T1 measurement of brain metabolites at 3T with a saturated-inversion recovery method

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Introduction: *In vivo* magnetic resonance spectroscopy (MRS) provides metabolic assessments of changes that occur in diseased or abnormal brain tissues. Accurate measurement of metabolite longitudinal relaxation times is important for optimization of imaging parameters for *in vivo* MRS and MRSI experiments. Knowledge of metabolite T1s is also necessary for correction of T1 losses if absolute quantification is to be performed. Most metabolite T1 measurements are performed with either inversion recovery or progressive saturation scheme that requires at least one of the data points to be acquired with a very long repetition time (6-10s) [1-2]. In addition, progressive saturation requires large number of data points for accurate fitting of the T1 relaxation curve. In this study, a magnetization reset sequence was added to the inversion/MRS localization sequence so that a steady state inversion recovery MRS signal can be acquired using a shorter TR (2s), thus drastically reducing the total scan time required for *in vivo* metabolite T1 measurement.

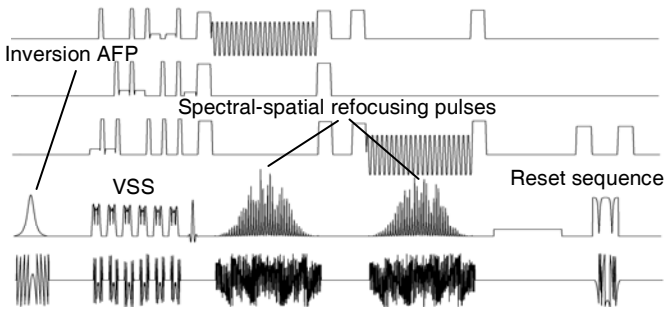

Figure 1. The saturated-inversion MRS sequence used in this study.

Methods: Pulse sequence: A nonselective hyperbolic secant inversion pulse was added in front of the standard PRESS localization pulse sequence that includes outer volume suppression (figure 1). Dual-band spectral spatial refocusing pulses were used in place of the conventional 180° refocusing pulses to provide lipid suppression and attenuated water refocusing [3]. This eliminated the conventional water suppression sequence used prior to the localization thus allowing shorter inversion time to be used even in the presence of the outer volume suppression pulses. A magnetization reset sequence was added after the gradient spoiler following readout [4-5]. The reset sequence contains a nonselective saturation pulse, a BIR4-90° pulse that is insensitive to B1 variation, and a gradient spoiler. The acquisitions with inversion and without inversion were interleaved (since signal was saturated for each TR) and signal from the two acquisitions were subtracted [4]. The resulted signal can then be related to T1 by the following: $\ln(S_{diff}) = -t_{inv}/T1 + C$, where S_{diff} is the difference of the measured signal between the acquisition with and without inversion, t_{inv} is the inversion time and C is a constant related to the steady state signal. A straight line is then fitted to the $\ln(S_{diff})$ vs. t_{inv} plot using a least squares method. T1 can then be determined from the slope of this linear relationship. Parameters: All studies were performed on a GE 3T scanner (GE Healthcare, Waukesha WI). Three different phantoms each with a single resonance of known T1s (Diagnostic Sonar, Livingston, UK) as well as five healthy volunteers were examined. Phantom T1 measurements were performed using a quadrature T/R head coil with inversion times of 200, 400 and 600ms from an 8cc voxel with 32 averages of the interleaved acquisitions. In vivo T1 measurements were performed using an 8 channel phased-array head coil for signal reception and the body coil for RF transmission. For each volunteer, T1 measurements were performed from 8cc voxels in both occipital GM and occipital WM with inversion times of 100, 300, and 500ms. 32 averages of the interleaved acquisitions were obtained. Total acquisition time for the three point T1 measurement for each voxel was ~8 minutes. All T1s were calculated from the peak heights of the spectra.

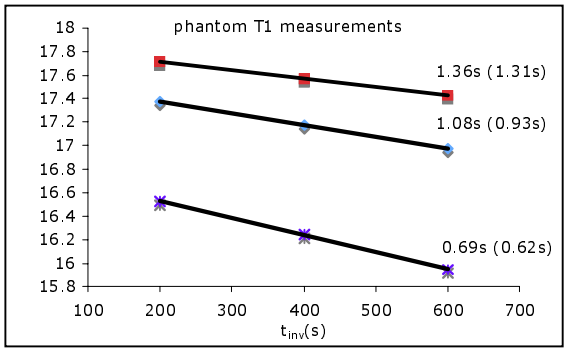

Figure 2. Semilog plot of signal recovery vs inversion time in the saturated-inversion recovery experiment for T1 measurement in three T1 phantoms, along with the least squared fid lines (average R^2 = 0.999). The measured T1s are in excellent agreement with the known values (in brackets).

subjects	GM choline	GM creatine	GM NAA	WM choline	WM creatine	WM NAA
vol1	1.18	1.94	1.47	0.98	1.96	1.64
vol2	1.06	1.22	1.25	1.62	1.52	1.78
vol3	0.93	1.40	1.44	1.60	1.54	1.47
vol4	1.27	1.50	1.41	1.62	1.62	1.36
vol5	1.11	1.78	1.24	0.98	1.72	1.31
average	**1.11**	**1.57**	**1.36**	**1.36**	**1.67**	**1.51**
S.E.	0.07	0.17	0.06	0.20	0.10	0.11

Table 1. T1 values (in seconds) of brain metabolite at 3T measured from occipital gray matter and occipital white matter tissues of five healthy volunteers using saturated-inversion recovery pulse sequence.

Results and Discussions: The T1 measurements performed on the three T1 phantoms demonstrated excellent agreement with the known T1 values (figure 2). T1s of the three major brain metabolite (choline, creatine, and NAA) measured from the occipital GM/WM were similar to what has been reported at 3T (table 1) [1-2]. Also similar to prior studies, a scattering of T1 values was observed between subjects. While only three data points provided excellent least squares fits to the phantom data (average R^2 = 0.999), more data points may be desired for *in vivo* measurements (average R^2 = 0.948). Since the acquisition time was reduced by using a much shorter TR in this saturated-inversion recovery scheme, additional data points can be acquired while total scan time can still be kept under what is typically used with progressive saturation or inversion recovery methods.

References:

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