An Analytic Description of Factors Affecting MOLLI's Accuracy Using a Time-Weighted Average Model of T_1 Relaxation

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PURPOSE: To develop an analytic description of factors affecting the accuracy of the MOLLI sequence.

THEORY: The MOdified Look-Locker Inversion recovery (MOLLI) sequence is widely used for in-vivo cardiac T_1 mapping and consists of multiple balanced steady-state free precession (bSSFP) images following a single inversion pulse[1]. The apparent relaxation time constant (T_1^*) is multiplied by a Look-Locker correction factor to calculated $T_1 = (B/A-1)T_1^*$, intended to account for magnetization perturbation by the readouts. Despite this correction, MOLLI T_1 values are known to have systematic errors that depend on heart rate, flip angle, T_1, T_2, inversion efficiency, off-resonance, and magnetization transfer[1-6]. Analysis of these sources of error has been limited to Bloch equation simulations or phantom experiments which only empirically describe each source of error independently. We hypothesize that the apparent longitudinal relaxation rate ($R_1^* = 1/T_1^*$) can be described in terms of the driven relaxation rate during the image readouts (R_1') and the true relaxation rate during the intervals between imaging (R_1), as a time weighted average (TWA) of the two rate constants (R_1' and R_1), thus enabling an analytic description of T_1^*. For a given flip angle (θ), true T_1 and T_2 values and a MOLLI duty cycle (D) defined as the fraction of time per heartbeat spent acquiring data (which is determined by repetition time (TR), number of phase encode lines, and heart rate), the TWA model predicts:

$R_1^* = DR_1' + (1-D)R_1$, where the driven relaxation rate (R_1') is given by[7]: $R_1' = R_1\cos^2(\theta/2) + R_2\sin^2(\theta/2)$ [Eq 1, 2]

METHODS: Simulations: The TWA model was validated by comparison of predicted T_1^* values with Bloch equation simulations of the MOLLI sequence, using a single flip angle and actual sequence parameters (see below) over a wide range of T_1s (300–3000 ms) T_2s (30–250 ms), flip angles (10–70º), total phase encode lines (50–150), and heart rates (30–120 bpm). Additional simulations were also run to match phantom experiments, with a distribution of flip angles to emulate realistic slice profile effects. Equation 2 describes distinct R_1' values for each flip angle and for realistic slice profiles we propose that the resulting multi-exponential distribution of R_1's can be approximated as a single mono-exponential R_1' by taking the average of all R_1', weighted by the flip angle distribution and the relative signal intensity (approximated as sin(θ/2)).

Phantoms: 14 $NiCl_2$ doped agarose phantoms with a range of physiologic T_1 and T_2 values were imaged on a 1.5T Siemens Aera MRI scanner. Spin echo experiments using 10 s TR with 14 TIs spanning 100–2000 ms and 7 TEs spanning 11–200 ms were used to calculate gold standard T_1 and T_2 values respectively. MOLLI imaging was performed in the same session with common sequence parameters: 1.305/2.63 ms TE/TR, 35º flip angle, 360×270 mm field of view, 192×112 matrix, 78% phase resolution, 7/8 partial Fourier, rate 2 GRAPPA, 120 ms starting TI, 80 ms TI increment, 2 Look-Locker sets of 5 images separated by 10 recovery heartbeats to avoid incomplete T_1 recovery, and a simulated heart rate of 60 bpm. MOLLI was repeated with 8 flip angles (10–70º) and also with 8 simulated heart rates (30–120 bpm) to vary R_1' and the duty cycle, respectively.

Analysis: To calculate T_1^*, both Look-Locker sets from MOLLI data were fit concurrently to a three-parameter exponential: Signal = A−Bexp(−TI/T_1^*), where T_1^* was matched between sets but A and B were independent. MOLLI T_1 values were calculated in the standard fashion by fitting the combined Look-Locker sets and applying Look-Locker correction. TWA model T_1^* was predicted for each experiment using the above equations.

RESULTS: The TWA model of T_1^* had excellent agreement with single flip angle simulations over all parameters tested with an average difference of −6±6 ms. In phantom experiments, very good agreement was found between TWA T_1^* and simulation T_1^* (−2±6 ms), as well as between measured T_1^* from phantoms and both TWA T_1^* and simulation T_1^* (−6±15 ms and -8±17 ms respectively, **Fig. 1**). Look-Locker corrected T_1 values generally underestimated T_1 when compared to spin echo, particularly for short T_2 (44–74 ms) phantoms and increasing error with larger flip angles and higher heart rates (range: −146 to 34 ms error).

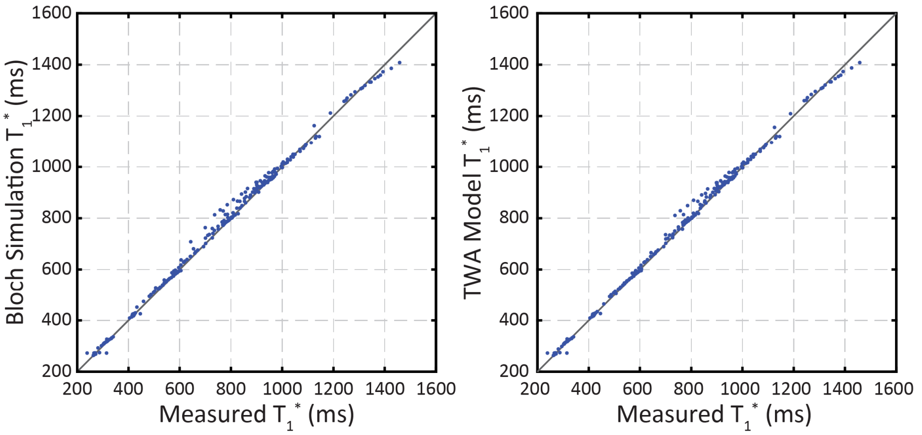

Fig. 1. Comparison of Bloch simulation T_1^* (left) and TWA model T_1^* (right) with measured T_1^* in phantoms with 10–70º flip angle and 30–120 bpm MOLLI acquisitions.

DISCUSSION: The TWA model was validated against Bloch equation simulations across a wide range of multiple sequence parameters and agreement between measured T_1^* and TWA T_1^* suggests the weighted mono-exponential R_1' approximation is a reasonable description of slice profile effects. The TWA model provides an analytic framework for calculating the effect of T_1, T_2, flip angle, and duty cycle, which have only been empirically characterized in the past. For example, the duty cycle relationship in the TWA model describes how T_1^* changes with heart rate without the use of an empirical correction factor[8] (even when allowing for complete recovery between Look-Locker sets). The TWA model also explains the decrease in T_1^* values observed with increased phase encode lines through the effect on duty cycle as well as the interaction of T_1, T_2, and flip angle in T_1^* error.

The Look-Locker correction factor is used in MOLLI to account for errors in T_1^*, but fails to yield accurate T_1 values in all cases, particularly with short T_2 or poor inversion efficiency. While the TWA model can analytically calculate T_1^*, it does not describe the error in the Look-Locker correction or provide an equivalent correction factor by which the true T_1 can be calculated with acquired MOLLI data. Nevertheless, the TWA model provides an algebraic equation describing the effects of many of MOLLI's sources of error on T_1^* and yields intuitive insight into how many of these previously described sources of error interact.

CONCLUSION: MOLLI's apparent T_1^* can be described using a time-weighted average model of pure T_1 relaxation and driven T_1' relaxation and provides intuitive insight and a quantitative basis for analyzing factors affecting MOLLI T_1 values.

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