Kirsten M. Becker*, Jeanette Schulz-Menger, Tobias Schaeffter, Christoph Kolbitsch

In vivo myocardial tissue characterization of all four chambers using high-resolution quantitative MRI

Abstract: Quantitative native T_1 Mapping of the myocardium without the application of contrast agents can be used to detect fibrosis in the left ventricle. Spatial resolution of standard native T_1 mapping is limited by cardiac motion and hence is not sufficient to resolve small myocardial structures, such as the right ventricle and the atria. Here, we present a novel MR approach which provides cardiac motion information and native T_1 maps from the same data. Motion information is utilized to optimize data selection for T_1 mapping and a model-based iterative reconstruction scheme ensures high-resolution T_1 maps for the entire heart. Feasibility of the approach was demonstrated in three healthy volunteers. In the T_1 maps, the myocardium of all four chambers can be visualized and T_1 values of the left atrium and right chambers were comparable to left ventricular T_1 values.

Keywords: T_1 mapping, myocardial tissue characterization, magnetic resonance imaging

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1 Introduction

Cardiovascular Magnetic resonance imaging (CMR) is an important modality for diagnosis of cardiovascular diseases. Fibrosis is considered to play a role in various cardiomyopathies, such as arrhythmias [1]. Qualitative CMR is used in clinical routine to detect fibrosis by late gadolinium enhancement imaging (LGE) in the ventricles and atria [2], but is limited to focal fibrosis. Recently, quantitative CMR (T_1, T_2 and T_2* mapping) has become an important modality for myocardial tissue characterization [3,4]. Post-contract T_1 mapping offers a method to assess focal and diffuse fibrotic tissue and post-contrast T_1 times are suggested to be associated with atrial and ventricular fibrosis in arrhythmic patients [5-7]. However, contrast agents are required and observed T_1 times are strongly depend on the contrast dose and delay time between contrast administration and measurement.

Native T_1 mapping overcomes these limitations. Its main challenge is cardiac motion which strongly limits the achievable in-plane spatial resolution to approximately 2.0 x 2.0 mm^2 and therefore it is commonly only used in the left ventricle. For imaging of smaller structures, such as the right ventricle or the atria, with a thickness of less than 3 mm [8], spatial resolution is not sufficient.

In order to minimize cardiac motion, MR image acquisition is commonly restricted to the quiescent phase of the cardiac cycle (i.e. mid-diastole). The correct beginning and duration of data acquisition has to be set prior to the data acquisition and hence can only be estimated prospectively.

Here we demonstrate the feasibility of a high-resolution (1.0x1.0 mm² in-plane resolution) native T_1 mapping technique, that allows for mapping of all four chambers non-invasively. Cardiac motion information (cine images) is obtained from the same data prior to T_1 reconstruction. The motion information is utilized to select only data with minimal cardiac motion for T_1 mapping specifically for each subject and scan. This minimizes motion-induced blurring and optimizes the amount of data available for T_1 mapping. A model-based iterative reconstruction technique is used to obtain accurate T_1 maps obtained directly from the MR raw data. This ensures high quality T_1 maps even from highly undersampled MR data.

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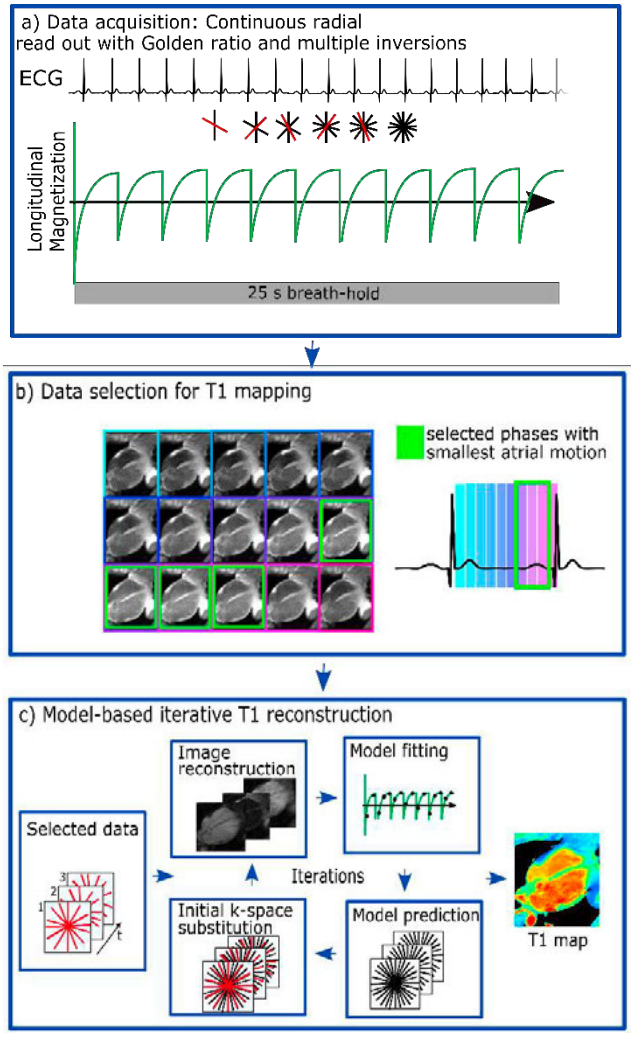

Figure 1: a) Data selection for T_1 mapping. b) Based on the cine image of the same acquisition, data for T_1 mapping within a window with minimal cardiac motion was selected. c) T_1 was estimated using model-based iterative reconstruction.

2 Methods

2.1 Data acquisition

2D data acquisition is performed continuously, with a spoiled gradient echo sequence. At constant time intervals, inversion pulses were applied (Figure 1a). Radial golden-ratio based data sampling with an angle increment of 111.25° between successive spokes allows for flexible reordering of the data. A recorded ECG signal was used for retrospective gating of the data to specific cardiac phases.

2.2 Image reconstruction

Due to the small thickness of the atrial wall, even small cardiac motion can strongly impair the reconstructed T_1 maps. In order to be able to select data with minimal cardiac motion, dark blood functional cine images showing the changes of the heart during the cardiac cycle were reconstructed prior to T_1 mapping from the same raw data (Figure 1b) [9]. Cine reconstruction was performed using an iterative kt-SENSE approach [10]. Based on the cine images, a time frame for T_1 mapping was selected, where cardiac motion was minimal (Figure 1b). The length of this frame is flexible and can be optimized for each subject. T_1 maps of the selected data were reconstructed by model-based iterative reconstruction (Figure 1c) [9,11]. The iterative process includes:

1. Image reconstruction for all selected time points.
2. T_1 estimation by pixel-wise three-parameter fitting to a signal model. The signal model describes the behaviour of the spoiled gradient echo signal of the longitudinal magnetization during continuous data acquisition and multiple inversions.
3. Model prediction for all time points.
4. Substitution of the model predictions by the initial k-space data for data consistency.

The iterative process was stopped after a fixed number of iterations.

2.3 In vivo imaging

The proposed approach was evaluated in three healthy volunteers (3 males, aged 29.7 ± 3.5 years). Within a 25 s breath-hold, 2D slices were acquired with the following settings: in-plane resolution: 1.0x1.0 mm², FOV: 320x320 mm² with 2-fold oversampling in radial direction, slice thickness: 8.0 mm, flip angle: 5°, TE/TR: 2.03/5.3 ms and a fixed interval between inversions of 2276 ms. Slices were oriented in four-chamber view (4ChV) and a short axis through both atria (ASAX).

Cine images were reconstructed with 15 cardiac phases. Data for T_1 mapping were selected in a window between 300 and 360ms per cardiac cycle, depending on cardiac motion. For comparison purpose, T_1 mapping was also performed by a common T_1 mapping technique for mapping of the left ventricle, a 3(3)3(3)5 modified Look Locker inversion recovery (MOLLI) [12] in ASAX view in one of the subjects with the following settings: FOV: 360x307 mm², slice thickness: 8.0 mm, in-plane resolution: 2.1x1.4 mm² and

integrated motion compensation. T_1 values were assessed in a manually drawn region-of-interest in the septum, left and right atria and right ventricle in 4ChV.

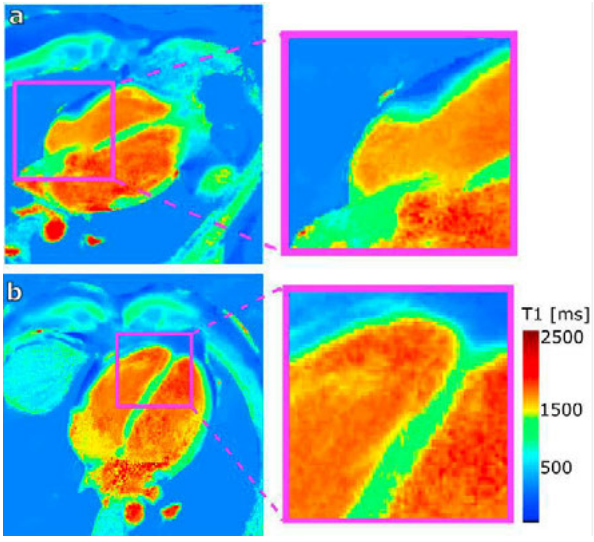

Figure 2: T_1 maps of two subjects in 4ChV. The myocardium of the right atrium can be visualized (a), as well as the myocardial wall of the right ventricle (b).

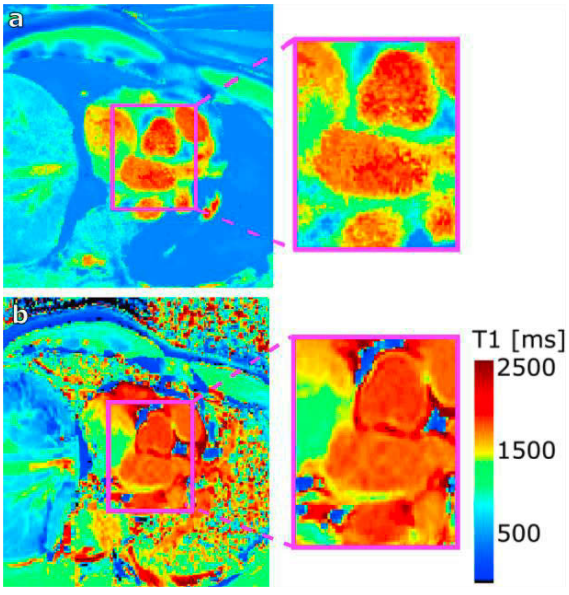

Figure 3: a) T_1 map in ASAX. In this orientation, the myocardium of the left atrium can be visualized. b) T_1 map of the same subject obtained by a MOLLI sequence. Here, the myocardium of the left atrium cannot be fully distinguished.

3 Results

High-resolution T_1 maps of the four chambers could be reconstructed for all subjects. T1 maps obtained by our approach and the MOLLI sequence are presented in figure 2 and 3. The result of the voxel-wise fit is shown in figure 4. R^2 of the fit was larger than 0.9 in all voxels within the heart. T_1 values in the three subjects are shown in table 1. In figure 5 a T_1 map is shown in 4ChV, together with a qualitative anatomical image from the same raw data and same cardiac phase and the overlay of the two images.

Table 1: T_1 values obtained by our approach in all chambers in the three subjects (mean ± standard deviation within the region-of-interest).

Subject	T_1 septum [ms]	T_1 right ventricle [ms]	T_1 left atrium [ms]	T_1 right atrium [ms]
1	1230 ± 84	1288 ± 91	1263 ± 89	1272 ± 143
2	1287 ± 73	1258 ± 85	1281 ± 90	1234 ± 126
3	1260 ± 76	1287 ± 67	1290 ± 76	1291 ± 135

4 Discussion

Small structures, such as the myocardium of the right ventricle and both atria can be seen in the T_1 maps. In ASAX orientation, myocardium of the left atrium can be visualized by our T_1 mapping approach, whereas left atrial myocardium cannot be identified in the standard MOLLI T_1 map (Figure 3b), which could possibly be explained by lower resolution and residual cardiac motion during data acquisition. T_1 values of the chambers were in the range of septal T_1 in the same subjects and high R^2 values for all myocardial voxels suggest

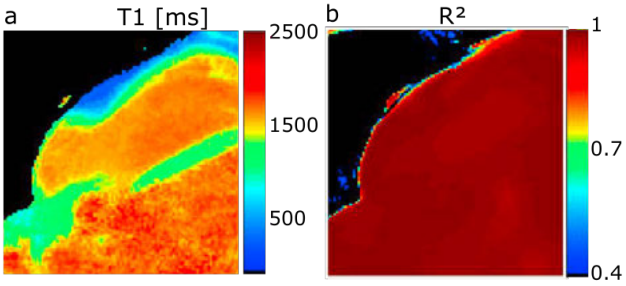

Figure 4: Result of the voxel-wise T_1 fitting. a) The T_1 Map is masked by the R^2 map (b). Only T_1 values with a R^2 of larger than 0.9 are visualized. R^2 is larger than 0.9 in the entire heart.

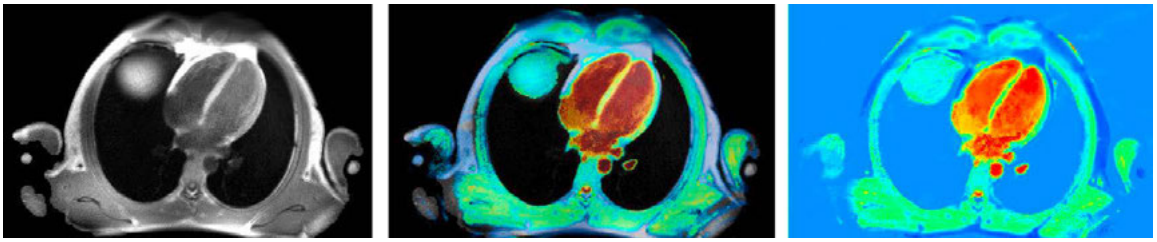

Figure 5: Qualitative anatomical scan, anatomical scan overlaid with the T_1 map of the same acquisition and the T_1 map (left to right).

a robust fit. The standard deviation of T_1 values within the atrial region-of interest is higher than in the septum. This could be explained by the smaller number of voxels in the right atrial region-of-interest.

The overlay of T_1 Map and structural image allows to immediately relate the T_1 values to its underlying anatomy without any misregistration errors due to varying breath-hold positions and could be used for further analysis of the T_1 map.

So far, cine images have only been used to select the quiescent phase of the heart but they could also be utilized to obtain motion information to correct for cardiac motion. This would allow for more data to be used for T_1 mapping in each cardiac cycle and achieve a clinically feasible scan time.

Evaluation in patients with atrial and ventricular fibrosis has to be performed in future research.

5 Conclusion

The feasibility of native T_1 mapping in both ventricle and atria was demonstrated for the first time. In the future, we will investigate the extension of the technique to 3D in order to further improve the accuracy of T_1 maps especially in regions with complex geometry, such as the atria. This will ensure native T_1 mapping can be used as non-invasive biomarker for diffuse and focal fibrosis in the whole heart in patients with arrhythmias.

Author Statement

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