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Validation of the shortened modified look locker inversion recovery (Sh-MOLLI) sequence for cardiac gated T1 mapping

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Background

T1-mapping of the myocardium can potentially detect, quantify and monitor subtle diffuse pathology without the use of contrast agent. One proven method is the MOLLI (Modified Look-Locker Inversion-recovery) technique, offering single-slice T1-mapping based on three sequential inversion-recovery (IR)-prepared experiments in a 17-heartbeat breath-hold. However, long breath-holds can limit clinical application in patients. We propose and test a novel variant (Sh-MOLLI) that is approximately two times faster.

Materials and methods

10 normal volunteers (7 males; age 35 ± 7 years) underwent CMR imaging at 1.5 T (SIEMENS, Avanto) using MOLLI [Messroghli. JMRI. 2007:26(4):1081-6] and Sh-MOLLI. Basal, mid-cavity and apical short-axis T1 maps were obtained. Sh-MOLLI was implemented as 3 IR experiments split over 9 heartbeats to collect 5+1+1 images at TI = 100+[0,1,2,3,4]*Heartbeat_Interval, 180, 360 ms. IRs were separated by only one heartbeat. Typical SSFP readout parameters: TE = 1.1 ms, TR = 206 ms, flip angle = 35°, FOV = 340 × 116 mm, matrix 192 × 116, interpolated voxel size 0.9 × 0.9 × 8 mm. Sh-MOLLI samples from the second and third IR are taken into account only if T1 estimate is shorter than the heartbeat interval, and they improve standard error of fit. Nonlinear fitting was implemented in C++ directly in the image reconstruction pipeline utilizing parallel processing with T1 maps available for viewing on the console immediately after acquisition. Offline post-processing involved manual tracing of endo- and epi-cardial contours to calculate T1 statistics in myocardial segments 1 to 16 of the AHA 17-segment model.

Results

T1-maps produced by either method did not differ visually. T1-estimates were similar in all but 3 segments (Fig. 1). Across all 160 segments pooled together, Sh-MOLLI T1-estimates were lower by 10.2 ± 24 ms (i.e. -1%, p <

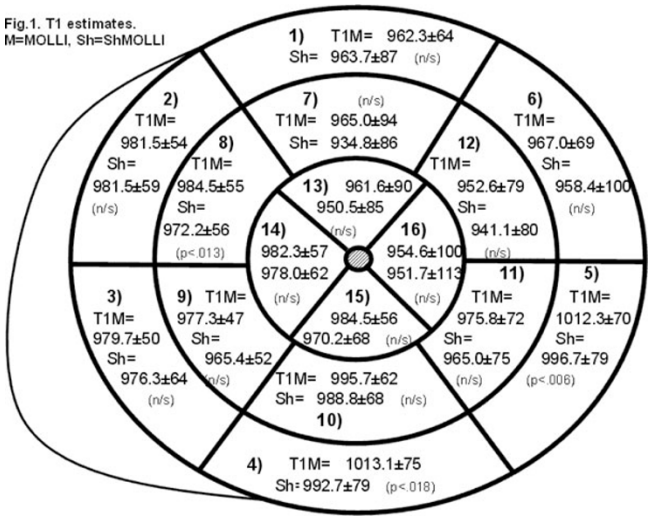

Figure 1
T1 estimatees.

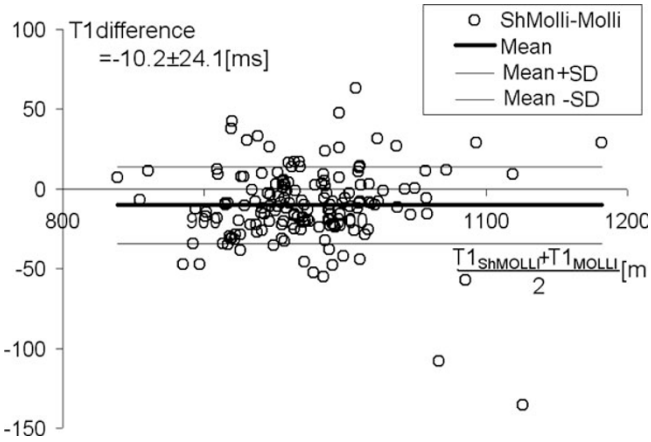

Figure 2
Bland-Altmand plos. T1:ShMOLLI-MOLLI

0.001, see Fig 2). Sh-MOLLI showed an 8% larger variation in T1-estimates.

Discussion

The main advantage of Sh-MOLLI is a near two-fold increase in speed of acquisition. The additional variation in T1-estimates is much less than the 25-50% expected from the reduced number of samples - likely due to the fact that Sh-MOLLI is less susceptible to movement artifacts accumulated within shorter breatholds. Further underestimation of T1 values is only minor, especially when compared to the known bias of MOLLI, which is in the order of -5%. Simulations and phantom measurements (not presented here) showed that the bias in Sh-MOLLI T1 estimates is relatively stable across a wide range of T1 values and independent of heart rate variation.

Conclusion

The proposed Sh-MOLLI sequence is fast, clinically applicable, and can generate robust, quantitative single breathhold T1 maps of the human myocardium with high resolution.