ShMOLLI: Shortened Modified Look Locker Inversion recovery for cardiac T1 mapping – From theory to normal human myocardium

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INTRODUCTION: T_1-mapping of the myocardium can provide quantitative assessment of changes in the myocardium, with potential to detect, quantify and monitor subtle diffuse pathology without the use of contrast agents. Cardiac T_1-mapping is complicated by movement, which limits the resolution of inversion time (TI) sampling to a heartbeat interval. One method is the MOLLI technique (Modified Look Locker Inversion recovery (IR)), which offers accurate T_1-mapping over a wide range of T_1 values using a single long breath-hold [1]. It typically utilises three sequential IRs to provide 3+3+5 TI samples/separated by 3 heartbeat breaks for the recovery of longitudinal magnetization (sampling scheme 3/3+3/3+5). However, this amounts to a long 17 heartbeat breath-hold, which can limit clinical application in certain patients with cardiac disease. We propose and test a novel variant of MOLLI that is approximately two times faster.

METHODS: Simulation: Look-Locker and incomplete magnetization recovery effects were simulated in IDL (Interactive Data Language, ITT Visual Information Solutions) for T_1=50-2600ms. Assuming realistic SNR, we found that T_1 values longer than the heartbeat interval are adequately estimated from the first IR experiment; the additional IR epochs are necessary only for estimating the short T_1 values where long stopping periods are not necessary. Thus we tested Short MOLLI (ShMOLLI), which is based on a 5/1+1/1+1 sampling scheme and combines minimal recovery times with conditional data reconstruction (Fig.1), against the original MOLLI method [1]. Nonlinear fitting was prototyped in IDL (simulations) and implemented in C++ directly in the image reconstruction pipeline utilizing parallel processing, with T1 maps available for viewing on the console immediately after acquisition.

Experimental: Fifteen 50ml Agarose+NiCl gel phantoms[2] with T2~60ms and T1 70-2300ms were studied in a 1.5T MR scanner (Avanto, Siemens Medical Solutions). The heart rate (HR) was varied artificially between 40-100 BPM. Imaging parameters: FOV=217x290mm, resolution 1.1x1.1x8mm on a 256x256 matrix (interpolated from 128x128 acquisition), flip angle=35deg, TR/TE=206/0.98ms. A Spin echo sequence with TI=33, 100, 300, 900, 2700, 5000 ms, TE/TR=6.3/10000ms was used as reference.

Normal Controls: 10 normal volunteers (7 males; age 35±7years) underwent CMR imaging at 1.5T using the ShMOLLI and MOLLI methods. Basal, mid-cavity and apical short-axis T1 maps were generated. A single slice, which was perceived "best quality" at the time of scanning, was additionally repeated 2 times at the end of the protocol to assess short-term variability of the estimates. Images were collected with SSFP, typically: TE=1.1ms, TR=206ms, flip angle=35º, FOV=340x220mm, matrix 192x124, interpolated voxel size 0.9x0.9x8mm. Offline post-processing involved manual tracing of endo- and epi-cardial contours to calculate statistics of T1 estimates in myocardial segments 1 to 16 of the AHA 17-segment model for comparison with previously published estimates [3].

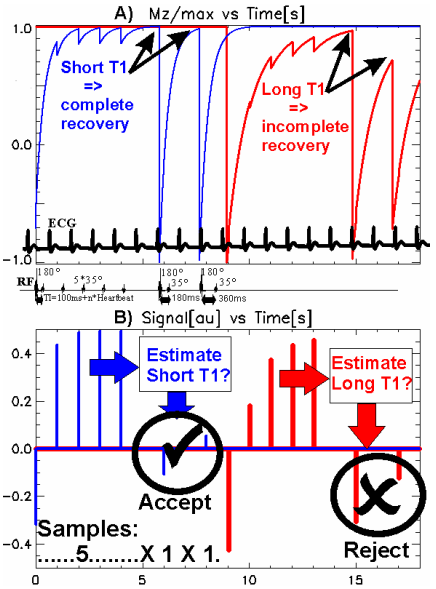

Fig.1. A) Evolution of the longitudinal magnetisation during ShMOLLI acquisition for short T_1 (blue) and long T_1. (red/offset for clarity) B) Decision on validity of the additional signal samples can be taken on-the-fly.

RESULTS & DISCUSSION: ShMOLLI is characterized by a negative bias of about 4% in T1 estimates. In both simulation and phantom measurements the ShMOLLI bias is independent of T1 values and heart rate, making any corrections much simpler than in the case of MOLLI (Fig. 2). The simulated variability of T1 estimates for Sh-MOLLI (Fig. 2A, whiskers) is about 40% larger than that for MOLLI, as expected due to a reduced number of TI samples. Our *in-vivo* MOLLI T1 estimates concur closely with previously published estimates [3] both in average values and variability (Fig. 3). As predicted from simulations, ShMOLLI produces slightly lower T1 estimates than MOLLI (Δ=-10.2±24ms, i.e. ~1%, p<0.001, N=160 segments). However, the *in-vivo* variability of ShMOLLI T1 estimates (whiskers in Fig.3) is only 8% larger. Direct estimates of short-term T1 variability are the same for ShMOLLI and MOLLI (SD=6.6ms and 7.2ms, respectively; p=0.54). This is most likely due to the advantages of shorter imaging time and decreased body movement offered by the ShMOLLI method that outweigh the statistical penalty for obtaining fewer measurements.

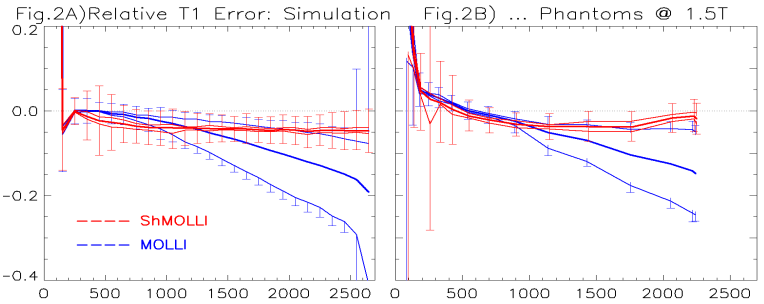

Fig. 2. T1 estimation errors. Thick centre lines: average bias. Thin lines: bias range due to heart rate variation (HR=40-100 BPM). Whiskers: worst case SD across all HR.

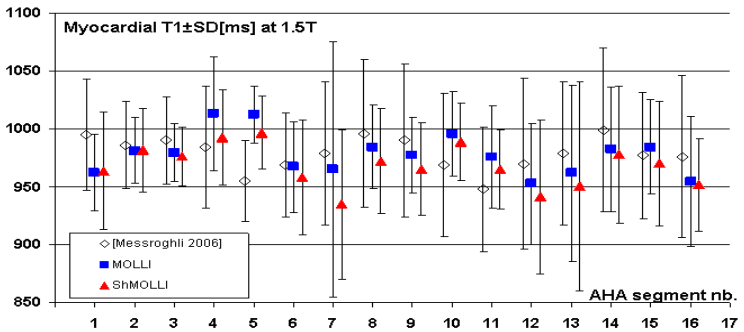

Fig. 3. Measured T1 relaxation times in AHA myocardial segments.

CONCLUSION: The new ShMOLLI sequence, using conditional reconstruction of incomplete recovery periods, is fast, practical, and can generate robust, quantitative myocardial T1 maps in a single 9 heartbeat breath-hold with high resolution.

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References: [1] Messroghli. Magn Reson Med 2004. 52:141-6.
[2] Cochlin. Proceedings of 11th Annual ISMRM Meeting 2003. 885. **[3]** Messroghli. Radiology 2006. 238:1004-12.