Implementation of a robust method to derive unbiased T1 maps from MOLLI sequence and Bloch equations simulations.

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Introduction

Myocardial T_1 mapping is a technique that has recently emerged in cardiac MR protocols and enables an accurate diagnosis and quantification of myocardial fibrosis [1]. The MOLLI sequence has been widely used for this purpose but is known to underestimate high T_1 values [2]. In the standard post-processing approach of the sequence, T_1-fitting of the data is performed by a non-linear least square fit to the exponential recovery curve $A - B.\exp(-TI/T_1^*)$, where TI is the measured inversion time for each acquired image. T_1^* is the effective time constant which includes the effect of the image readout and is related to the T_1 as $T_1 = T_1^* (B/A - 1)$. This Look-Locker correction can be derived analytically in the case of FLASH readout with continuous RF [3]. However, unlike typical Look-Locker scans, MOLLI is played using non-continuous bSSFP readout, resulting in intermittent free recovery of magnetization. As the longitudinal recovery curve has modulated and unmodulated parts, MOLLI exhibits a complex response to scan and intrinsic tissue parameters (nominal flip angle, inversion efficacy, T_2) that are not properly modeled in this standard approach. The goal of our study was first to quantify the error made on T_1 estimation with this standard post-processing using Bloch equations simulation of the MOLLI sequence. Then, we proposed a robust approach, applicable *in vivo* in the context of cardiac MR, to derive unbiased T_1 maps using the simulations, experimental data points of the MOLLI sequence and the acquisition of T_2 and B_1 maps.

Materials & Methods

Bloch equations simulation of the MOLLI sequence was implemented in Matlab as described in [4] and [5] using actual acquisition and timing parameters. First, this simulation was used to emphasize the deviation between true T_1 and T_1 values determined by the standard post-processing approach, as a function of T_1, T_2, nominal flip angle, and inversion efficacy $\eta = \cos(\pi$ - inversion pulse). Then, to derive an accurate T_1 map, simulated datasets were adjusted on experimental MOLLI data points, using T_2 and B_1 parameters obtained with other specific MR sequences.

Five Gd-DOTA doped agar phantoms with a broad T_1 distribution were used for MR experiments on a 3T whole-body scanner (Tim Trio, Siemens Healthcare). True T_1 values were assessed using a standard inversion recovery turbo spin echo (IR-TSE) sequence with 15 inversion times (from 100 to 9000ms). The MOLLI sequence was acquired with a standard implementation consisting of 3 inversion sets of 3, 3 and 5 images, TE/TR = 1.25/2.5ms, nominal flip angle = 35°, TI_{min} = 100ms with 80ms increment and a simulated 60bpm heart rate. T_2 maps were generated with a T_2-prepared TrueFISP [6] using 3 T_2 preparation times (0/25/55ms). 3D B_1 transmit field maps were obtained with a standard AFI sequence (TR_1+TR_2=100ms, TR_2 =5TR_1, TE=2.75 ms, nominal flip angle: 60°).

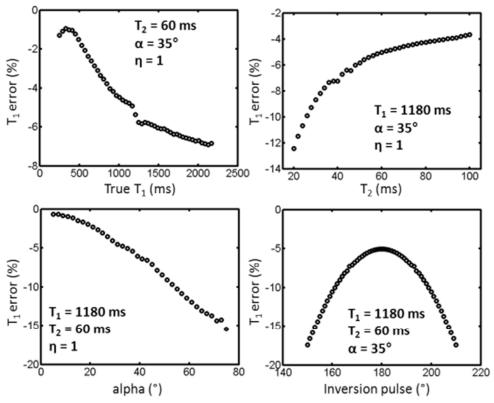

Figure 1: Simulated deviations between true T_1 and T_1 values determined by the standard post-processing approach, as a function of T_1, T_2, nominal flip angle, and inversion efficacy.

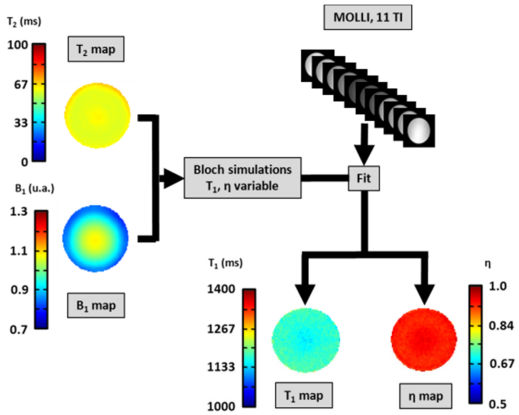

Figure 2: Description of the new post-processing approach of the MOLLI sequence to derive T_1 and η maps.

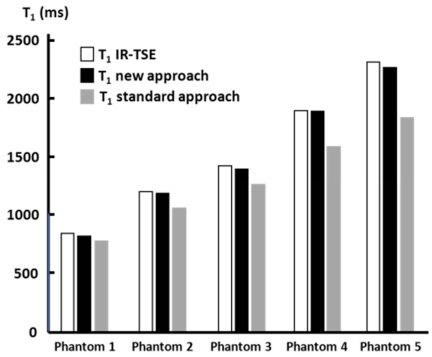

Figure 3: T_1 values determined on five different phantoms using a gold standard IR-TSE sequence, the standard post-processing of MOLLI sequence and our new approach.

Results

As depicted by figure 1, the standard post-processing approach of MOLLI sequence is quite sensitive to sequence parameters (bSSFP readout scheme, nominal flip angle, inversion efficiency) but also to the tissue T_2. Although discrepancies might be weak for small T_1, large T_2 using low nominal flip angles and with good inversion efficiency, they could become higher than 15% for large T_1 values, high nominal flip angle and poor inversion efficiency. Figure 2 represents a flow chart of the new method to derive T_1 and η maps based on the adjustment of simulated datasets on MOLLI experimental data. Results obtained on phantoms shows that our new post-processing approach was much more efficient to precisely determine a large range of T_1 values (Figure 3). The error made with the standard approach was found between 8% and 13% (depending of the T_1) while the maximum deviation was less than 2% using the new method.

Discussion & Conclusion

Systematic errors on T_1 values reported by the users of the MOLLI sequence are largely due to the post-processing procedure that does not take into account the bSSFP readouts interleaved with relaxation periods. In this study, we showed on phantoms that a proper simulation of the sequence combined with T_2 and B_1 mapping allowed for an accurate quantification of the T_1 without interfering with the acquisition parameters (by decreasing the nominal flip angle or the number of phase encoding steps). For *in vivo* applications, the T_2-prepared TrueFISP can be acquired in one breath-hold in less than 10 R-R periods, and a B_1 mapping sequence based on Bloch-Siegert shift [7] can be implemented to fit in another breath-hold. Further work will cover in vivo applications. For example, diffuse fibrosis might slightly affect myocardium T_1 values and its diagnosis could be improved using our new approach considering the large T_1 windows that can be accurately assessed without T_2 bias. Furthermore, estimation of parameters like the extracellular volume fraction (which mostly relies on T_1 mapping) would greatly benefit from this precise T_1 quantification method.

References

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