Rapid Method for Mapping the Longitudinal Relaxation Time

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Introduction Mapping the longitudinal relaxation time (T_1) usually involves curve fitting the time constant of the relaxation equation $M_z(t) = M_0 \exp(-t/T_1) + M_{eq} [1 - \exp(-t/T_1)]$, where M_0 and M_{eq} are the initial and the equilibrium magnetization, respectively. Conventionally, this curve is sampled by repeated use of the inversion recovery (180°-τ-90°; $M_0 = -M_{eq}$) or the saturation recovery (90°-τ-90°; $M_0 = 0$) pulse sequence. The drawbacks are that for both of the pulse sequences the flip angle of the RF pulses are required to be at specific values and M_{eq} has to be measured, which takes extra time and may introduce error. In particular, these methods are time consuming because (i) each repetition obtains only one sample point and (ii) a long delay between repetitions is required to allow full recovery of the magnetization. In this work, we develop a rapid T_1 mapping method which transforms the fitting curve to a decay exponential and does not have these drawbacks.

Methods Consider a simple pulse sequence which has two RF pulses of flip angle α. The two pulses are separated by evolution time τ. The NMR induction signal after the first and the second pulse is proportional to the volume integral of M_0 and $M_0 \exp(-\tau/T_1) \cos \alpha + M_{eq} [1 - \exp(-\tau/T_1)]$, respectively. After a delay D for magnetization recovery, a 180° pulse is executed to invert the magnetization so the initial magnetization becomes $-M_0$. Then the two-pulse sequence is repeated; the signals are subtracted from those of the first two-pulse sequence. After dividing the signal of the second α-pulse by $\cos \alpha$, the final signals of the two α-pulses are proportional to $2M_0$ and $2M_0 \exp(-\tau/T_1)$, respectively. Thus the curve for data fitting is transformed from the conventional recovery exponential to a decay exponential; the latter can be easily and directly fitted with semi-log coordinates. Note that the M_{eq} dependence is eliminated so measuring M_{eq} is not required. If the inversion RF pulse does not turn the magnetization to exactly $-M_0$, the factor 2 in the final signals becomes $(1+\beta)$, where $0 < \beta < 1$. Since T_1 is the quantity of interest, the value of $(1+\beta)$ can be arbitrary (although $\beta = 1$ has higher signal intensity). Thus the T_1 fitting will not be affected by the accuracy of the inversion pulse. For the same reason, a fully recovered magnetization is not necessary so the recovery delay D can be shortened for time-saving. The pulse sequence can be expanded to have q α-pulses to obtain q samples for the curve fitting in one scan. The general theory is given in Ref. [1]; it is shown that the results agree with that by the inversion-recovery method. In Ref. [1], the k-space is sampled by a low-flip-angle pulse-train method. In this work, the k-space is sampled by a single-shot pulse sequence so a larger value of α can be used for better signal-to-noise; a spiral pulse sequence [2] was employed for this purpose. In addition, the original method is extended to multi-slice acquisition by scheduling the acquisition of each slice evenly during an evolution time τ (i.e., the number of slices is τ-dependent). The experiment was performed at 1.5 T. The actual flip angle was obtained from a map constructed by solving a trigonometry relation between the intensity of the images from a single α-pulse and a single 2α-pulse. The number of curve-fitting samples was $q = 3$; the samples were equally spaced by τ.

Results and Discussion Figure 1 presents the anatomic image and the T_1 map of the brain of a healthy volunteer. The variation of the contrast in the T_1 map agrees with the distribution of the gray and write matter shown in the anatomic image. They also capture the well-known feature that the T_1 value of the gray matter is a few hundred ms longer than that of the white matter. Sample T_1 values (averaging over nine pixels) are given in the map, including the gray matter 1090 ms, the write matter 680 ms, and the cerebrospinal fluid (CSF) 3210 ms. The data for the entire six slices were acquired in less than 2.5 s. In summary, the present method can successfully obtain data for T_1 mapping in a very short period of time with reasonable accuracy.

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References [1] J-J Hsu and IJ Lowe, J Magn Reson **169**, 270 (2004). [2] GH Glover and S Lai, Magn Reson Med **39**, 361 (1998).

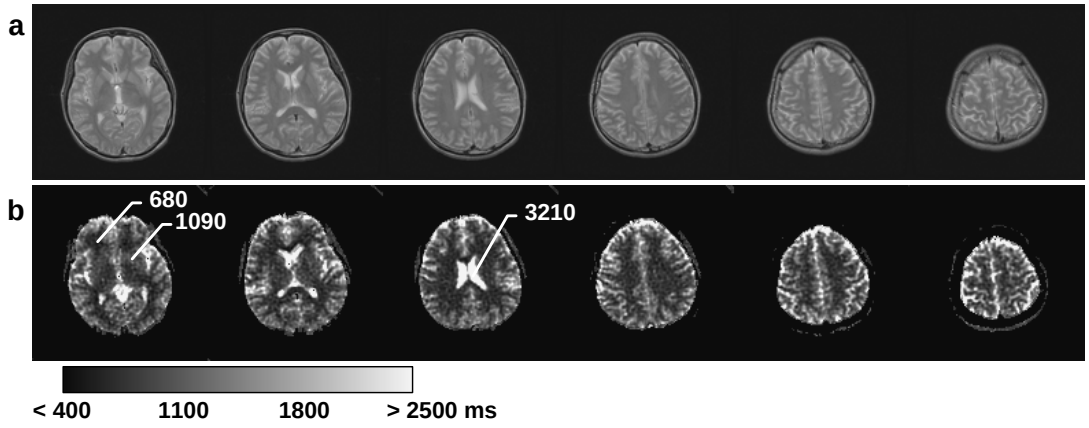

Figure 1 (**a**) Anatomic image by fast-spin-echo MRI (size 256×256, T_E = 68 ms, T_R = 4 s). (**b**) T_1 map by the present method (size 128×128, α = 30°, τ = 350 ms, D = 350 ms, T_E = 6 ms). The sample T_1 values are given in ms. In (**a**) and (**b**), the slice thickness is 5 mm, the gap between slices 5 mm, and the field of view 24 cm. The entire T_1 map of six slices was taken with one scan in ~2.5 s.