Free-Breathing Post-Contrast Three-Dimensional T₁ Mapping: Volumetric Assessment of Myocardial T₁ Values

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Purpose: To develop a three-dimensional (3D) free-breathing myocardial T_1 mapping sequence for assessment of left ventricle diffuse fibrosis after contrast administration.

Methods: In the proposed sequence, multiple 3D inversion recovery images are acquired in an interleaved manner. A mixed prospective/retrospective navigator scheme is used to obtain the 3D Cartesian k-space data with fully sampled center and randomly undersampled outer k-space. The resulting undersampled 3D k-space data are then reconstructed using compressed sensing. Subsequently, T₁ maps are generated by voxel-wise curve fitting of the individual interleaved images. In a phantom study, the accuracy of the 3D sequence was evaluated against two-dimensional (2D) modified Look-Locker inversion recovery (MOLLI) and spin-echo sequences. In vivo T₁ times of the proposed method were compared with 2D multislice MOLLI T₁ mapping. Subsequently, the feasibility of high-resolution 3D T₁ mapping with spatial resolution of 1.7 \times 1.7 \times 4 mm³ was demonstrated.

Results: The proposed method shows good agreement with 2D MOLLI and the spin-echo reference in phantom. No significant difference was found in the in vivo T₁ times estimated using the proposed sequence and the 2D MOLLI technique (myocardium, 330 ± 66 ms versus 319 ± 93 ms; blood pools, 211 ± 68 ms versus 210 ± 98 ms). However, improved homogeneity, as measured using standard deviation of the T₁ signal, was observed in the 3D T₁ maps.

Conclusion: The proposed sequence enables high-resolution 3D T_1 mapping after contrast injection during free-breathing with volumetric left ventricle coverage. **Magn Reson Med 000:000–000, 2014.** © **2014 Wiley Periodicals, Inc.**

Key words: myocardial T₁ mapping; diffused fibrosis; navigator gating; quantitative cardiac MRI

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DOI 10.1002/mrm.25124

Published online 00 Month 2014 in Wiley Online Library (wileyonlinelibrary. com).

INTRODUCTION

Focal myocardial scar due to ischemic or nonischemic heart disease can be assessed using late gadolinium enhancement on cardiac MR (CMR) (1-3). This technique relies on differences in contrast washout between infarcted and healthy myocardium for visualization of necrotic tissue. However, late gadolinium enhancement imaging cannot identify diffuse or interstitial myocardial fibrosis in patients with nonischemic disease where the collagen deposition is commonly diffused across the myocardium and is not focal. Quantitative myocardial T₁ mapping is an emerging technique that allows assessment of diffuse fibrosis in the myocardium. The concentration of a gadolinium contrast agent is inversely proportional to the postcontrast T_1 time (4). This enables inference from postcontrast T₁ quantification on the collagen content and allows both the identification of focal and diffuse fibrosis in the myocardium (5,6).

Quantitative T₁ mapping is commonly performed by acquiring a series of inversion recovery images with different inversion times. The image intensities are then fit to a T_1 relaxation curve to estimate voxel-wise T_1 maps. The two-dimensional (2D) Look-Locker imaging sequence (7) is most commonly used for evaluation of myocardial T_1 times. In this technique, a series of T_1 weighted images is acquired after the application of a single inversion pulse. However, due to cardiac motion, different images are acquired at different heart phases, allowing only regional-wise calculation of T₁. The modified Look-Locker inversion recovery sequence (MOLLI) addresses this limitation by employing image acquisition with electrocardiography (ECG) triggering to a specific cardiac phase. This allows for a voxel-wise T_1 estimation. However, a relatively long scan time is required to provide a sufficient sampling of the T₁ curve due to recovery periods of the longitudinal magnetization. The shortened MOLLI sequence (8) was proposed for the acquisition of myocardial T₁ maps in reduced scan times. The gradual reduction of recovery periods in combination with a conditional data-exclusion scheme allows T₁ mapping in nine heartbeats. An alternative way to overcome the problem of long recovery periods is to employ saturation recovery, for example, in an ECGtriggered Look-Locker approach as proposed by Song et al. (9) or repeated in every heart beat as proposed by Chow et al. (10) and Slavin et al. (11). All of the

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Grant sponsor: National Institutes of Health; Grant number: R01-EB008743-01A2; Grant sponsor: Deutsche Telekom Stiftung (S.W.).

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Received 7 June 2013; revised 18 November 2013; accepted 18 December 2013



FIG. 1. **a**: Sequence diagram depicting the interleaved acquisition of multiple segmented inversion recovery images with different inversion times. **b**: The spatially aligned images can be used to generate T_1 maps by performing a voxel-wise curve fitting. The crosses on the inversion recovery curve correspond to different images acquired along the recovery curve with predefined inversion times. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

aforementioned methods employ 2D imaging during a single breath-hold per slice limiting the spatial resolution, coverage, and signal-to-noise ratio (SNR) compared to three-dimensional (3D) imaging. However, volumetric 3D T₁ mapping is very challenging due to long scan times and spatial misregistration induced by respiratory motion between the acquisitions of images with different inversion times.

Several recent studies reported the development of 3D sequences for in vivo myocardial T₁ mapping. A variable flip angle T₁ mapping method for 3D imaging in mice was proposed by Coolen et al. (12). Five sets of images are acquired subsequently with different flip angles to generate varying T_1 -weighted contrasts, in 10 min per image set. Each image set was acquired with retrospective cardiac gating to obtain one image per heart-phase per flip-angle. In Warntjes et al. (13), the T₁ quantification from the interleaved acquisition of phase images in the phase-sensitive inversion recovery (PSIR) technique (14) was proposed. The acquisition of one phase-sensitive inversion recovery 3D volume was performed during prolonged breath-holds of \sim 24 s. The subsequent acquisition of two 3D inversion recovery images with different inversion times was used for T_1 quantification by Coniglio et al. (15). The acquisition was free-breathing, with the use of navigator (NAV) triggering for respiratory motion compensation. However, to shorten the scan time and reduce spatial misregistration, these studies used two imaging datasets for estimation of the T_1 maps, which can adversely impact the accuracy of T_1 maps (16). Therefore, alternative 3D T_1

mapping sequences—which enable the acquisition of a higher number of images with different inversion times along the recovery curve while providing sufficient registration between images—are desired.

In this study, we sought to develop a free-breathing 3D T_1 mapping sequence for volumetric assessment of diffuse myocardial fibrosis. Phantom and in vivo imaging experiments were performed to evaluate the feasibility of the proposed sequence.

METHODS

3D T₁ Mapping

Figure 1 shows the schematic of the proposed imaging sequence. To enable the acquisition of spatially resolved T₁ maps, multiple inversion recovery 3D k-space datasets are acquired with different inversion times in an interleaved manner. An ECG-triggered segmented data acquisition is performed to fill in the 3D k-space data matrices. To compensate for respiratory motion, we propose to use NAV gating and prospective slice tracking with a 7-mm gating window for the central parts of the k-spaces with a conventional reject/re-acquire scheme. In the outer k-space, we propose to use prospective slice tracking but without reacquisition of any k-space segment, regardless of the prospective NAV signal. Figure 2 shows the schematic of this data acquisition scheme. In order to guarantee the same signal recovery throughout the acquisition of each segment, we propose to repeat the central k-space segment with all inversion times if



FIG. 2. The prospective NAV-gating scheme for the central k-space acquisition. The interleaved acquisition of k-space segments is repeated with all inversion times in the same order until one instance with each inversion time was acquired inside the gating window. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

one was NAV-rejected due to respiratory motion. However, only one instance of a k-space segment will be used in case of multiple NAV-accepted acquisitions of the same k-space segment for a given inversion time. For data acquired in the outer k-space, those segments, which are associated with a NAV signal outside the 7mm acceptance window, were identified retrospectively and discarded (17). This approach results in 3D k-space datasets, which are fully sampled in the central k-space and randomly undersampled in the outer region of the kspace. Each 3D k-space data matrix is then reconstructed low-dimensional-structure using self-learning and thresholding (18). In this improved compressed sensing reconstruction algorithm for cardiac MR, patient- and anatomy-specific sparsifying transforms are generated from the central k-space low resolution data and are iteratively refined.

A model of the incomplete recovery of the longitudinal magnetization was derived by iteratively applying the Bloch-equations to simulate the whole recovery curve. Perfect inversion of the longitudinal magnetization was assumed in the model.

$$S_{-1}(M_0, T_1) = S_{initial}(M_0, T_1)$$

$$S_{i+1}(M_0, T_1) = M_0(1 - (1 - (1 - S_i(M_0, T_1) \quad [1])$$

$$\times e^{-(T_{RR} - T_{inv,i})/T_1}) e^{-T_{inv,i}/T_1}, \quad i = 0, 1, \dots, 4$$

where M_0 is the spin density, T_1 is the longitudinal relaxation time, and $T_{inv,i}$ is the inversion time corresponding to the *i*th image. T_{RR} is the R-R interval length computed from the heart rate at the beginning of the scan. $S_{initial}$ represents the initial longitudinal magnetization transient steady state, which is reached after running cycles of the 5 inversion times repeatedly and is a function of M_0 and T_1 . The fitting was performed by fitting ($S_0(M_0, T_1), S_1(M_0, T_1), \ldots, S_4(M_0, T_1)$) to the signal vector (I_0, I_1, \ldots, I_4) for a single voxel in the five T_1 weighted images in order to derive voxel-wise T_1 maps from the reconstructed 3D images.

Phantom Imaging

All studies were performed on a 1.5T Philips Achieva (Philips, Best, The Netherlands) system using a 32-

channel cardiac coil array. The phantom consists of a bottle filled with water, copper sulfate, and sodium chloride and a number of vials containing different liquids. The T_1 values of this phantom ranged from ~200 to 500 ms, a range typically expected for postcontrast T_1 mapping (6). The following phantom experiment was performed to study the accuracy of the proposed 3D T_1 mapping sequence and to confirm the consistency of the T_1 estimation along the slice encoding dimension.

The phantom was imaged using the proposed 3D T₁ mapping method, a multislice 2D MOLLI sequence, and a 2D inversion recovery spin-echo sequence. The 3D T_1 mapping sequence used a balanced steady state free precision imaging readout (repetition time [TR]/echo time $[TE] = 3.0 \text{ ms}/1.3 \text{ ms}; \text{ flip angle} = 35^{\circ}; \text{ resolution} = 1.7 \times$ $2.1 \times 2 \text{ mm}^3$; field of view [FOV] = $200 \times 100 \times 20 \text{ mm}^3$; scan time = 1:50 min; encodings per segment = 20) with five inversion times linearly spread between 140 and 500 ms. For MOLLI, the 3-3-5 scheme with optimized parameter values (TR/TE = 3.0 ms/1.3 ms; flip angle = 35° ; inplane resolution = $1.7 \times 2.1 \times 2 \text{ mm}^3$; slice thickness = 2 mm; $FOV = 200 \times 100 \text{ mm}^2$; SENES factor = 2) as described by Messroghli et al. (19) was used, and the T_1 maps were generated using exponential fitting with maximum likelihood estimation (20) and a flip angle independent correction of the measured T_1 value (21). For reference, an inversion recovery spin-echo sequence was performed using the following parameters: TR/TE = 10 s/100 ms; in-plane resolution = $1.2 \times 1.2 \text{ mm}^3$; slice thickness = 8 mm; FOV = 300×131 mm²; flip angle = 90° ; 15 inversion times between 100 and 3000 ms. Additionally, the bottle phantom was scanned along its long axis with the 3D sequence (TR/TE = 2.6 ms/1.0 ms)ms; flip angle = 35° ; resolution = $1.7 \times 2.1 \times 10 \text{ mm}^3$; $FOV = 300 \times 300 \times 100 \text{ mm}^3$; scan time = 3:10 min; acquisition matrix = $173 \times 146 \times 13$; encodings per segment = 20) and 2D MOLLI (FOV = $300 \times 300 \text{ mm}^2$; inplane resolution = $1.7 \times 2.1 \text{ mm}^2$; slice thickness = 10mm; TR/TE = 2.6 ms/1.03 ms; flip angle = 35° ; SENSE factor = 2). All scans were performed using a simulated ECG with a heart rate of 60 bpm.

The average T_1 estimation for each phantom compartment was compared between the different sequences. Because the T_1 values in the phantom are supposed to be homogenous, the variability within each phantom compartment, as assessed by the standard deviation within a manually drawn region of interest (ROI), was used as a measurement for signal homogeneity. The same ROI was used for all sequences.

In Vivo Imaging

The study was approved by the institutional review board and written informed consent was acquired prior to each examination. In a prospective study, we recruited nine healthy adult subjects (male, n=4; female, n=5; age, 34.3 ± 17.2 y) and three subjects with suspected cardiac disease (male, n = 1; female, n = 2; age, 62.3 ± 8.33 y) undergoing clinical cardiac MR examinations. All subjects were imaged using both the 3D T₁ mapping and multislice MOLLI sequences 5 to 15 min after administration of 0.2 mmol/kg gadobenate dimeglumine (MultiHance, Bracco SpA, Milan, Italy). The sequences were performed in randomized order to mitigate the impact of contrast washout in between scans. The 3D T₁ mapping sequence consisted of five imaging datasets acquired using five different inversion times linearly spread between 135 and 500 ms. Images with equal spatial resolution to MOLLI were acquired using the following sequence parameters: TR/TE = 2.6 ms/1.0 ms; flip angle = 35° ; resolution = 1.7 × $2.1 \times 10 \text{ mm}^3$; FOV = $300 \times 300 \times 100 \text{ mm}^3$; acquisition matrix = $173 \times 146 \times 13$; this resulted in a nominal scan time of 3:10 min at a heart rate of 60 bpm and 100% gating efficiency for the acquisition of the central k-space. Furthermore, to demonstrate the feasibility of an improved spatial resolution, high-resolution maps were acquired in five subjects using the following parameters: resolution = $1.7 \times 1.7 \times 4 \text{ mm}^3$; FOV = $300 \times 300 \times 100 \text{ mm}^3$; TR/TE = 3.0 ms/1.3 ms; acquisition matrix = 173 \times 146 \times 13; nominal scan time = 9:00 min at 60 bpm and 100%efficiency. The central k-space area was chosen to cover 15% of the ky encodings and 25% of the kz encodings for both 3D sequences. Multislice 2D MOLLI was performed using the following parameters: FOV = $300 \times 300 \text{ mm}^2$; in-plane resolution = $1.7 \times 2.1 \text{ mm}^2$; slice thickness = 10mm; TR/TE = 2.6 ms/1.0 ms; flip angle = 35° ; SENSE factor = 2; total breath-held scan time (without rest periods in between breath-holds) = 2:40 min.

Data Analysis

T_1 Measurements

ROIs were manually drawn in the T_1 maps for quantitative assessment of the T_1 times and the homogeneity in the myocardium and the left and right ventricle. The homogeneity of the estimated T_1 was assessed as the standard deviation within an ROI.

A paired Student *t*-test was used for assessment of statistical significance of the difference between the average estimated T_1 times in the myocardium and the homogeneity within the blood pools. A *P* value of <0.05 was considered significant.

Spatial Alignment

To study the spatial alignment of the images with different inversion times, five images per slice were selected

Table 1 Phantom Measurements

	Vial 1	Vial 2	Vial 3
2D spin-echo	271 ± 1.5	327 ± 0.9	421 ± 2.0
2D MOLLI	$\textbf{279} \pm \textbf{12.7}$	$\textbf{323} \pm \textbf{17.2}$	438 ± 19.8
3D T1 mapping	264 ± 7.8	$\textbf{328} \pm \textbf{7.3}$	441 ± 5.9

Data are presented as the mean \pm standard deviation of T₁ times (ms) from 2D MOLLI and the proposed 3D T₁ sequence compared with measurements from a 2D spin-echo sequence.

for further analysis (all inversion times for the 3D sequence and the images 2, 4, 6, 8, and 10 for MOLLI). A software tool was developed in MATLAB (MathWorks, Natick, Massachusetts, USA) to manually draw closed contours around the left ventricle (LV) in each image separately. The LV center point was estimated as the centroid of this contour for each inversion time. For each slice, the distance between the estimated center point in two successive images with different inversion times was assessed. The motion for one slice was quantified as the average value of these distances. The spatial registration in the entire dataset was represented by the average, the minimum, and the maximum of this estimation among the slices of a dataset.

RESULTS

Phantom Imaging

Table 1 shows the T_1 times determined with the 3D T_1 mapping sequence, MOLLI, and the inversion recovery spin-echo sequence in phantom. Both MOLLI and the 3D sequences resulted in T_1 values close to the calculated T_1 from the spin-echo sequence with a relative difference of 0.3%–5% and 1%–4%, respectively. The standard deviation of the assessed T_1 time within the phantom compartments was reduced by 40%–70% using a 3D measurement compared with 2D MOLLI in the phantom experiment. Figure 3 shows the T_1 measurements along the slice-encoding dimension. The proposed 3D sequence shows a slight corruption of the T_1 values at the end of the FOV. The variation in the MOLLI T_1 time estimates across the slices is within the range of the inslice variation.

In Vivo Imaging

Figure 4 shows multiple slices of representative 3D T_1 maps acquired in a healthy subject in comparison with a multislice MOLLI sequence. The white arrow indicates artifacts at the epicardial border caused by motion between different T_1 -weighted images. Figure 5 shows the T_1 times of the proposed 3D sequence versus MOLLI in all subjects. The standard deviation within the blood pools was significantly decreased by using the proposed 3D method compared to MOLLI from 28 ± 11 ms variation with MOLLI to 8.5 ± 4.1 ms with the proposed method (P < 0.05).

Figure 6 shows representative T_1 -weighted images of an example slice of the proposed 3D technique and MOLLI. Substantial motion can be observed in the MOLLI images, due to improper breath-holding. The interleaved 3D



FIG. 3. **a**: Bottle phantom containing a homogenous liquid, with approximate slice locations. **b**: T_1 times in the bottle phantom along the slice-encoding dimension using a 2D multislice technique and the proposed 3D technique, with the slice locations indicated in panel a. The standard deviation represents the in-plane variation within a region of interest in the bottle. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

acquisition is free of motion, as the myocardial border remains stationary among the images. The motion quantification of the average displacement between two images by tracking the LV center point showed values between 0.40 ± 0.05 mm and 1.5 ± 0.9 mm, with an average of 1.0 ± 0.63 mm among all slices (standard deviation over the different subjects) for 2D T₁ mapping. For the 3D data set, the offset was between 0.48 ± 0.15 mm and 0.78 ± 0.25 mm with a mean value of 0.63 ± 0.15 mm.

The scan time for the proposed sequence was 4:00 min on the average at low resolution and 10:40 min at high resolution. The average scan time for the multislice MOLLI sequence was 9:45 minutes, including the rest periods between breath-holds.

Figure 7 shows representative slices of a highresolution 3D T_1 map acquired in 9:26 min. Visually improved image quality can be observed with a full LV coverage.



FIG. 4. T_1 maps acquired in a healthy subject using the proposed 3D sequence (top row) and multislice 2D MOLLI (bottom row). Both sequences result in comparable T_1 measurements in the myocardium (352 ± 34 ms versus 340 ± 68 ms for 3D versus 2D). Visually improved homogeneity can be observed in T_1 maps acquired using 3D approach. Motion artifacts caused by poor breath-holding can be seen at the epicardial border in the 2D T_1 maps (white arrow). [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]



FIG. 5. In vivo T_1 times assessed in the left ventricular myocardium (left) and the left and right ventricular blood pools (right) of all subjects (including healthy subjects and patients with suspected cardiac disease) with 2D MOLLI and the proposed 3D T_1 mapping method. The identity line is indicated in green. The sequences were performed in randomized order. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

DISCUSSION

We proposed a novel 3D myocardial T_1 mapping approach based on interleaved 3D acquisitions with a joint prospective-retrospective compressed-sensing motion correction. The interleaved acquisition of multiple T_1 -weighted inversion recovery images in combination with a novel navigator gating scheme ensures spatial alignment of these images and enables the generation of 3D T_1 maps by performing a voxel-wise curve fit on a compressed sensing reconstruction of the acquired undersampled data. The proposed 3D sequence leads to T_1 maps with whole heart coverage in free-breathing.

The higher signal-to-noise ratio compared with 2D imaging, due to the increased excitation volume beneficially affects the T_1 fit and the quality of the T_1 maps. This enables a reduction in the number of T_1 -weighted images, which are required for a reliable T_1 map. Five different inversion times were chosen empirically as a trade-off between T_1 map quality and scan time.

In the proposed sequence, the magnetization preparation and the image data readout are always applied within one heart cycle. This inherently limits the range of applicable inversion times to typically 100–700 ms. For estimation of long T_1 times, this may lead to an insufficient fit conditioning. Hence, the scheme presented herein is only suitable for application in postcontrast T_1 mapping.

The time between two inversion pulses in the proposed scheme is less than the duration of one heart cycle. This time is too short to allow for full recovery of the longitudinal relaxation curve after the last magnetization preparation. In order to obtain unbiased T_1 times, a two-parameter signal model was derived from the Bloch equations, incorporating the insufficient recovery of the longitudinal magnetization. This enabled close agreement of the proposed sequence with the spin-echo measurements in phantom. However, due to the small number of sampling points on the T_1 recovery curve, no three parameter model could be employed. In the presence of substantial field



FIG. 6. Selected T_1 -weighted images of the same slice acquired with the proposed free-breathing 3D T_1 mapping sequence (top row) and a breath-hold multislice MOLLI (bottom row) in a healthy subject. The respective inversion times are indicated in the lower right corner of each image. Although the subject was asked to hold his breath during the scan, motion of the epicardial border with respect to the red reference line, presumably caused by respiratory motion drift, can be seen in the lower row. The epicardial border is stationary with the proposed technique. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]



FIG. 7. Representative slices (right panel) of a 3D high-resolution ($1.7 \times 1.7 \times 4 \text{ mm}^3$) T₁ map of a healthy subject acquired in 9:26 min compared with a low-resolution 2D MOLLI T₁ map (left panel).

inhomogeneities or susceptibilities, the sequence could be used with an increased number of images and a three parameter model in order to take inversion efficiency into account.

3D T_1 mapping inherently requires longer scan times per acquisition compared to 2D imaging. For T₁ quantification after contrast injection, these scans may be affected by contrast changes due to the transient nature of contrast uptake during the scan, in particular for imaging early after contrast injection, where the T_1 times after a bolus injection change the fastest (22). Imaging in the presence of major contrast changes among the different k-space parts might impact the accuracy and/or cause blurring/artifacts. To mitigate this problem, the acquisition of the central k-space area in the proposed 3D sequence is performed at the beginning of the scan. Because the central k-space contains most of the information about the image contrast, the outer k-space area is less susceptible to changes in the contrast, minimizing the apparent image artifacts. Note that while a 3D acquisition inherently suffers from artifacts caused by contrast changes, the T₁ quantification across the LV is still uniform and comparable among the slices. Contrast changes during the lengthy process of volumetric coverage with a 2D sequence may cause substantially different estimation of the T₁ time in different slices. This potentially hampers the comparison of the T_1 times across the entire LV volume.

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In the proposed sequence, the actual magnetization signal is highly dependent on the magnetization history and consequently highly dependent on the order of the applied inversion times. To minimize the corruption introduced by insufficient recovery, it was crucial that the same recovery scheme is maintained for the central k-space and the outer k-space. Therefore, dummy interleaves are performed for the repeated acquisitions of a kspace segment in the central k-space, even after data for the respective interleaf was already NAV-accepted.

In T_1 mapping, a spatial misalignment of the different T_1 -weighted images leads to motion artifacts in subendocardial and subepicardial regions and reduces the effective resolution of the T_1 map. The slice with the best breath-hold showed a decreased amount of motion compared with the NAV-gated free-breathing datasets. However, the average amount of motion in the free-breathing datasets was found to be less than in the breath-hold datasets. With MOLLI 2D T_1 mapping, numerous breathholds were required to provide full-heart coverage. This demanding procedure can lower the effectiveness of the subject's breath-hold, inducing pronounced misalignment in the presence of incomplete breath-holds. Additionally, long breath-holds are known to suffer from a linear drift in foot-head direction in the order of 0.4 mm/s (right diaphragm) (23). Accordingly, the quantitative analysis showed a particular prominent difference between the maximum amounts of motion in the 2D breath-hold approach compared to 3D T₁ mapping, indicating slices with imperfect breath-holds. Furthermore, it is commonly known that the position of the heart varies between multiple breath-holds (24,25), which prevents reformatting or continuous volume analyses among slices with the 2D multislice approach.

The problem of spatial misregistration of the images can be mitigated by applying a retrospective image registration. However, compared with prospective image alignment, this postprocessing complicates the image reconstruction, since image registration algorithms are sensitive to the applied similarity measures and the regularization parameters, and require to compromise between accuracy, precision, and reliability (26). In particular, if 2D imaging is applied, the effectiveness of image registration algorithms is lowered by in-plane motion and the associated displacement of anatomical features.

The rest periods necessary between subsequent breathholds lead to prolonged scan times for LV coverage with the 2D multislice sequence (up to 10 min). Although the acquisition window per cardiac cycle was reduced in the 3D sequence, the scan time for the same volume during free-breathing was shortened substantially.

2D T₁ mapping methods such as MOLLI or shortened MOLLI are acquired in a nonsegmented, single-shot data acquisition. Despite the application of acceleration techniques, this leads to long acquisition windows (around 200 ms) that often exceed the duration of the middiastole quiescence. Therefore, cardiac motion artifacts could adversely impact the image and T₁ map quality. The proposed 3D T₁ mapping scheme uses a segmented data acquisition, which enables the use of a subjectspecific acquisition window to reduce cardiac motion. Furthermore, the segmented data acquisition allows for resolutions beyond single-shot imaging, potentially allowing for improved localization of abnormal T₁ times and reduced partial-volume effects.

We have noticed some degree of blurring in 3D T_1 images, which may be associated with compressed sensing-based reconstruction or processing of raw data without additional filtering that is present on the commercially available reconstructions. Although better reconstruction techniques can potentially reduce this artifact, subendocardial areas are commonly excluded for T_1 measurements to avoid partial voluming effect because of cardiac motion.

In the present study, the selected inversion times of the different interleaves were linearly distributed. A comprehensive evaluation of the optimal inversion time distribution could benefit the T_1 fit conditioning that may further improve estimation of the T_1 maps.

This study has several limitations. Similar to other studies on myocardial T_1 mapping, the proposed technique was carefully evaluated using phantom experiments, which are necessary to confirm unbiased and accurate T_1 quantification in a controlled and idealized setting. However, deviations of the phantom from in

vivo imaging (e.g., T₂ and magnetization transfer effects, susceptibilities, and field inhomogeneities), as well as the impact of cardiac and respiratory motion, limit the generalization of the phantom results. In myocardial postcontrast T₁ mapping, the "true" T₁ time in vivo cannot be assessed. Furthermore, no patients with known or suspected diffuse fibrosis were recruited for this study. It was beyond the scope of this study to establish postcontrast T_1 times in the healthy and fibrotic myocardium. However, the proposed technique showed reduced intramyocardial variation in vivo, as well as reduced intravial variation of T₁ times in phantom. This suggests that the proposed technique may be more suitable for discriminating between healthy and fibrotic tissue over conventional 2D myocardial T1 mapping, although this was not studied.

CONCLUSION

We have demonstrated the feasibility of a free-breathing 3D myocardial T_1 mapping sequence for volumetric assessment of the LV T_1 values. The resulting 3D T_1 maps, acquired after contrast injection, allowed whole heart coverage with less motion artifacts compared with the 2D breath-hold multislice sequences.

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