3D Saturation Recovery Imaging for Free Breathing Myocardial T_1 Mapping

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Introduction: T_1 mapping overcomes limitations of late gadolinium enhancement for the detection of diffuse fibrosis in the myocardium[1]. Several myocardial T_1 mapping methods have been proposed recently, however most of them are limited to 2D breath-hold acquisitions with associated limitations in signal-to-noise ratio (SNR) and spatial resolution. The MOdified Look-Locker Inversion recovery (MOLLI) approach has been the most widely used method[2], however systematic T_1 errors have been reported which can be mitigated by using Saturation recovery single SHot Acquisition (SASHA)[3]. In this work, we extend the 2D SASHA to 3D using a 1D diaphragmatic navigator for respiratory motion correction and segmented *k*-space acquisitions. The proposed free breathing 3D SASHA method was compared to breath-hold 2D SASHA and 2D MOLLI in healthy volunteers and a T_1 phantom.

Methods: The 3D SASHA sequence was implemented as an ECG-triggered and respiratory gated and corrected radiofrequency spoiled gradient echo sequence. Nine 3D images were acquired at different delay times (0 to 700ms) from the saturation pulses, plus an image acquisition prior to any saturation pulses to estimate the magnetization after an infinite delay. Imaging parameters of the 3D SASHA sequence include; FOV=300×300×80mm^3, spatial resolution=1.5×1.5×8mm^3, α=30°, TR/TE=5.2/2.6ms and nominal scan time=5:10min. A 6 mm window and 0.6 tracking factor was used for the respiratory gating and slice tracking. 7 healthy volunteers were scanned on a 1.5T clinical scanner comparing the proposed free breathing 3D SASHA to 2D SASHA and 2D MOLLI. Both 2D scans were acquired during breath holding. For the phantom experiment, 3D SASHA, 2D SASHA and 2D MOLLI were used to scan 12 vials with different T_1 values ranging from 250 to 1600 ms. Reference T_1 values for the phantom experiments were generated with a gold standard spin echo sequence.

Results: Figure 1 shows the results from the phantom experiments. A good agreement was observed between the gold standard and 2D SASHA (y=1.0x-33, r^2=0.98) and 3D SASHA (y=1.0x-25, r^2=0.99). However, systematic T_1 underestimation was found for 2D MOLLI (y=0.8x+5, r^2=0.99) which increased linearly with T_1. Short-axis T_1 maps using 2D MOLLI, 2D SASHA and 3D MOLLI from one healthy subject are shown in Figure 2. Average T_1 values of the myocardium and blood from the 7 healthy subjects are shown in Table 1. T_1 values were larger for the SASHA acquisitions than for MOLLI, however the agreement between 2D and 3D SASHA was excellent. The average scan time of the 3D SASHA sequence for the 7 volunteers was 9:21±0:38mins.

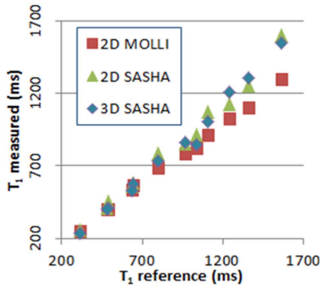

Figure 1. Measured T_1 of 2D MOLLI, 2D SASHA and 3D SASHA vs. reference T_1 in phantom

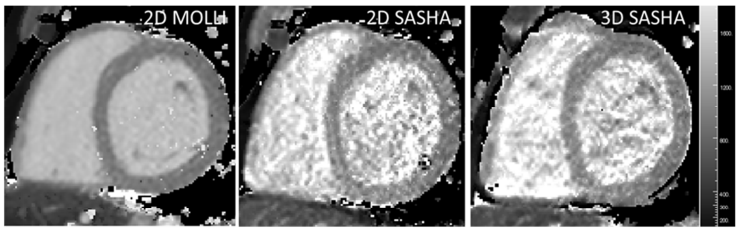

Figure 2. T_1 maps from one healthy volunteer. 2D MOLLI and 2D SASHA acquired during breath holding. 3D SASHA acquired during free breathing. All T_1 maps are windowed to the same dynamic range (0<T_1<2000).

Discussion: The proposed 3D SASHA sequence allows for accurate T_1 quantification of the whole left ventricle without the need for breath holding. Due to the 3D encoding, the SNR of 3D SASHA was in general higher than 2D SASHA in an otherwise SNR-starved sequence, as saturation pulses and relatively short delay times are used in the SASHA sequence. Future work will focus on reducing the scan time using compressed sensing and evaluating the performance of 3D SASHA in patients with myocardial scar.

In conclusion, free breathing 3D SASHA overcomes the need for breath hold acquisitions, improves the SNR compared to 2D SASHA and provides more accurate T_1 maps than 2D MOLLI.

Table 1. Average measured blood and myocardium T_1 in 7 healthy subjects

	Myocardium	Blood
2D MOLLI	952±16	1510±39
2D SASHA	1103±51	1618±171
3D SASHA	1065±19	1639±118

References: 1 Kellman, JMRI, 2012. 2 Messroghli, JMRI, 2007. 3 Chow, ISMRM, 2012.