Breath-Held Myocardial T1 Mapping Using Multiple Single-Point Saturation Recovery

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Introduction: Changes in myocardial T_1 values have been demonstrated in a number of cardiac diseases. T_1 mapping, which is commonly performed by acquiring images at several time points after magnetization preparation, has shown promise for quantifying these T_1 changes. The challenge for cardiac T_1 mapping is obtaining sufficient sampling of the T_1 relaxation curve in a single breath-hold. Traditional approaches use inversion recovery (IR) or saturation recovery (SR) to collect either single or multiple data points after each preparation. Balanced SSFP (bSSFP) readouts are typically necessary to maximize SNR. Because IR must incorporate dead time to allow full magnetization recovery, T_1 mapping using single-point IR cannot be performed in a single breath-hold (1). Multi-point or Look-Locker (LL) IR is feasible in a breath-hold; however, the required dead time necessitates both partial Fourier and parallel imaging as well as long data acquisition windows (~200 ms) (2). Breath-held SR LL imaging, which obviates any dead time and uses shorter data acquisition windows without parallel imaging, has also been reported (3). However, LL techniques measure "apparent" T_1 (T_1*), which is a function of T_1 and T_2 for bSSFP, rather than the true T_1. This work demonstrates a cardiac T_1 mapping method that measures true T_1 directly and efficiently in a single breath-hold using multiple single-point SR with long delay times.

Methods: The proposed pulse sequence uses of a series of SR experiments, each consisting of a non-slice-selective saturation pulse, a delay time TS during which free T_1 relaxation occurs, and a bSSFP data acquisition period (Fig. 1). Images were acquired at four delay times, which has been shown to be effective for SR (4). Short TSs were acquired within a single heartbeat (Fig. 1a). Longer TSs, which have previously been unachievable in cardiac imaging, were performed across heartbeats and were therefore heart-rate dependent (Fig. 1b). In order to accurately measure long TSs, individual heartbeats were timed by repeatedly playing out wait pulses during non-imaging portions of each cardiac cycle. The following parameters were used for all T_1 mapping scans: TE/TR 1.7/3.9 ms, 45° flip angle, 256 x 160 matrix, 0.75 phase FOV, 0.5 NEX, 38 views per segment, 2 segments, and ECG triggering. Validation of T_1 measurements was performed on an agarose phantom with a reference T_1 measured by IR spin-echo imaging. Images were acquired at TSs of 300, 1300, 2300, and 4300 ms for a simulated heart rate of 60 beats per minute (bpm) and at 300, 900, 1500, and 4500 ms for 100 bpm. To measure the T_1 of normal myocardium, mid-ventricular short-axis slices were imaged in two healthy volunteers. For Volunteer 1, images were acquired at TSs of 200, 300, 1670, and 3137 ms, which required 1, 1, 2, and 3 heartbeats, respectively. The scan time was 14 heartbeats (7 heartbeats per segment). For Volunteer 2, the TSs were 300, 500, 1591, and 3744 ms, requiring 1, 1, 2, and 4 heartbeats, respectively, in 16 heartbeats. Non-contrast-enhanced T_1 mapping was also performed on a patient with hypertrophic cardiomyopathy (HCM) with TSs of 400, 600, 1457, and 3232 ms, which required 1, 1, 2, and 4 heartbeats, respectively. The scan time was 16 heartbeats. Regions of interest (ROIs) were drawn on the image for each TS, and T_1 values were calculated by fitting the ROI measurements to a three-parameter model for longitudinal relaxation, $A - B \exp(-TS/T_1)$.

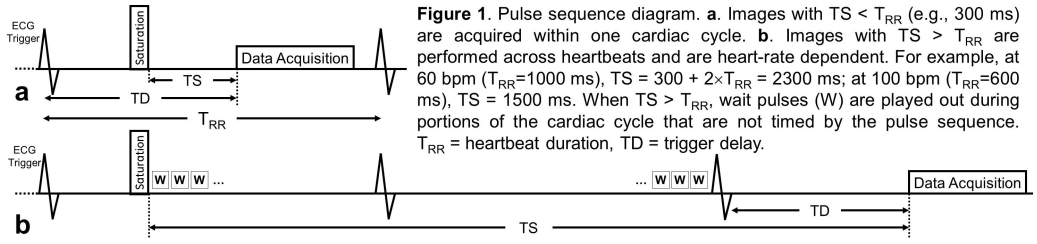

Figure 1. Pulse sequence diagram. **a**. Images with TS < T_{RR} (e.g., 300 ms) are acquired within one cardiac cycle. **b**. Images with TS > T_{RR} are performed across heartbeats and are heart-rate dependent. For example, at 60 bpm (T_{RR}=1000 ms), TS = 300 + 2×T_{RR} = 2300 ms; at 100 bpm (T_{RR}=600 ms), TS = 1500 ms. When TS > T_{RR}, wait pulses (W) are played out during portions of the cardiac cycle that are not timed by the pulse sequence. T_{RR} = heartbeat duration, TD = trigger delay.

Results: T_1 mapping of the agarose phantom yielded a T_1 of 2036 ms at 60 bpm and 2035 ms at 100 bpm, compared with the reference value of 1999 ms. The T_1 of normal myocardium measured around the left ventricle for the two volunteers were 1188 and 1205 ms, respectively (Fig. 2a). In the HCM case (Fig. 2b), the average T_1 was 1471 ms in the hypertrophic region and 1380 ms in the more remote myocardium.

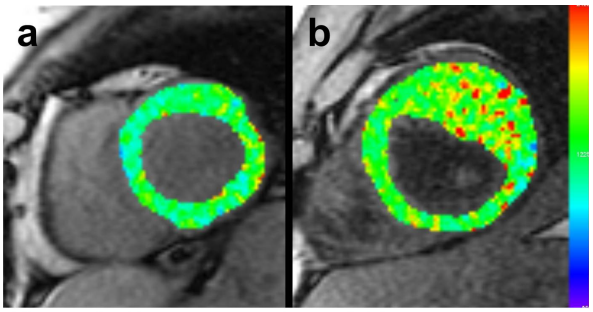

Figure 2. Non-contrast-enhanced T_1 maps a. Normal myocardium in a healthy volunteer. **b**. Hypertrophic cardiomyopathy. Color map range: 50 – 2400 ms.

Discussion: This work has demonstrated the feasibility of performing breath-held myocardial T_1 mapping using multiple single-point SR. Long delay times, which are the key features of this method, were achieved by allowing T_1 relaxation to occur across multiple heartbeats. The accuracy of these delay times was assured, even in the presence of intra-scan heart rate variability, by using the pulse sequence to measure the duration of each heartbeat in real time. Phantom validation yielded T_1 values within 2% of the reference value for heart rates of 60 and 100 bpm. The T_1 of unenhanced normal myocardium was slightly longer than literature values (1,5); however, previous single-point methods have been limited to using TS < T_{RR}, which is suboptimal for curve fitting (6). Although, in this study, data was not acquired during heartbeats that were spanned by a TS (Fig. 1b), the use of a slice-selective saturation pulse would enable a multi-slice acquisition by allowing additional slices to be imaged during these unused heartbeats.

References 1. Iles, JACC, 52:1574 (2008). 2. Messroghli, MRM, 52:141 (2004). 3. Slavin, SCMR, p.189 (2007). 4. Song, ISMRM, p. 3653 (2010). 5. Blume, JMRI, 29:480 (2009). 6. Zhang, JMRI, 8:675 (1998).