High-resolution three-dimensional ANGIE T1 mapping of the heart

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Target audience: Clinicians and scientists working on cardiac T1 mapping.

Introduction: Assessment of fibrosis in thinner myocardial structures such as the right ventricular (RV) and left atrial walls would be valuable in disorders such as pulmonary hypertension, congenital heart disease, and atrial fibrillation. However, current cardiac T1 mapping techniques[1,2,3] have limited spatial resolution because data are acquired within a breathhold. We recently developed an Accelerated and Navigator-Gated look-locker Imaging sequence for cardiac T1 Estimation (ANGIE)[4], which enables high-resolution T1 mapping by removing the breathhold constraint. However, high resolution 2D imaging is limited by low SNR and restricted coverage of the heart. A 3D acquisition provides higher SNR along with greater coverage of the heart. However standard 3D navigated techniques have prohibitively long scan times. Thus, the aim of the present study was to extend ANGIE to perform high-resolution three-dimensional (3D) T1 mapping of the heart within a clinically acceptable scan time.

Methods: ANGIE uses navigator-gating and a segmented readout to enable free breathing acquisition with high spatial resolution[4]. An adaptively driven undersampling strategy with an image reconstruction algorithm that combines compressed sensing (CS) with local low-rank sparsity[5,6] , partial Fourier and parallel imaging (SENSE) was developed to achieve high acceleration for 3D ANGIE. The reconstruction problem was formulated as the following optimization equation:

$$\mathbf{m}^* = \arg\min_{\mathbf{m}} \|\mathcal{F}_u C_i \mathbf{m} - \mathbf{d}\|_2 + \lambda_1 (\textstyle\sum_b \|\mathbf{m_b}\|_*) + \lambda_2 \left\|\mathbf{m} - |\mathbf{m}| * e^{-2\pi i \varphi_{\text{lowres}}}\right\|_2$$

where $\mathbf{m}$ is the image after coil combination, C_i is the individual coil sensitivity profile, $\mathbf{d}$ is the measured k-space data, $\mathbf{m_b}$ is a small region of $\mathbf{m}$ reformatted into a Casorati matrix, $\| \quad \|_*$ is the nuclear norm operator, and φ_{lowres} is the low resolution phase image computed from the center fully sampled k-space region. The reconstruction algorithm was evaluated for a range of acceleration rates by retrospectively undersampling a fully-sampled 3D ANGIE dataset. High-resolution (1.3-1.4x1.3-1.4x4mm^3) native T1 mapping of the heart using 3D ANGIE was compared with 2D ANGIE and 2D MOLLI in six healthy volunteers. All imaging was performed on a 1.5T system (Avanto Siemens) using a 32-channel phased-array receiver coil. Imaging parameters for 3D ANGIE included: matrix size=224x224x14 (including 2 partitions for slice oversampling), encoding lines per readout = 32, number of inversion times=12, initial TI =175ms, TI increment =70ms, and partial Fourier reduction factor of 3/4 along the phase encode direction. An acceleration rate of 7 was chosen based on the results from reconstructions of the fully-sampled dataset. 2D MOLLI (2.5-2.6x2-2.1x4mm^3) and 2D ANGIE (1.3-1.4x1.3-1.4x4mm^3) scans were also performed at three different short-axis slice positions.

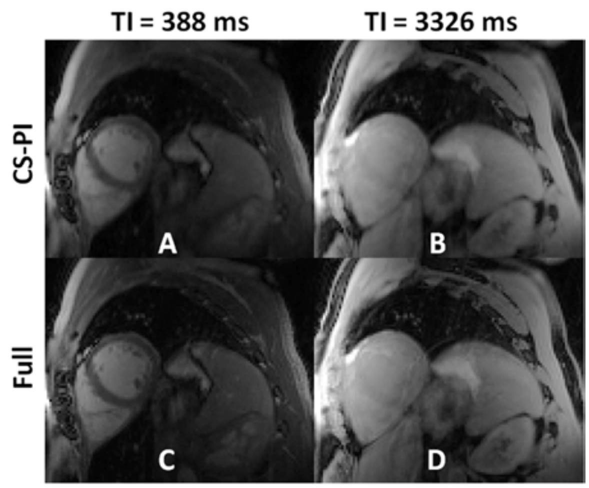

Figure. 1. Example reconstruction results from a retrospectively undersampled (Rate=10) 3D ANGIE dataset. CS-PI reconstructed (**A-B**) and fully-sampled (**C-D**) images from a single partition at two inversion times. The image reconstruction algorithm effectively suppressed aliasing artifacts and retained spatial resolution.

Results: Figure 1 illustrates example reconstructed (A-B) and fully sampled (C-D) images from a retrospectively accelerated 3D ANGIE dataset. The image reconstruction algorithm effectively suppressed aliasing artifacts and retained spatial resolution, illustrating the capability of achieving a high acceleration rate using the proposed reconstruction algorithm. Figure 2 illustrates example T1 maps from a healthy volunteer acquired using all three techniques at three different slice positions across the ventricles. 2D MOLLI (Fig. 2G-I) provided high SNR but incomplete definition of the RV wall, whereas 2D ANGIE (Fig. 2D-F) provided good definition of the RV wall but lower SNR. Three-dimensional ANGIE (Fig. 2A-C) provided good definition of the RV wall as well as high SNR. The left ventricular myocardium and blood T1 estimates using 3D ANGIE (LV: 985 ± 66 ms, blood: 1466 ± 52 ms) were in close agreement with 2D MOLLI (LV: 984 ± 75 ms, blood: 1474 ± 80ms). The RV T1 estimates using 3D ANGIE (991 ± 87 ms) were in close agreement with 2D ANGIE (997 ± 109 ms). Table 1 summarizes the scan time results. The acquisition time for 3D ANGIE was 6.4 ± 1.4 mins, while for 2D ANGIE was 2.1 ± 0.8 mins (per slice) illustrating the improvement in acquisition time per unit slice.

Conclusions: Three-dimensional ANGIE provides accurate high-resolution (1.3x1.3x4mm^3) T1 maps of the human heart with high SNR and low acquisition time per unit slice.

References: (1) Messroghli et al: MRM 2004. (2) Chow et al: MRM 2014. (1) Weingartner et al: MRM 2013. (4) Mehta et al: MRM 2014. (5) Chen et al: MRM 2014. (6) Trzasko et al: Proc. Int. Symp. MRM 2011.

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Table. 1. Scan time results

	MOLLI	2D ANGIE	3D ANGIE
Scan Time	12 (hb)	2.1 ± 0.8 mins	6.4 ± 1.4 mins
Accel. Rate	1.7	2.0	7.0
Navigator Efficiency (%)	-	57 ± 14	67 ± 15
Number of slices	1	1	12

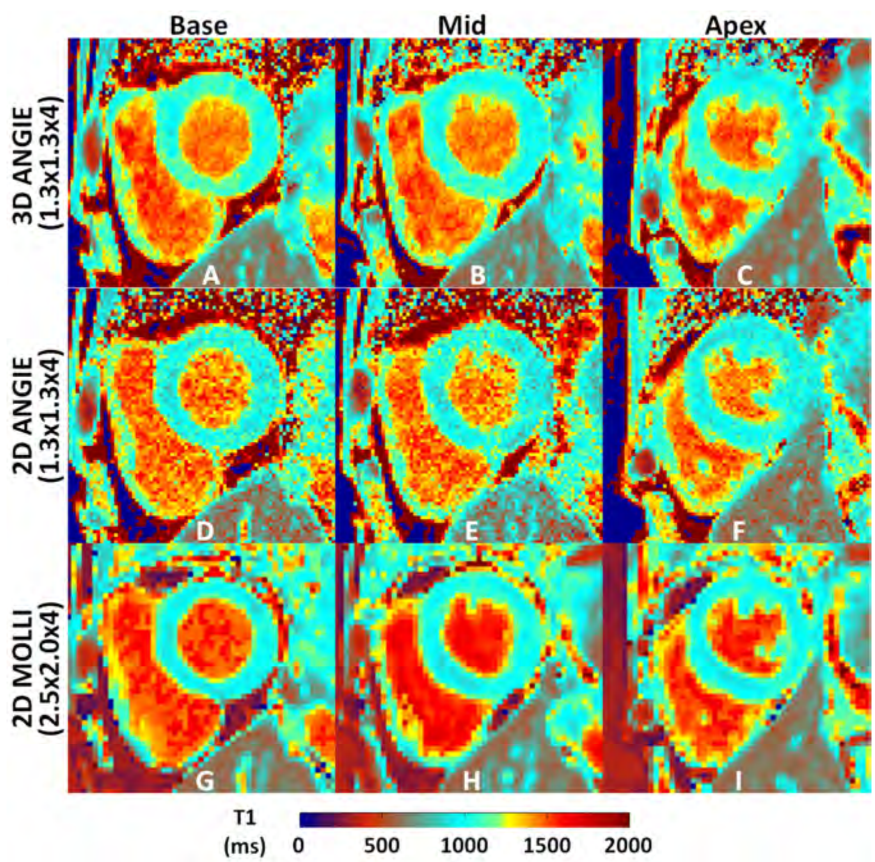

Figure. 2. Comparison of T1 mapping techniques in a healthy volunteer. Example native T1 maps from a healthy volunteer at three different slice positions acquired using 3D ANGIE (**A-C**), 2D ANGIE (**D-F**) and 2D MOLLI (**G-I**). 2D MOLLI provided high SNR but incomplete definition of the RV wall, whereas 2D ANGIE provided good definition of the RV wall but lower SNR. However, 3D ANGIE provided both good definition of the RV wall as well as high SNR.