Single Scan T1 and T2* Mapping without Flip Angle Correction

P. Mörchel[1], G. Melkus[1], M. Flentje[2], and P. M. Jakob[1,3]

[1]Experimental Physics 5, University of Würzburg, Würzburg, Bavaria, Germany, [2]Radiation Oncology, University of Würzburg, Würzburg, Bavaria, Germany, [3]Research Center for Magnetic Resonance Bavaria (MRB), Würzburg, Bavaria, Germany

Introduction: Quantitative magnetic resonance imaging is a powerful tool for investigating a large variety of biological phenomena. Thus, big efforts have been made during the recent years in order to develop fast methods for the quantitative assessment of various MR parameters. Two very important parameters are the T_1 and T_2* relaxation times. Here a new method for the simultaneous measurement of T_1 and T_2* maps is presented. Various approaches towards the simultaneous acquisition of T_1 and T_2* have been made [1, 2]. But all of these methods need the computation or measurement of flip angle maps in order to correct for B_1 inhomogeneities. The presented method is robust against variations in flip angles due to B_1 inhomogeneities of the resonator. Moreover, this sequence is time efficient since both parameters can be measured in the time a single conventional T_1 measurement [3] would take. Another advantage is that there are no misregistration artifacts due to motion which can occur during the consecutive measurement of the single parameters T_1 and T_2*.

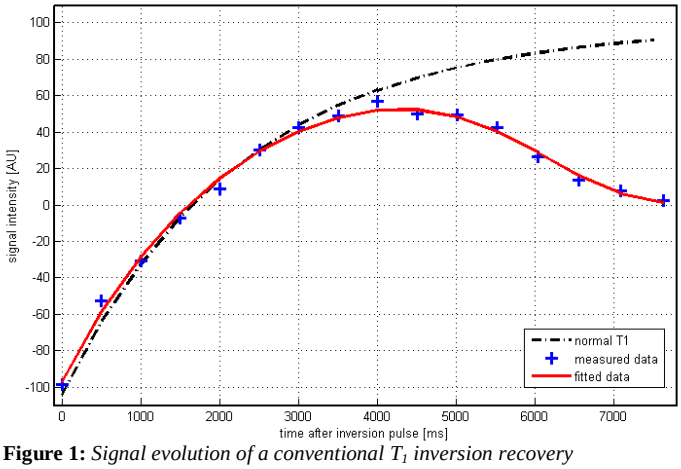

Figure 1: *Signal evolution of a conventional T_1 inversion recovery experiment (dash-dot line). Measured data (plus sign) and the corresponding fit (solid line) of the combined T_1/T_2* measurement of one typical pixel of a tumor transplanted to a mouse leg at 17.6 T.*

Material and Methods: The proposed method uses the large dynamic range of the inversion recovery experiment for the T_1 sampling and the robustness of single echo acquisition for the T_2* acquisition. We implemented this using an inversion recovery snapshot FLASH sequence [3, 4] including a T_2* measurement using single echo acquisition with exponentially increasing echo times. The conventional inversion recovery snapshot FLASH sequence applies a 180° inversion pulse followed by a series of FLASH modules for sampling the T_1 relaxation curve, which relaxes towards M_0* instead of M_0 due to the subsequent FLASH excitation pulses. In the method introduced here the echo times within these FLASH modules (and with it the repetition times of the FLASH modules) are increased exponentially with increasing time between the inversion pulse and the FLASH module. This results in a signal decay with the time constant T_2* during the sampling of the inversion recovery T_1 curve (solid line in Figure 1). The exponential increase is adjusted such that nearly the complete dynamic range of the inversion recovery curve is covered. This is achieved by keeping the echo time close to its minimal value at the first half of the acquisition. During the steady state tail of the T_1 signal, the echo time of the FLASH modules then rapidly increases, which leads to the T_2* decay and allows the calculation of T_2* values (Figure 1). Since the consecutive excitation pulses of the single FLASH sequences are no longer equidistant and thus the signal does not relax towards a steady state, the analytic equations introduced by Deichmann [4], which implement a correction for these effects, do not apply for this model.

We therefore implemented a fitting algorithm which simulates the pulse sequence with the known timings and thus allows the calculation of the resulting signal of the sequence. This enables the fitting of the parameters M_0, T_1, and T_2* by minimizing the mean square error of the measured data and the simulated signal.

Results: Figure 1 depicts the measured data (plus signs) and the corresponding fit (solid line) of one typical pixel using the combined T_1/T_2* measurement of a tumor transplanted to a mouse leg at 17.6 T. The diagram demonstrates that the fitting model simulating the pulse sequence describes the data very well. In Table 1, mean ROI values derived from the single parameter measurements of several Magnevist doped water phantoms (probe 1 to 3) are compared with the values obtained from the combined T_1/T_2* acquisition at 17.6 T. The small errors of average 0.55% and 3.30% for the T_1 and T_2* measurements, respectively, confirm the robustness of the method. The last row in Table 1 shows the relaxation values of a ROI in a tumor. The slightly higher error in the T_2* measurement can be attributed to thermal variations of the gradient system since the single T_2* measurement was performed using a multi gradient echo sequence which causes the system to heat. Computed relaxation maps of the combined method compared to the single parameter measurements of the segmented tumor are shown in Figure 2.

Probe	T1 single [ms]	T1 comb. [ms]	error [%]
1	97.01	97.55	0.55
2	90.18	90.98	0.88
3	91.70	91.50	0.22
Tumor	2668.01	2610.58	2.15

Probe	T2s single [ms]	T2s comb. [ms]	error [%]
1	42.42	44.94	5.94
2	48.90	50.33	2.92
3	49.00	49.50	1.02
Tumor	19.99	19.91	0.38

Table 1: *T_1 and T_2* values of a ROI of different Magnevist doped water phantoms (1-3) and a tumor measured using a normal inversion recovery method (T_1 single), a multi gradient echo sequence (T_2* single), and the combined T_1/T_2* method (T_1 comb. and T_2* comb.).*

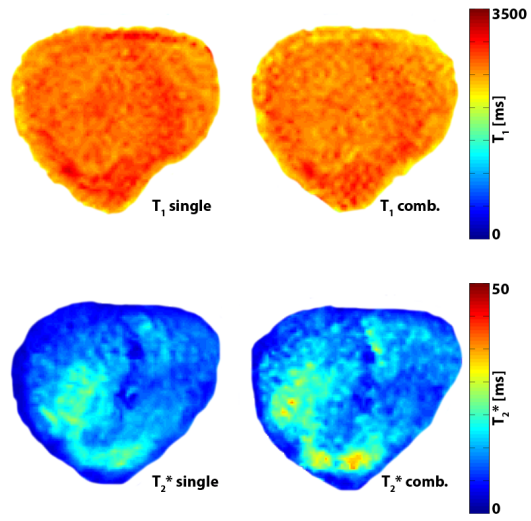

Figure 2: Comparison of T_1 and T_2* maps of the single and the combined measurement methods of a tumor transplanted to a mouse leg at 17.6 T.

Conclusion: In this study, a robust method for the simultaneous measurement of T_1 and T_2* maps was developed. The applicability of this sequence was confirmed using measurements on several phantoms and in vivo. This method allows for the acquisition of T_1 and T_2* in the time a single T_1 measurement would take. In future work, this method will be adapted to in vivo measurements of mice allowing a simultaneous measurement of the BOLD effect and perfusion using spin labeling methods.

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References: [1] Warntjes J.B.M et. al. MRM 2007, 57:528-537; [2] Ishimori Y et. al. JMRI 2003:18:113-120; [3] Look DC, Locker DR. Rev. Sci. Instrum. 1970:41:250-251; [4] Deichmann R et. al. JMR 1992, 96:608-612.