T_1 Mapping: Should We Agree To Disagree?

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INTRODUCTION: The longitudinal relaxation time T_1 is an important MR biomarker for characterizing tissue, and an integral part of many quantitative MRI protocols[1] (e.g. quantitative magnetization transfer). A recent study[2] reported that three commonly used methods for T_1 mapping (Inversion Recovery[3] (IR), Look-Locker[4] (LL), Variable Flip Angle[5] (VFA)) measure similar T_1 values in phantoms, but exhibit significant disagreement *in vivo* (Fig. 1). In this work we report simulations demonstrating that inaccuracies in B_1 mapping and incomplete spoiling could explain the T_1 variations observed *in vivo*.

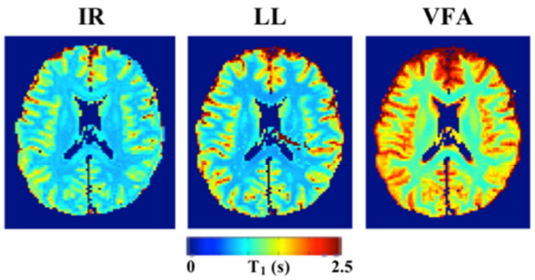

Figure 1: *Single slice T_1 maps (IR, LL, VFA) of a healthy volunteer in a single session[2].*

METHODS: Bloch simulations were implemented using the Matlab software package (MATLAB2011a, The Mathworks Inc.) and were based on 100 spin isochromats with true T_1/T_2 values of 825.5/100 ms. The T_1 value corresponds to the mode of the white matter (WM) values reported in a recent study using IR[2] at 3 T. The IR pulse sequence used TI = 30, 530, 1030, 1530 ms and TR/TE = 1550/11 ms. Steady state was ensured by repeating the sequence 200 times. The nominal inversion and saturation pulse flip angles were 180°/90°. The timing of the LL sequence was identical to the IR, with 5° excitation pulses. The VFA sequence used four nominal flip angles of 3°, 10, 20°, 30°, RF phase increment = 117°, TR/TE = 15/3.5 ms. The nominal flip angles were scaled with experimental whole brain B_1 data (actual flip angle method[6]) from a healthy subject at 3 T; the median B_1 scaling factor observed over the whole brain was 0.89. Prior to each pulse for VFA and following the inversion pulses in IR and LL, imperfect spoiling was simulated by dephasing the spins 80-100% of a 2π fully dephased state. Prior to fitting, to account for inaccuracies in B_1 mapping, we scaled the flip angle from 0.9 to 1.1 of its true value (flip angle error factor). *In vivo* data from 10 healthy subjects on a 3 T Siemens Tim Trio using identical acquisition parameters as described above was compared with these simulations.

RESULTS: Figure 2 shows the relationship between the fitted T_1 values and a range of flip angle variations for IR, LL and VFA using a partial dephasing factor of 0.9. Figure 3 shows the relationship between the fitted T_1 values and the partial dephasing factors using a flip angle underestimation of 0.95. The black dotted lines in Figs. 2 and 3 indicate the simulation parameters used to generate the data in Fig. 4, which shows a comparison between the mode WM T_1 and the simulated T_1 values.

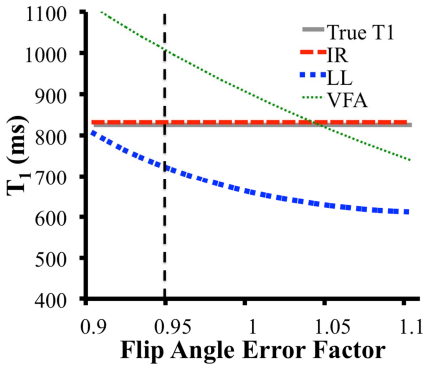

Figure 2: *The relationship between fitted T_1 and flip angle error (after B_1 correction) for IR, LL and VFA using a partial dephasing factor of 0.9. The vertical line indicates where the simulation parameters for Fig. 2 and Fig. 3 are identical.*

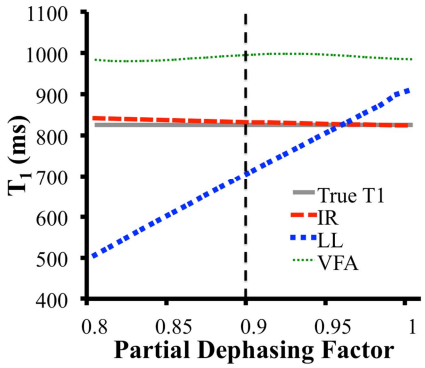

Figure 3: *The relationship between fitted T_1 and partial dephasing factor for IR, LL and VFA for a flip angle error factor of 0.95. The vertical line indicates where the simulation parameters for Fig. 2 and Fig. 3 are identical.*

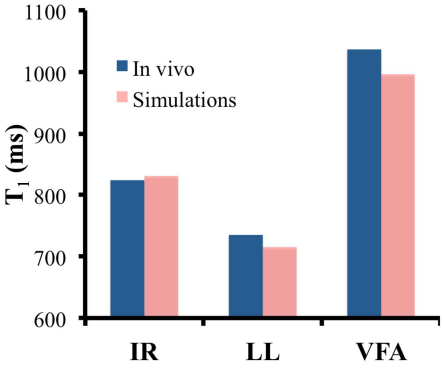

Figure 4: *Comparison between the mode WM T_1 measured in 10 healthy subjects[2], and simulations with similar parameters. The simulation values correspond to parameters represented by the vertical dashed line in Figs. 2 and 3.*

DISCUSSION: The bar graph in Fig. 4 shows that the simulations follows a similar trend in T_1 values compared to the *in vivo* WM T_1. Overall, simulations suggest that LL typically underestimated T_1, and VFA overestimated T_1. For all the simulated parameters, T_1 measured with IR is very stable and only slightly deviates from the true T_1. Error in B_1 mapping has been shown[7] to be sensitive to factors such as RF pulse shape, slice-select gradients and B_0 inhomogeneities. Incomplete or variable dephasing could result from factors like diffusion anisotropy in WM tracts[8], which could explain the agreement between T_1 methods in phantoms but not *in vivo*[2]. Our simulations did not account for magnetization transfer effects, which have also been shown to cause T_1 map inaccuracies in VFA[9]. Including MT in VFA leads to an increase in fitted T_1 values, hence worsening the predicted disagreement between VFA and IR.

CONCLUSION: Our simulations predict a systematic bias between the three most common T_1 mapping techniques due to inaccurate B_1 mapping and/or spoiling, and these same trends are observed *in vivo*. We observe that T_1 is underestimated with LL, overestimated with VFA, and very accurate with IR (if a proper fitting model is used[3]). This work highlights the importance of accurate B_1 mapping, robust spoiling methods, and proper calibration with the IR gold standard. As these effects can be site/scanner specific, we strongly suggest acquiring at least one gold standard IR map, in addition to any other T_1 mapping protocols used in the studies, to account for the T_1 bias. This is particularly important to consider when using T_1 maps with other quantitative techniques, as the T_1 bias could have a significant effect on other parameters of the quantitative model.

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