Metabolite Proton T1 Relaxation Times in the Rat Brain in vivo at 17.2 Tesla

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Introduction

At high magnetic field, ^{1}H MR Spectroscopy benefits from an increase in sensitivity and spectral resolution by an intrinsic increase of the Signal-to-Noise Ratio and a higher chemical shift dispersion. At ultra-high magnetic fields such as 17.2 T, it is crucial to establish T_1 and T_2 relaxation times in order to optimize MRS acquisition parameters and to achieve proper quantification. Knowledge of T_1 times is also necessary for choosing optimal inversion delay times for the acquisition of metabolite-nulled spectra through single- or double-inversion schemes. Here, we present measurements of T_1 relaxation times of 20 metabolites in the rat brain *in vivo* at 17.2T.

Methods

MRS Acquisitions. A total of 6 Dark-Agouti rats were studied under isoflurane anesthesia (1-2% in pure O_2). Body temperature was monitored and maintained at 37° ± 0.5°. All Experiments were performed on a 17.2 T/26 cm Bruker BioSpec MRI scanner (Ettlingen, Germany) using a home-made 20 mm diameter single-loop surface coil transceiver. Anatomical images were acquired for positioning using a RARE sequence covering the entire brain. ^{1}H MR Spectra were acquired with a LASER[1] sequence (TE/TR =16.5/5000 ms, 128 averages, 2048 points) from a volume of 50 µL (5x5x2mm^3) containing mostly cerebral cortex and contributions from the corpus callosum and the hippocampus. Local B_0 field homogenization on the same volume was done using mapshim and local-shim Bruker routines (water linewidth = 23 ± 3 Hz). T_1-weighting was introduced by incorporating a non-selective adiabatic inversion pulse before the signal excitation pulse. A total of 9 T_1-weighted inversion recovery spectra were acquired (TI = 109, 264, 500, 750 1000, 1250, 1500, 2000, 3000 ms). Water suppression was done using a WET module[2] with numerically optimized flip angles and delays. Metabolite-nulled spectra were acquired at TE=16.5 ms using a double inversion scheme (TI1/TI2/TR= 2600/600/5000ms).

Data Analysis. After removal of the residual water signal using the HLSVD[3] algorithm, each MR spectra was analyzed using LCModel[4] and a set of simulated spectra. Simulations were performed using a spin simulation software developed by R.A. de Graaf, (MRRC, Yale School of Medicine) and Matlab (MathWorks, Natick, MA, USA). Due to their difference in T_1 values, Cr-CH3 and Cr-CH2 signals were accounted separately. The line shapes of macromolecules were parameterized[5] and implemented in LCModel. T_1 relaxation times were calculated by fitting the metabolites concentrations to a mono-exponential recovery function.

Results and Discussion

Figure 1.a shows examples of our T_1-weighted MR spectra at five different inversion times. Figure 1.b shows the fitted macromolecule resonance groups. Figure 2 recapitulates the majority of T_1 relaxation times calculated for metabolite and macromolecule resonance groups (see Fig.1.b for definition). One can observe that overall the T_1 values are rather similar for most metabolites which are centered to 1690 ms, with the exception of Taurine (2212 ± 99 ms) and Cr-CH2 (1152 ± 32 ms). The T_1's of macromolecules are circa 700 ms. Compared to T_1 values measured in the rat brain *in vivo* at lower magnetic field such as 9.4 or 11.7 Tesla[6], our values are slightly longer which is consistent with the Bloembergen-Purcell-Pound theory of dipolar relaxation[7].

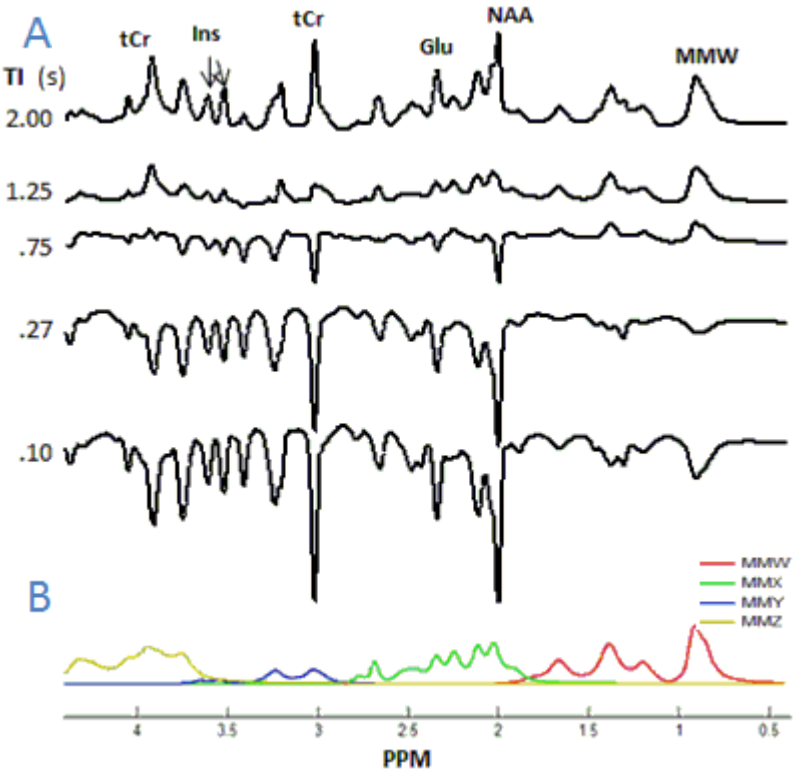

Fig.1 A.T_1-weighted spectra with increasing inversion times at TE = 16.5 ms. **B.** Macromolecule resonance groups fits used in LCModel.

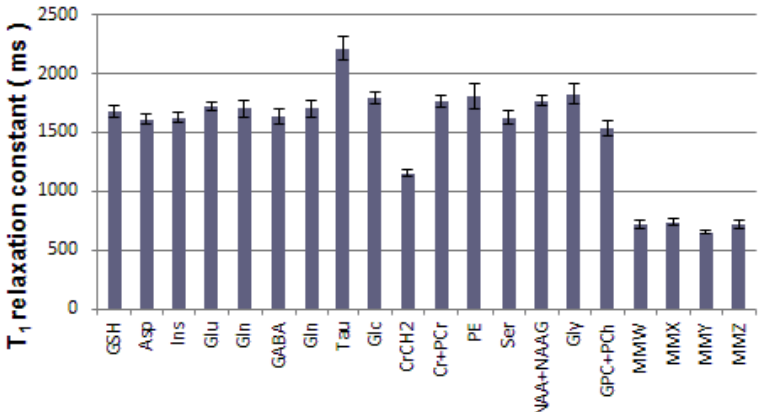

Fig.2 T_1 measured values found for several metabolites and macromolecules at 17.2 T. Error bars show the standard deviation. Macromolecule groups are shown in fig.2.

References :

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