An Intuitive Model of Several Factors Affecting Accuracy of MOLLI T_1 Values

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INTRODUCTION The MOdified Look-Locker Inversion recovery (MOLLI) sequence (1) and its variants are commonly used for quantitative cardiac T_1 mapping to detect myocardial fibrosis. However, MOLLI sequences have been shown to have systematic T_1 errors dependent on factors such as heart rate (2), T_2 values (3), T_1 values (4) and inversion efficiency (4). The interaction of these effects is not well understood and potential dependencies on other pulse sequence parameters have not been considered. We propose a model for predicting systematic MOLLI errors that incorporates the effects of T_1, T_2, and other sequence parameters to provide an intuitive understanding of how these factors affect MOLLI T_1 errors.

THEORY The MOLLI sequence consists of several "Look-Locker sets", each containing a single inversion pulse followed by several single-shot balanced steady-state free precession images at various inversion times (TI), separated by several heartbeats for magnetization recovery. T_1 values are calculated by fitting a three-parameter exponential recovery model and applying the "Look-Locker correction" (5), intended to account for magnetization attenuation from multiple imaging readouts after a single inversion pulse.

We propose that the errors in MOLLI T_1 values are directly related to the magnitude of magnetization perturbation caused by imaging. The perturbation of imaging readouts can be characterized by comparison to pure T_1 recovery that would occur over the same time period in the absence of an imaging readout. Specifically, M_{diff} is defined as the difference in normalized longitudinal magnetization following first imaging readout as compared to pure T_1 recovery over the same time (Fig. 1). The degree of perturbation is determined by both tissue properties such as T_1 and T_2 as well as imaging parameters such as repetition time and the number of k-space lines acquired.

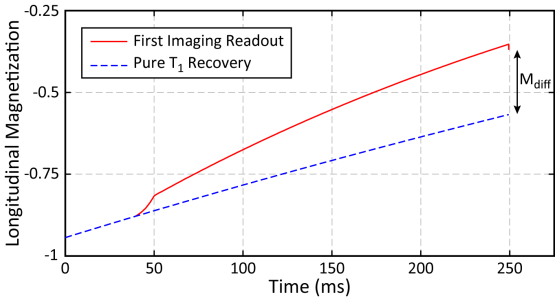

Fig. 1 M_{diff} with pre-contrast myocardium-like T_1 and T_2 values. Dashed blue line shows pure T_1 recovery following inversion. Solid red line shows a bSSFP readout with linearly ramped opening RF pulses and a closing α/2 pulse.

METHODS Phantoms: 14 $NiCl_2$ doped agarose phantoms with a wide range of physiologic T_2/T_1 values simulating pre- and post-contrast blood and myocardium were imaged on a 1.5T Siemens Avanto. Spin echo experiments using a 10 s TR with 16 TIs spanning 100–5000 ms and 6 TEs spanning 11–200 ms were used to calculate gold standard T_1 and T_2 values respectively. Three variations of a "3-5" Shortened MOLLI (6) sequence were performed: 1) typical parameters with TE/TR of 1.03/2.43 ms and 86 acquired k-space lines per image, 2) rate 2 GRAPPA parallel imaging with 57 acquired k-space lines, and 3) a longer TE/TR of 1.24/3.06 ms. All 3 variations shared other common pulse sequence parameters: 2 inversion sets of 3 and 5 images with 3 recovery heartbeats between sets, 140 ms TI_{min}, 80 ms TI increment, 6/8 partial Fourier, 75% phase resolution, 35° flip angle, and a 60 bpm simulated heart rate. T_1 values were calculated using in-line T_1 maps with Look-Locker correction.

Simulations: Bloch equation simulations of the MOLLI sequence were used to calculate M_{diff} as described in the Theory and Figure 1. Simulations were performed in MATLAB for each phantom experiment using an adiabatic hyperbolic secant inversion pulse, spin echo T_1 and T_2 values, and actual imaging sequence parameters.

RESULTS Phantoms had a wide range of spin-echo T_1 (276–1453 ms) and T_2 (46–199 ms) values. MOLLI generally underestimated T_1 values compared to spin echo with a wide range of accuracy from a 12% underestimation to a 7% overestimation. Errors in MOLLI T_1 values were strongly related to M_{diff}, with increasing errors at larger M_{diff} values (Fig. 2). M_{diff} values varied greatly between phantoms due to a wide range of T_2/T_1 values (50/1145 – 122/276 ms), with larger perturbations for smaller T_2/T_1 ratios. Phantoms with T_2 and T_1 values similar to pre- and post-contrast blood and myocardium (circled markers in Figure 2) have widely different systematic errors ranging from a 10% underestimation in pre-contrast myocardium to 5% overestimation in post-contrast blood. M_{diff} and systematic T_1 errors were also affected by sequence parameter changes, with greater errors for longer readouts and up to 2% of errors in any given phantom were the result of parameter changes alone.

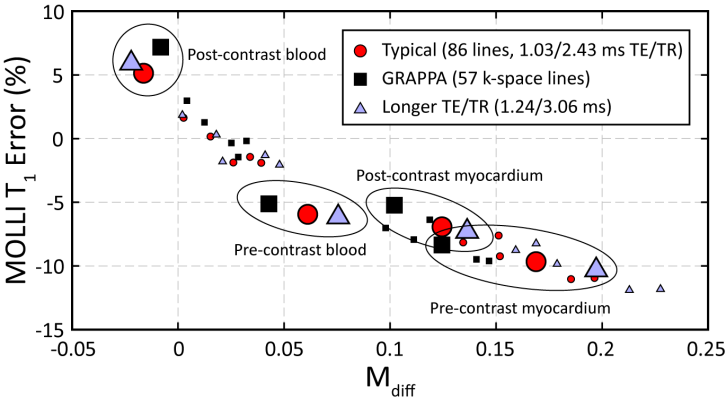

Fig. 2 MOLLI T_1 errors as a function of M_{diff} for all phantoms for different sequence parameters. Data for pre- and post-contrast blood and myocardium-like phantoms are shown with enlarged data points.

DISCUSSION AND CONCLUSION Large systematic errors in MOLLI T_1 values were strongly correlated with M_{diff}, a measure of magnetization perturbation caused by the imaging readout. M_{diff} is affected by both intrinsic tissue T_2/T_1 values and also commonly altered sequence parameters, such as TE/TR and the number of RF pulses. The Look-Locker correction factor is intended to correct for the effects of magnetization perturbation, although our data show that significant errors remain even after correction. The M_{diff} concept provides an intuitive understanding of how tissue relaxation and sequence parameter affect accuracy of MOLLI T_1 values, although other confounders such as heart rate may present yet additional sources of systematic errors.

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