

Validation of a Faster Modified Look-Locker Inversion-recovery (MOLLI) method for myocardial T1 mapping on 3T MRI

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Introduction : T1 mapping enables direct myocardial signal quantification and allows a better characterization of myocardial tissue composition on global or regional level. Modified Look-Locker Inversion-recovery (MOLLI) sequence described by Messroghli et al (MRM 2004, 52:141-146) provides high resolution T1 map of myocardium in native and post-contrast situation within a 17 heart-beat breath hold. However, long breath holds often limit clinical application in patients due to motion artifact and heart rate variability. In this study, we designed and tested a faster MOLLI method on 3T clinical machine.

Methods : Seven healthy normal volunteers (7 male, mean age 31±6.9 years) underwent cardiac MRI at 3T clinical machine (MAGNETOM Verio, Siemens AG Healthcare Sector, Erlangen, Germany). Original-MOLLI and fast-MOLLI were performed at same short-axial slice in basal and mid-ventricular level with single breath hold. Original-MOLLI was implemented as a three inversion-recovery (IR) sequence with the first and second blocks of 3 and the third blocks of 5 consecutive image acquisitions. On the other hand, fast-MOLLI was implemented as a two IR sequence with the first of 3 and the second of 5 images. Figure 1 show a scheme of fast-MOLLI sequence. T1 map was reconstructed using 11 (original-MOLLI) and 8 (fast-MOLLI) source images with different inversion time. SSFP (True-FISP) sequence was used for readout (single-slice, single-shot, TE/TR=1.1/2.5msec, flip angle 35°,FOV 320x223mm, matrix 192x256 and slice thickness 8mm). The True-FISP readout in MOLLI used short RF pulses and high bandwidth to minimize banding artifact. The T1 map was divided into 6 segments, and fan-shaped ROIs were set in each segment (Figure 2). Then, segment-based T1 was measured.

Results : The acquisition time of original-MOLLI and fast-MOLLI was 16.9 ± 2.4 sec and 10.0 ± 1.5 sec, respectively. Fast-MOLLI decreased by about one-third the acquisition time compared with original-MOLLI. In 2 segments of inferolateral wall, slight banding artifact near epicardium occurred at the similar location in original-MOLLI and fast-MOLLI. All but 2 of total 78 segments showed good image quality without artifact. T1 maps produced by original-MOLLI and fast-MOLLI did not differ visually. Mean T1 were similar in all segments (mean T1 : original-MOLLI 1142±50msec, fast-MOLLI 1140±43msec). Mean T1 at septal wall (1159 msec) was slightly longer than that of lateral wall (1129 msec), but no statistical difference among the segments. The Bland-Altman plot showed a good agreement between original-MOLLI and fast-MOLLI, with a mean difference of 0.59 ± 33.6 msec (Figure 3).

Discussion and Conclusion : Previous study at 1.5T MRI (Messroghli et al, Radiology 2006, 238:1004-1012) showed that the non-contrast normal myocardial T1 obtained by original-MOLLI method was 980±53msec. In this study, normal myocardial T1 at 3T machine was about 16% longer than that at 1.5T. The proposed MOLLI sequence is faster and clinically applicable, and can generate quantitative T1 map of myocardium with high resolution. T1 mapping using fast-MOLLI will be of great help to understand the myocardial tissue characterization in various heart diseases.

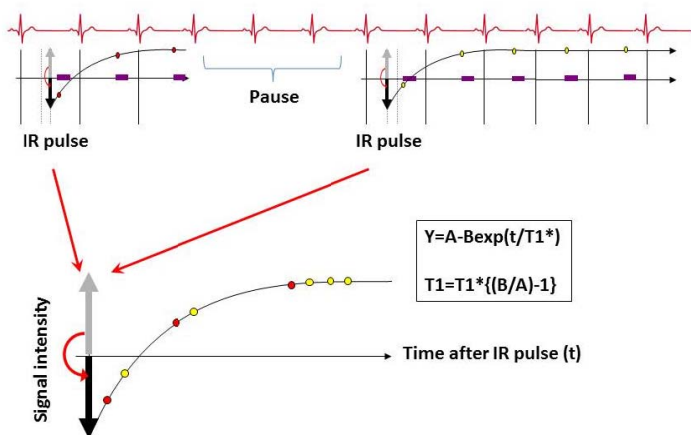


Figure 1. Scheme of the fast-MOLLI sequence. Fast-MOLLI was implemented as 2 IR sequence with the first of 3 and the second of 5 images. T1 map was reconstructed to apply algorithms to define the fitting curve using the 8 acquired voxels.

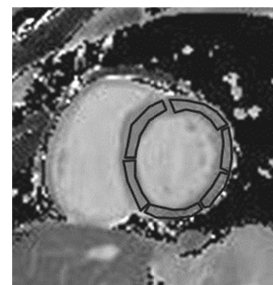


Figure 2. The T1 map was divided into 6 segments at each slice, and T1 was measured.

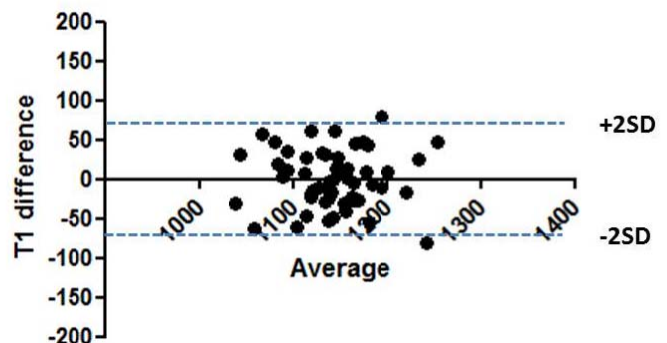


Figure 3. Bland-Altman plot analysis of segmented-based T1 between original-MOLLI and fast-MOLLI.