High Resolution Multi-slice Myocardial T_2 Mapping with Improved Scan Time Efficiency

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Introduction/ Purpose: Quantitative myocardial T_2 mapping allows non-invasive assessment of myocardial inflammation and edema [1]. In a typical T_2 mapping sequence, pixel-wise T_2 maps are generated by acquiring series of T_2 weighted images with different T_2prep echo times using an ECG triggered single-shot acquisition. Rest cycles are needed between each two successive images to allow full magnetization recovery, which results in a reduced scan time efficiency. In such sequence, multi-segment acquisition is difficult to be employed as it requires even more rest cycles between each two successive segments, which makes the scan time even longer. This reduces the feasibility of the multi-segment high-resolution T_2 mapping in clinical settings. Recently, a free-breathing multi-slice myocardial T_2 mapping sequence was proposed to increase the scan time efficiency of T_2 mapping sequence by combining a slice-selective T_2prep pulse and interleaved slice acquisition which eliminates the need of rest cycles for magnetization recovery. In this study, we sought to further extend the multi-slice T_2 mapping sequence to allow segmented acquisition to achieve higher in-plane spatial resolution within an acceptable scan time.

Methods

Imaging Sequence: **Fig. 1** shows the schematic of the proposed segmented data acquisition for multi-slice myocardial T_2 mapping, which consists of multiple slice-selective T_2prep prepared blocks with different echo times. Each block is acquired using an ECG triggered multi-shot acquisition, which is repeated for all k-space segments. This acquisition block is then repeated with different order of slices to acquire all slices at each echo time.

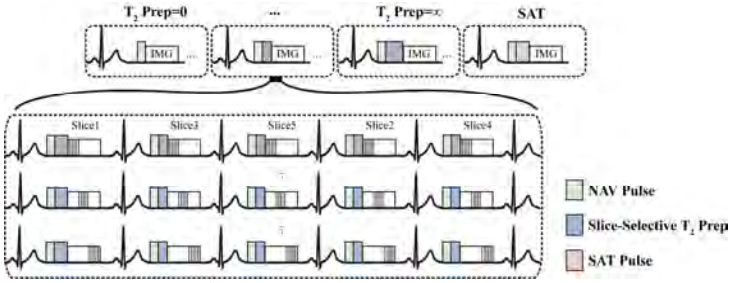

Figure 1. *Schematic of the high resolution multi-slice T_2 mapping sequence using segmented data acquisition. A series of T_2prep blocks (First block: T_2prep=0, last block: T_2prep=∞) which acquired after saturation pulse are acquired using a segmented data acquisition and repeated with different order of slices.*

Experimental Validation: To characterize the proposed sequence in terms of accuracy, precision, and reproducibility, vials of $NiCl_2$ doped agarose phantom with different T_1/ T_2 times were imaged five times repeatedly using a segmented data acquisition scheme and compared to a single-shot multi-slice T_2 mapping sequence (*single-shot*: TR/TE=2.7/1.3ms, voxel size=2x2mm^2, slice thickness=8mm, TFE factor=73, acquisition window=195.8ms/ *3-segments*: TR/TE=3.8/1.9 ms, voxel size=1x1mm^2, slice thickness=10mm, TFE factor=36, acquisition window=136.9ms, with bSSFP imaging readout, flip angle=85, FOV=280x280mm^2, linear k-space ordering, 10 linear ramp-up pulses, SENSE factor=2). Accuracy was defined as the difference between the mean T_2 value and the averaged reference T_2 (spin echo) in each vial. Precision was defined as the averaged standard deviation of T_2 in each vial. Reproducibility was defined as the standard deviation of T_2 over five repetitions. Statistical significances between sequences were assessed using a Wilcoxon signed rank test. To evaluate the spatial resolution, images were acquired using a high resolution phantom with single-shot, 3-segments, 5-segments acquisition which results in 2x2mm^2, 1x1mm^2, 0.7x0.7mm^2 in-plane spatial resolution, respectively (*single-shot*: TR/TE=2.7/1.4ms, voxel size=2x2mm^2, slice thickness=8mm, TFE factor=106, acquisition window=285ms/ *3-segments*: TR/TE=3.8/1.9ms, voxel size=1x1mm^2, slice thickness=10mm, TFE factor=60, acquisition window=229ms/ *5-segments*: TR/TE=4.8/2.4ms, voxel size=0.7x0.7mm^2, slice thickness=10mm, TFE factor=50, acquisition window=239ms, with bSSFP imaging readout, flip angle=85, FOV=380x412mm^2, linear k-space ordering, 10 linear ramp-up pulses, SENSE factor=2). To further investigate the feasibility of the proposed multi-shot sequence, an ex-vivo heart of an infarcted swine model were imaged using a multi-slice T_2 mapping sequence with different number of segments in k-space (*single-shot*: TR/TE=2.9/1.4ms, voxel size=2x2mm^2, slice thickness=8mm, TFE factor=41, acquisition window=117.5ms/ *3-segments*: TR/TE=3.9/1.95ms, voxel size=1x1mm^2, slice thickness=10 mm, TFE factor=23, acquisition window=89.7ms/ *5-segments*: TR/TE=6.1/3ms, voxel size=0.5x0.5mm^2, slice thickness=10mm, TFE factor=26, acquisition window=158ms, with bSSFP imaging readout, flip angle=85, FOV=200x152mm^2, linear k-space ordering, 10 linear ramp-up pulses, SENSE factor=2). T_2 maps were generated by voxel-wise curve-fitting of the signal with a three-parameter fit model [2].

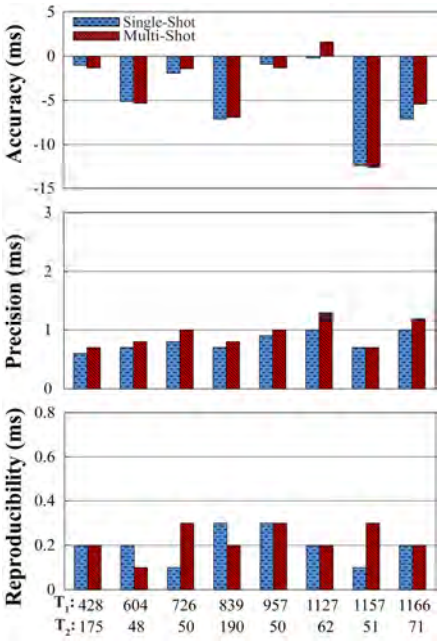

Figure 2. *Multi-shot sequence yields similar accuracy and reproducibility with reduced precision compared to the single-shot multi-slice myocardial T_2 mapping sequence in the phantom study.*

Results: In phantom study, the multi-shot T_2 mapping sequence provides similar accuracy and reproducibility ($p>0.05$) with lower precision ($p=0.002$) compared to a single-shot sequence (**Fig. 2**). The impact of the improved spatial resolution was shown in the phantom study (**Fig. 3**), as well as in the ex-vivo study (**Fig. 4**).

Conclusion: The proposed high resolution multi-slice T_2 mapping using segmented data acquisition allows higher in-plane spatial resolution with high efficiency in the scan time.

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References: [1]He,JMRI,2006, [2]Akçakaya,MRM,2014.

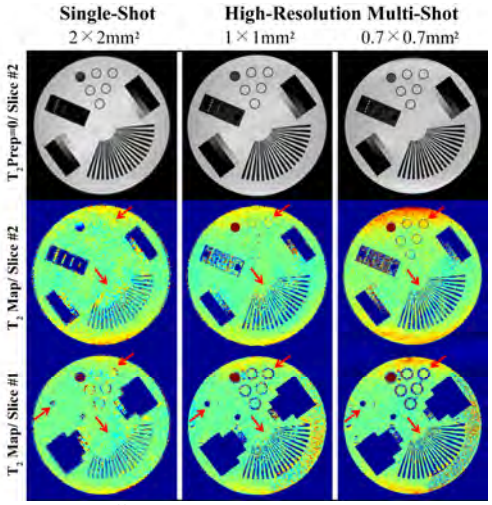

Figure 3. *Different phantom structures appear sharper in the high resolution T_2 maps acquired using the multi-shot acquisition compared to the single-shot sequence.*

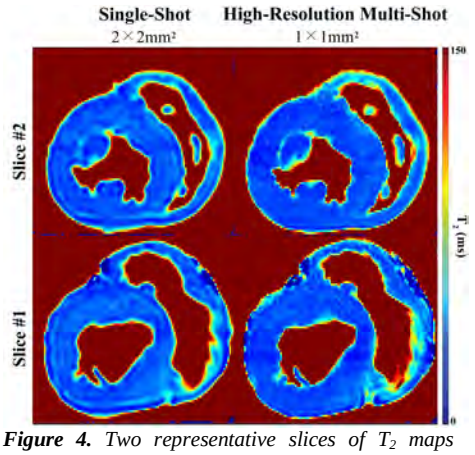

Figure 4. *Two representative slices of T_2 maps acquired from an ex-vivo infarcted heart of a swine model. Reduced partial voluming error is shown on the high-resolution T_2 maps which are acquired using the proposed multi-slice T_2 mapping sequence.*