Free-Breathing Multi-Slice Myocardial T1 Mapping Using Inversion Recovery Slice Interleaved Spoiled Gradient Echo Imaging

Sébastien Roujol[1], Jihye Jang[1,2], Tamer A. Basha[1], Sebastian Weingärtner[1,3], Sophie Berg[1], and Reza Nezafat[1]

[1]*Department of Medicine, Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, Massachusetts, United States,* [2]*Computer Aided Medical Procedures, Technische Universität München, Munich, Germany,* [3]*Computer Assisted Clinical Medicine, University Medical Center Mannheim, Heidelberg University, Mannheim, Germany*

Target Audience

Scientists and clinicians who are interested in myocardial tissue characterization.

Purpose/Introduction

Myocardial T_1 mapping shows promise for the detection of various cardiomyopathies. Native myocardial T_1 mapping sequences usually employed a balanced steady state free precession (b-SSFP) readout, which leads to increased susceptibility to the B_0 field inhomogeneity and generates regional variations in T_1 estimates[1]. Furthermore, the b-SSFP signal is T_2 dependent and sensitive to magnetization transfer, which can induce substantial bias in T_1 estimates[2,3]. Gradient recalled echo (GRE) imaging has been used in the initial Look-Locker sequence, but cannot provide pixel-wise T_1 estimates. Post-contrast T_1 mapping using GRE has been reported using successive inversion pulses[4] or saturation pulses[5]. However, advantages and disadvantages associated with the use of GRE sequence for native myocardial T_1 mapping remain to be investigated further. In this study, we sought to develop and evaluate a multi-slice T_1 mapping sequence using GRE readout and characterize its accuracy, precision, and reproducibility for in-vivo native myocardial T_1 mapping.

Materials and Methods

Proposed sequence: The slice-interleaved T_1 (STONE) sequence has been recently proposed to provide multi-slice T_1 mapping coverage with a novel free breathing inversion recovery (IR) scheme[6]. In this study, this approach is extended for simultaneous imaging of five slices under free breathing conditions using GRE readout. Each slice is first acquired without any magnetization preparation pulse to sample the fully recovered longitudinal magnetization. Subsequently, an IR experiment is performed where the 5 slices are acquired over the 5 heartbeats following the IR pulse using a slice interleaved ordering to minimize potential slice cross talk effect. This IR experiment is repeated 5 times using different slice order to obtain signal samples for each slice at TI, TI + 1 RR, TI + 2 RR, TI + 3 RR, TI + 4 RR (where RR denotes the interval time between two R-waves, and TI is the inversion time). This block of 5 IR experiments is finally repeated using a different TI. Prospective slice tracking using a respiratory navigator is used to compensate for respiratory motion.

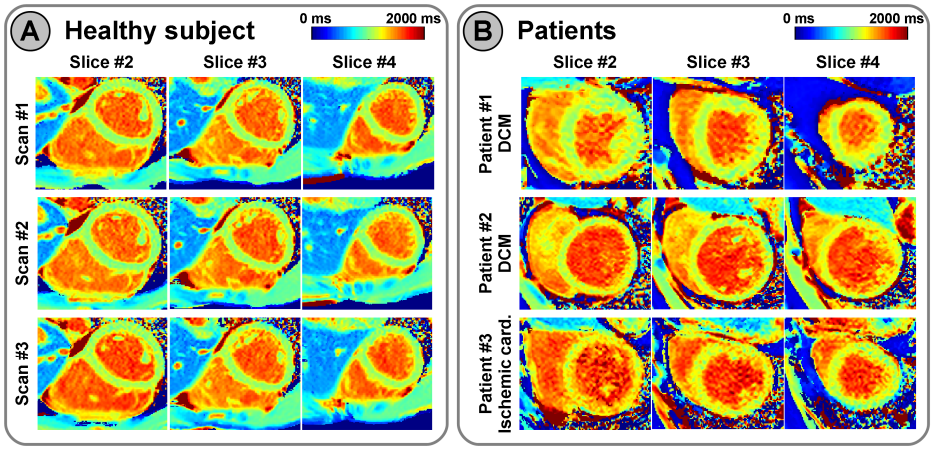

Figure 1. *(a) Example native T_1 maps obtained in three repetition of the proposed sequence in one subject. All T_1 maps show homogeneous T_1 signal over all myocardium, slices, and repetitions. (b) Example native T_1 maps obtained with the proposed sequence in 3 patients. Excellent native T_1 map quality was achieved in patients.*

Experimental evaluation: All data were acquired on a 1.5 T Phillips scanner. Nine healthy adult subjects (37±22 years, 4 males) were imaged 5 times with the proposed sequence and MOLLI to quantify the precision and reproducibility of each sequence. Sixteen patients (54±21 years, 13 males) referred for clinical CMR were imaged using the proposed sequence to show the feasibility in patients. The proposed sequence used a GRE imaging readout (5 slices, TR/TE/α=4.3/2.1ms/10°, FOV=280×272 mm^2, voxel size=2×2 mm^2, slice thickness=8 mm, number of phase-encoding lines=43, linear ordering, 10 linear ramp-up pulses, SENSE factor=2.5, half Fourier=0.75, bandwidth=382Hz/pixel). T_1 maps were reconstructed using a 2-point fit model and affine image registration. The MOLLI sequence used a 5-(3)-3 scheme with a b-SSFP readout and similar parameters (except TR/TE/α=2.6/1.3ms/70°, bandwidth=1785Hz/pixel, 1 slice). Image registration was performed using ARCTIC[7]. T_1 maps were reconstructed using a 3-point model fit with "Look-Locker correction".

Data Analysis: Precision was defined as the average (over the 5 repetition scans) of the standard deviation of T_1 estimates over a given slice. Reproducibility was defined as the standard deviation (over the 5 repetition scans) of the spatial average T_1 values in one given slice. Statistical tests were performed by means of Wilcoxon signed-rank tests (significance threshold at $p < 0.05$).

Results

Figure 1 shows example native T_1 maps obtained in 1 healthy subject (a) and 3 patients (b). All T_1 maps depicted excellent quality. In healthy subject (Figure 2), the proposed sequence yielded higher native T_1 times than MOLLI (1084±21ms vs. 1011±27ms, p=0.004) but with similar precision (64±10ms vs. 67±10ms, p=0.36) and reproducibility (18±9ms vs. 10±6ms, p=0.098).

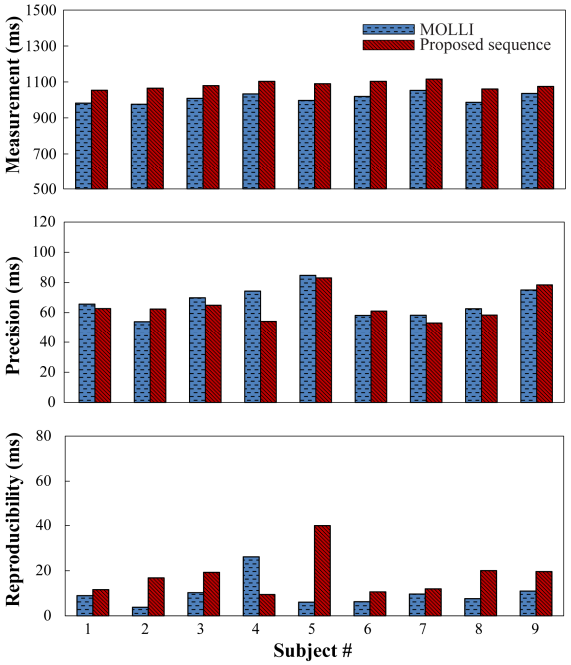

Figure 2. *Measurements, precision, and reproducibility of native T_1 mapping with the proposed sequence and MOLLI for each subject. Each metric was measured over the entire mid-ventricular slice in the proposed sequence and the single MOLLI slice.*

Conclusions

The proposed free breathing multi-slice T_1 mapping sequence yields similar in-vivo precision and reproducibility as MOLLI but with improved accuracy. In addition, the proposed sequence allows simultaneous imaging of 5 slices within free-breathing in ~100 sec.

Acknowledgements

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References

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