THREE DIMENSIONAL MYOCARDIAL T1 MAPPING DURING FREE-BREATHING

Sebastian Weingärtner[1,2], Mehmet Akçakaya[1], Warren J Manning[1], and Reza Nezafat[1]

[1]*Department of Medicine, Beth Israel Deaconess Medical Center and Harvard Medical School, Boston, MA, United States,* [2]*Computer Assisted Clinical Medicine, University Medical Center Mannheim, Heidelberg University, Mannheim, Germany*

INTRODUCTION: Myocardial T_1 mapping is an emerging diagnostic tool for detection of diffuse fibrosis. Conventionally, a two–dimensional (2D) T_1 mapping sequence with multiple T_1-weighted single-shot images during one breath hold per slice is used (1). However, these single-shot techniques inherently limit the spatial resolution, require numerous breath holds for sufficient coverage, and do not allow for volumetric coverage. In this study, we sought to develop a novel 3D free-breathing T_1 mapping sequence to address these limitations.

METHODS: ***Sequence:*** The proposed sequence consists of multiple interleaved, segmented inversion recovery SSFP image acquisitions. The effective inversion time is varied among the interleaves to create various T_1-weighted contrasts that allow for T_1 mapping. A k-space segment of one of the images is acquired per heart cycle with ECG-triggering.

Respiratory navigator (NAV) gating is performed with a two-fold scheme, as depicted in Figure 1. First, the central k-space is acquired at the beginning of the scan with prospective NAV gating. The n^{th} k-space segment for an interleaf is accepted only if the NAV signal is within the pre-defined gating window for that interleaf. The sequence moves onto the $(n+1)^{th}$ central k-space segment only if the n^{th} segment has been NAV-accepted for all the interleaves (corresponding to different inversion times). To ensure the longitudinal magnetization recovery trend remains the same throughout the scan, all interleaves for the n^{th} k-space segment are repeated (with a dummy cycle if it has already been NAV-accepted for that interleaf) in the same order, until each interleaf has been accepted for the n^{th} segment, and the sequence moves onto the $(n+1)^{th}$ segment. Subsequently, the outer k-space is acquired without any prospective respiratory motion compensation, and is retrospectively gated using the NAV signal, where measurements outside the gating-window are discarded.

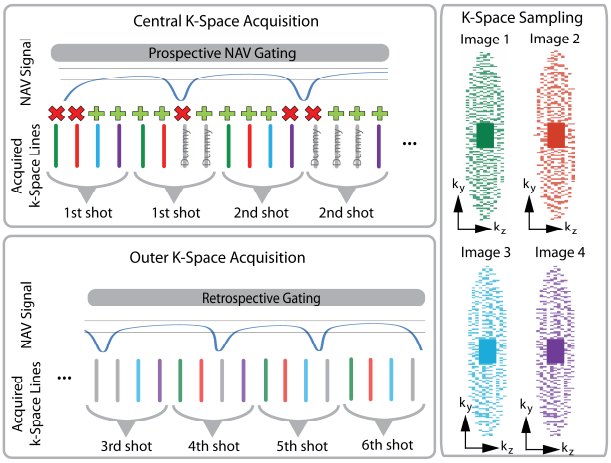

Fig. 1: *Respiratory navigating scheme of the proposed sequence: Central k-Space: All interleaves are repeated until individual acceptance of all interleaves with prospective gating. Outer k-space: Data is acquired without prospective motion compensation and is retrospectively gated, e.g. data that is acquired outside of the gating window is retrospectively discarded.*

This scheme creates an undersampled outer k-space with a fully sampled k-space center and can be reconstructed using a compressed-sensing algorithm (2). T_1 maps are obtained by voxel-wise curve fitting of a two parameter model of the longitudinal magnetization recovery curve to the image intensities.

Phantom Imaging: All imaging was performed on a 1.5T Philips Achieva system. Phantom measurements on a phantom with multiple compartments of different T_1s were performed to test the feasibility of the sequence for T_1 value estimation without any motion, and to compare the estimated T_1 values to those from the Modified Look-Locker (MOLLI) sequence (2).

In-Vivo Imaging: In-vivo 3D T_1 mapping was performed in six healthy subjects using the proposed T_1 mapping sequence 5-30 minutes after injection of Gd-BOPTA. The 3D T_1 mapping sequence was performed during free breathing with a resolution of $1.7\times1.7\times4mm^2$ (TR/TE = 3.0/1.28 ms), an acquisition window of 100 ms and a scan time of 5 minutes for 100% gating efficiency at a heart-rate of 60 bpm. For comparison 2D multi slice T1 maps were acquired using MOLLI (in-plane resolution 1.7×2.1 mm^2, slice thickness 10mm, SENSE rate 2). Images were quantitatively evaluated in terms of T_1 times, and signal homogeneity in the blood and myocardium.

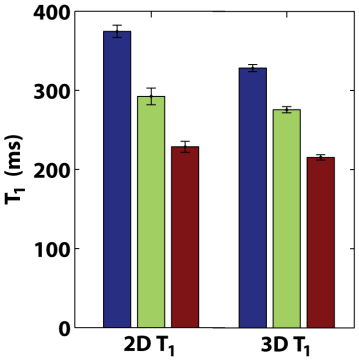

Fig. 2: *Phantom measurements comparing the proposed 3D T1 mapping sequence to 2D MOLLI in different phantom compartments.*

RESULTS: ***Phantom Imaging:*** Fig. 2 shows phantom measurements comparing the proposed T_1 mapping sequence to 2D MOLLI. It can be seen that the T_1 times of the proposed method are underestimating T_1 times by up to 12%. The error bars, that represent the variation within each phantom compartment, show that the proposed 3D method provides improved homogeneity compared to 2D T_1 mapping.

In-Vivo Imaging: Fig. 3 shows representative T_1 maps acquired in a healthy volunteer using the proposed 3D T_1 mapping sequence and multi-slice 2D MOLLI. The arrow indicates a MOLLI-slice that suffers from artifacts induced by improper breath holding. No statistical significant difference was found in the T_1 times of the myocardium, the left and right ventricles ($P > .09$). However the 3D T_1 maps show an average reduction of the T_1 variation in the ventricles by 37%. The acquisition time using the 3D T_1 mapping sequence was between 9 and 15 minutes and between 7 and 10 minutes using MOLLI (including rest periods between breath holds).

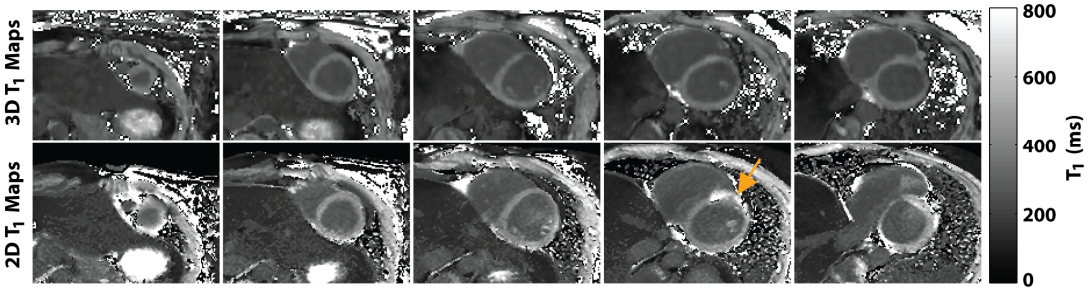

Fig. 3: *3D T1 maps acquired with the proposed technique compared to 2D multi-slice MOLLI. The arrow indicates an artifact induced by improper breath holding.*

CONCLUSIONS: We have proposed a novel sequence for 3D T_1 mapping, utilizing multiple interleaved, segmented inversion recovery image acquisitions. A joint prospective-retrospective navigator gating scheme for multiple interleaves enables free-breathing acquisition of 3D T_1 maps, which are unsusceptible to motion artifacts induced by improper breath holds. The 3D imaging sequence achieved improved homogeneity, coverage and resolution compared to 2D.

REFERENCES: 1. Messrohgli, D.R. MRM, 2004; 2. Moghari, M. MRM, 2012;