Free-Breathing Multi-Slice Myocardial T2 Mapping

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Introduction Quantitative myocardial T_2 mapping allows non-invasive assessment of myocardial inflammation/edema (1). Current implementations commonly use a T_2-prepared (T_2prep) SSFP sequence to acquire different T_2 weighted images at different echo times to generate the T_2 maps (2). To allow for full signal recovery before the application of a new T_2Prep, a rest period of several heartbeats is usually inserted without any data acquisition. For example, a 3 heartbeats rest period was used in the T_2 mapping sequence proposed in (1), resulting in the acquisition of only 3 T_2W images over 12 heartbeat acquisition (i.e. data acquisition efficiency of 25%). Therefore, to cover the entire left ventricle with 5 slices, the scan time is 60 sec of which 45 sec are a waiting time with no data acquisition. In this study, we propose a novel multi-slice T_2 mapping sequence by developing a slice-selective T_2Prep sequence, which allows interleaving the data acquisition of different slices in subsequent heartbeats. A slice-selective T_2Prep enables data acquisition for different slices and eliminates the need for rest period commonly used in conventional non-slice selective T_2 mapping sequences.

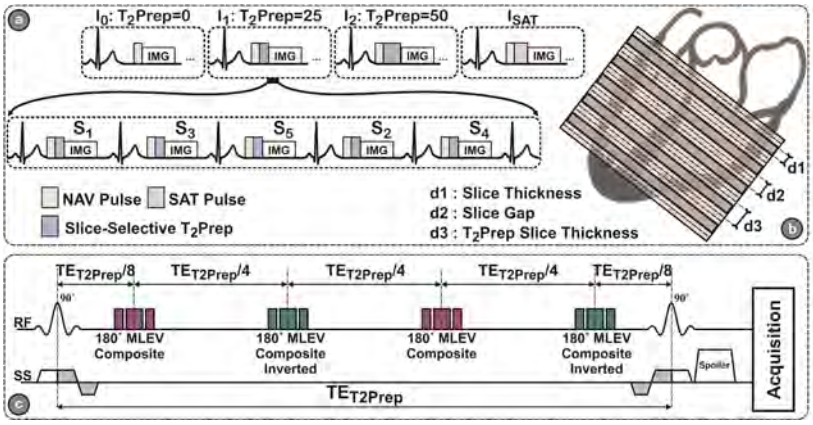

Fig 1. a) Sequence schematic using slice-selective T_2prep with b) an interleaved slice acquisition scheme. The imaging sequence uses a respiratory navigator (NAV) pulse for slice tracking by measuring respiratory motion of the right-hemi-diaphragm. The sequence consists of several T_2prep blocks, each with a specific T_2prep echo time. In each block, all slices are subsequently acquired in an interleaved fashion using ECG triggered T_2-prepared single shot imaging. The first block usually corresponds to T_2prep = 0, and the last block corresponds to T_2prep = ∞, where each image is acquired immediately after a saturation pulse (I_{SAT}). c) Schematic of the slice-selective T_2 magnetization preparation composite using 2 slice-selective 90° and -90° pulses with four non-selective composite MLEV refocusing pulses. The refocussing gradient for the second 90˚ pulse is reversed to achieve a perfect nulling for the gradients zero[th] moments in between the two 90˚ pulses.

Methods Pulse Sequence: Figure 1 shows the schematic of the proposed multi-slice T_2 mapping sequence, illustrated for the acquisition of 5 slices, with 4 different T_2prep echo times per slice.
Experiments: All imaging was performed on a 1.5T Philips Achieva MRI system using a 32-channel cardiac coil array. Phantom imaging was performed using $NiCl_2$ doped agarose vials, whose T_2/T_1 values spanned the ranges of values found in the blood and myocardium. Then, 10 healthy subjects were imaged using the proposed sequence, where a free-breathing ECG-triggered slice-selective T_2prep bSSFP sequence was used to acquire five short-axis slices with FOV = 320×320 mm^2, in-plane resolution = 2.5×2.5 mm^2, slice thickness = 8mm, slice gap = 4mm, TR/TE = 2.2/1.1ms, α = 40°, SENSE rate = 2, acquisition window = 140 ms. For comparison, a conventional breath-hold single-slice T_2prep bSSFP sequence was performed to image the middle of the 5-slices. All acquisitions were performed using the conventional 3-images with T_2prep echo times = 0, 25, 50 ms (2), with a SAT image added to compensate for the T_1 relaxation time during readout (3). T_2 maps were then generated using the 3-parameter fitting model (3).
Data Analysis: Images were transferred to a separate workstation for analysis. ROIs were defined on the different phantom vials, and T_2 values were estimated (3). In-vivo images were registered using non-rigid registration to compensate for residual in-plane motion, and T_2 values were calculated. Then, a myocardial segment based analysis was performed following the AHA segment model.

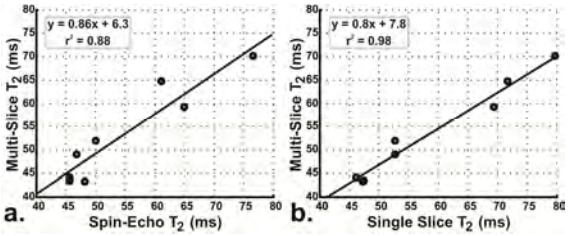

Fig 2. Regression analysis between estimated T_2 values in different phantom vials using the multi-slice sequence and reference T_2 values measured using a) spin echo and b) single-slice T_2 mapping sequences.

Results Fig 2 shows a strong correlation between the measurements from multi-slice T_2 sequence and both spin echo and single-slice sequences. In-vivo, the scan time for the proposed sequence was 4 heartbeats/slice compared to 13 heartbeats/slice in the conventional single-slice sequence. Fig 3 shows an example of the T_2 maps and bullseye quantifications obtained in one healthy subject. Fig 4 shows an example comparison between the single and multi-slice sequences in 3 healthy subjects. For each subject, the T_2 map generated from the single-slice sequence is compared to the T_2 map generated for the corresponding slice in the multi-slice sequence. The bullseye T_2 measurements are shown for each map.

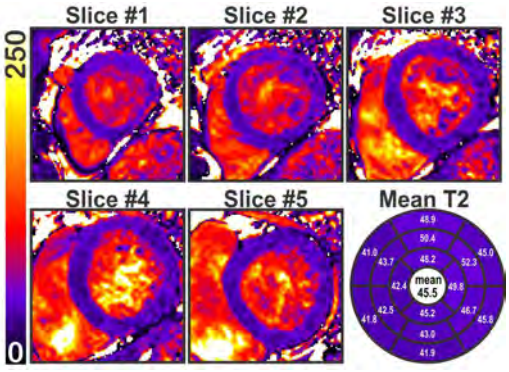

Figure 3. Representative example for the multi-slice T_2 maps/quantifications in a healthy subject.

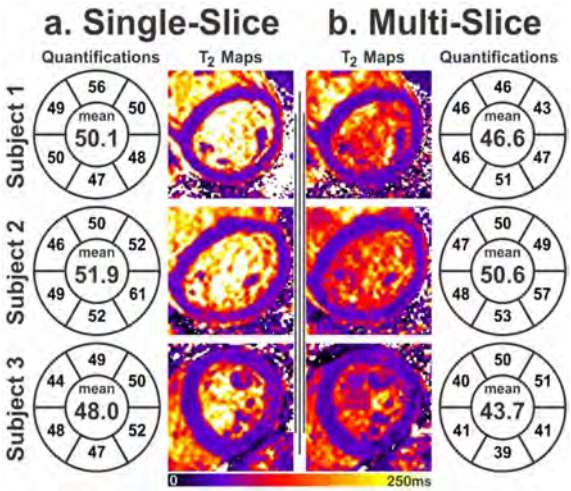

Fig 4. Example myocardial T_2 maps and T_2 measurements from single and multi-slice sequences in 3 healthy subjects. The values in each bullseye center represent the measurement value over the whole myocardium not the average of the segments values.

Conclusion
A novel multi-slice T_2 mapping pulse sequence was proposed to allow myocardial T_2 measurements over the entire left ventricle by imaging of 5 interleaved slices in 20 heartbeats.

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References
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