Characterization of Modified Look Locker (MOLLI) using Bloch simulations and corroboration with scan measurements

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Introduction: Recently, it has been shown that T1 mapping can differentiate between diffuse fibrosis and normal myocardium [1]. T1 mapping using the Modified Look Locker Imaging (MOLLI) technique [2] has found favor in cardiac imaging as a more reliable alternative to standard segmented Look Locker (LL). MOLLI is more robust to cardiac motion as data are acquired in the same quiescent window of several cardiac cycles as opposed to data acquisition over the entire cardiac cycle with segmented LL. A subsequent work [3] explored optimization of parameters to improve accuracy of calculated T1 values. The approach to optimization was purely experimental based on performing phantom scans while varying scan parameters. Such an approach could fail to be comprehensive in the covered parameter space as well as the parameters thought to influence T1 values. For example, the effect of T2 on the accuracy of T1 has not been determined although a relationship likely exists. In this work, we develop a Bloch simulation based characterization of the MOLLI sequence and evaluate T1 accuracy for several different scan parameters. We corroborate T1 values obtained from simulation with values obtained from scanning phantoms. Based on simulations and scanning results, it is shown that the simulation is a valuable tool in understanding the accuracy of MOLLI derived T1 values given different scan conditions.

Materials and Methods: The typical MOLLI acquisition consists of 11 images acquired as three sets of 3, 3 and 5 non-segmented balanced SSFP acquisitions over the corresponding number of consecutive R-R intervals. Each of the three sets includes two or more dummy R-R cycles after acquisitions to allow recovery of longitudinal magnetization. The similarity with standard LL is that one inversion pulse precedes each of the three sets of image acquisitions. However, unlike typical LL scans, acquisition is not continuous resulting in intermittent free recovery of magnetization. Since the longitudinal recovery curve has modulated and unmodulated parts, MOLLI exhibits a complex response to scan parameters.

Phantoms: Three agar-$NiCl_2$ phantoms mainly with different T2s were prepared by varying the amount of agar in each of them using the figure in [4] as a nomogram. Accurate T1 values for the phantoms were determined using gold standard inversion recovery spin echo (IR-SE) imaging. T2 values were determined using a multi-echo spin echo sequence. The T1 and T2 values so determined were then used in the Bloch simulations for MOLLI.

Simulations: Bloch calculations for balanced SSFP acquisition were implemented where an inversion pulse is followed by dead time (if any), dummy acquisitions to the center of k-space (first sampled point), followed by the acquisition echo train. The first sampled point corresponds to TI_{min} while the subsequent two or four (for the last set) sampled points were one R-R interval apart. The second set was implemented similar to the first set except that the initial magnetization was derived from the recovered magnetization of the previous set (after including 2 dummy R-R intervals) and the first sampled point was at (TI_{max} + (TI_{max}–TI_{min})/2). The third set was similarly simulated with the first TI at TI_{max} followed by four sampled points each 1R-R interval apart. To derive the T1 resulting from the MOLLI acquisition, all sampled data points were merged together and a three parameter fit based on Nelder-Mead minimization was used to find T1. Correction for the 3 parameter model as

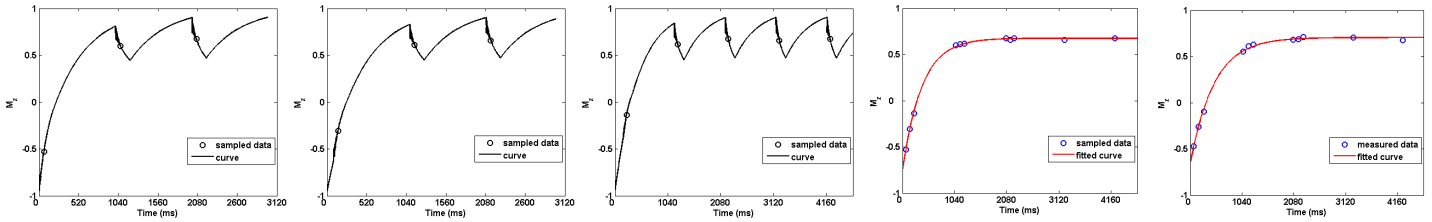

Fig 1: Simulated longitudinal magnetization for the three MOLLI data sets (3-3-5 acq), the final merged set with fit and comparable acquired data with fit (right).

described in [2] was performed.

MRI experiments: The three agar-$NiCl_2$ tubes were scanned on a Philips 3T Achieva scanner using the MOLLI sequence with 11 image acquisitions. Other scan parameters were: FOV=20cm, TI_{min}=66.2ms, TI_{max}=270ms, flip α=35°, b-SSFP TR/TE=2.6/1.3ms, 20 dummy pulses, centric encoding, acquisition etl=50, SENSE=2, R-R interval = 1sec. Variation in flip angle, TI_{max}, shot duration (acq etl) and linear vs centric encoding were studied through simulations and phantom experiments.

Results: T1/T2 from IR-SE and multi-echo SE scans were determined to be 490/50ms, 468/21ms and 334/12ms for the three phantoms. Figure 1 shows the simulated sampled points and longitudinal magnetization curve (post-inversion) for the three sets and the combined data with the corresponding three parameter fit for the second phantom and given scan parameters. Comparison with acquired data for the same phantom shows excellent agreement (after normalization of scales). Figure 2 shows the predicted and measured values when TI_{max} and flip angle were varied; increasing dummy acquisitions for centric encoding (Centric 1=20; Centric 2=30) or increasing shot duration for linear encoding (Linear 1=231ms; Linear 2=318ms) results in increased underestimation of T1 values. For all centric-encoded experiments, the error for the two phantoms with similar T1s but different T2s (phantoms ph2 and ph3) approached significance with mean measured error of 4.7% vs 3.5% when compared to IR-SE values. Linear encoding shows a strong inverse relationship between T1 inaccuracy and T2 value again based on T1 values in ph2 and ph3. For the two linear encoding scans, the measured error was 15.7% and 9.3% for ph2 and ph3, respectively. Good agreement was found between the predicted and measured T1 values in all experiments ($p<0.05$).

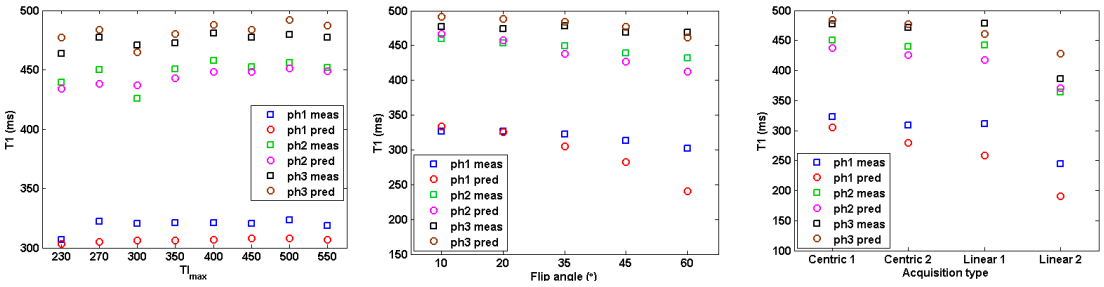

Fig 2: Variation in measured and predicted T1 values with inversion time (left), excitation angle (center) and encoding (right)

Discussion: Motion effects are discounted in the Bloch simulations done here. Predictions made from the model would need to be tempered accordingly. For example, increasing TI_{max} seems to improve accuracy but would result in increased motion related inconsistencies. Simulation results are at resonance. The off-resonance T1 values would be different. Linear **k**-space encoding results in considerable underestimation for short T2 species but may reduce artifacts in tissues with long T2. Increasing flip angles decrease T1 accuracy but SNR would be increased. Although Bloch simulations cannot predict the exact value, the trend and correspondence between simulated and measured values is excellent in all cases. A different variant of the standard MOLLI acquisition (for example, one with 3-3-3 acquisitions) can be straightforwardly simulated along the same lines as presented here.

References: [1] Iles L et al. *J Am Coll Cardiol.* 2008; 52:1574-80. [2] Messroghli DR et al. *Magn Reson Med* 2004;52:141-146. [3] Messroghli DR et al. *J Magn Reson Imag*. 2007; 26:1081-6. [4] Cochlin L et al. *Procs. ISMRM* 2003; 885.