Intrinsic Accuracy of Myocardial T1 Quantification with Modified Look-Locker Inversion Recovery (MOLLI)

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Introduction: T1 mapping in the heart for quantitative tissue characterization as an important input parameter for clinical differential diagnosis remains a major challenge. The use of the MOLLI technique (1) enables the generation of an accurate T1 map within a single breathhold in a wide range of T1 values. The intrinsic accuracy of the technique has been characterized in phantoms and in control subjects (2). However the theoretical analysis of this scheme in terms of accuracy is still pending. We present a detailed analysis of the signal behavior of the MOLLI technique and give estimates of the accuracy limits.

Method: The MOLLI acquisition scheme was simulated based on Bloch equations for on-resonant spins. Typical parameter settings taken from the clinical implementation of the technique (17 heart beats (hbs), SSFP with steady state preparation, 3 inversions with acquisition hbs (3-3-5), relaxation hbs (3-3-0), TR 3 ms, 100 phase encoding lines per image, 11 inversion times (TI) with minimal TI 150 ms, TI shift 50 ms) were fed into the simulation routine. The resulting signal curves for transversal magnetization were fit with a non-linear least squares 3-parmater T1 curve fit. The agreement of the resulting apparent T1 values with the input T1 of the simulation was analyzed with respect to varying flip angles (5...80 degrees), heart rates (RR 500...1000 ms) and T1 values (200...1000 ms).

Results: With increasing flip angle (T1=1000 ms), a systematic underestimation of T1 is observed (Tab. 1). This underestimation is independent from the specific T1 value itself, as can be seen from table 2. For a clinical protocol as stated above, the deviation of the apparent T1 from the true T1 is 3.0% for a 20° acquisition flip angle, 5.3% for 30° and 7.8% for 40° (see also Tab. 1). For higher flip angles, a pseudo steady state is established resulting from free T1 relaxation and intermittent SSFP readouts. For 50° the underestimation exceeds the 10% level. For fixed flip angle (α=30°), but varied input T1 values, a high level of agreement is achieved over a wide range of T1 values (Tab. 2). The influence of the heart rate on the apparent T1 is shown in Tab. 2.

Discussion: The quantification of T1 with MOLLI without any correction that accounts for the magnetization disturbance from free T1 relaxation due to SSFP acquisitions results in good agreement for lower flip angles. The systematic character of underestimation in T1 implies that a comparison of acquisitions with identical protocols will still reliably reveal relative differences in T1, even for higher flip angles where a significant deviation from the true T1 value will occur without additional corrections. Further investigations are required to analyze the influence of T2 on the T1 quantification with MOLLI. Improvements in scan efficiency can be expected if a correction based on the simulated signal evolution is taken into account and therefore higher flip angles can be used. The aim of reducing the interference of the SSFP readout with the free T1 relaxation implies to reduce the number of phase encoding lines per image, e.g. by using parallel imaging.

References: (1) Messroghli DR et al. Magn Reson Med. 52:141-146 (2004). (2) Messroghli DR et al. Proc. #200, SCMR 2006.

Flip angle α [deg]	5	10	20	25	30	35	40	50	60	80
T1 (fit) [ms]	996	993	970	959	947	934	922	901	886	869
Rel. diff [%]	0.4	0.7	3.0	4.1	5.3	6.6	7.8	9.9	11.4	13.1

Table 1 : Effect of varying excitation flip angle α on the deviation of apparent T1.

T1(true)[ms]	50	100	200	400	600	800	1000
T1 (fit) [ms]	50	100	199.8	390	569	788	947
Rel. diff [%]	0.0	0.0	0.1	2.5	5.2	1.5	5.3

RR [ms]	1000	900	800	700	600	500
T1 (fit) [ms]	947	941	926	920	893	887
Rel. diff [%]	5.3	5.9	7.4	8.0	10.7	13.0

Table 2 : Effect of varying input T1 value (left) and varying heart rate (right)on the deviation of apparent T1 from input T1 value.

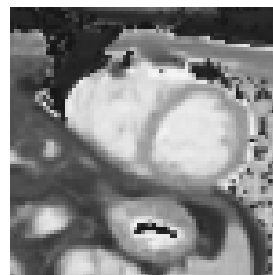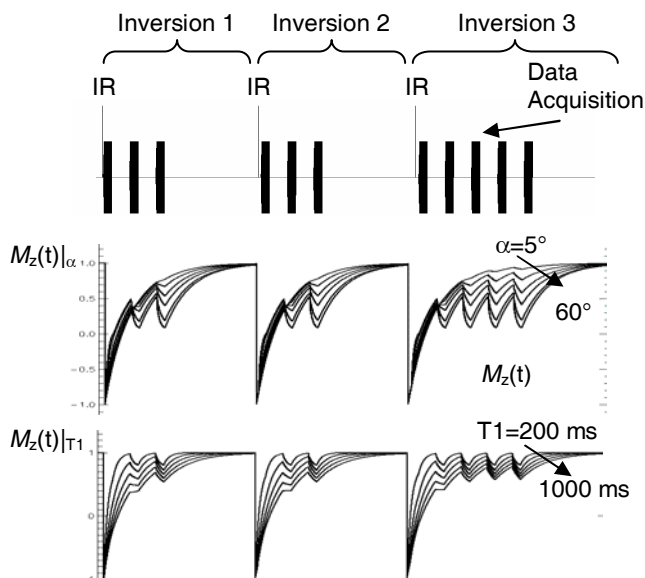*Figure 1: Left: MOLLI acquisition scheme and magnetization curves as function of flip angle α (5°...60°) and T1 relaxation time (200 ms ... 1000 ms).*
Right: MOLLI T1 map of mid short axis view in healthy volunteer acquired on a Siemens Sonata 1,5T clinical scanner within a single breathhold.