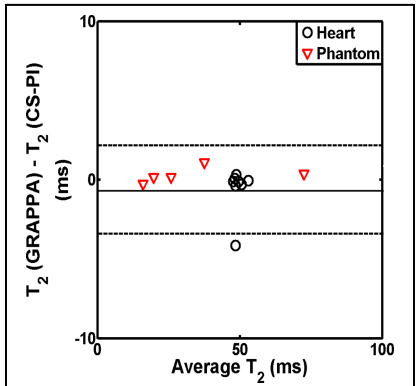

Fig. 2: Bland-Altman analysis of T_2 measurements obtained with the GRAPPA and Joint CS-PI techniques. Units in ms.

Conclusion: This study demonstrates the feasibility of performing accelerated T_2 mapping with relatively high spatial resolution (e.g., 1.6 mm x 1.6 mm) using the joint CS-PI technique. We hypothesize that an improved spatial resolution will minimize partial volume effects and permit better regional assessment of T_2 in the heart. While this study was motivated to perform high spatial resolution T_2 measurement in the heart, this accelerated pulse sequence can be useful for other clinical applications, particularly body imaging (e.g., liver, kidney). Future work includes continued validation of the accelerated T_2 mapping pulse sequence, optimization of the CS-PI reconstruction algorithm, and additional patient recruitment.

References: [1]. Carr, H, et al. Phys Rev 1954;94:630–638. [2]. Meiboom, S, et al. Rev Sci Instrum 1958;29:688–691. [3]. Kim, D, et al. MRM 2009; 62: 300-306. [4]. Lustig M, et al. MRM 2007;58:1182-1195. [5]. Otazo R et al. ISMRM 2009; 378. [6]. Griswold MA, et al. MRM 2002;47:1202-1210.

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