# T2 relaxation of coupled spin resonances of cerebral metabolites in rat brain at 9.4 T

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## Introduction

Knowledge of $T_2$ relaxation time of metabolites is essential for proper quantitation of metabolite concentrations in localized proton spectroscopy, especially at moderate and long echo times, such as those used in spectral editing. While the $T_2$ relaxation time of singlets, such as creatine and NAA, has been characterized in several studies [1, 2], similar information is lacking from less well represented metabolites of lower concentration. The aim of this study was to measure the $T_2$ relaxation time of coupled spin resonances of cerebral metabolites in rat brain in vivo at 9.4 T.

## Methods

*Theory.* Measurements of $T_2$ relaxation time of singlet resonances are straightforward due to the absence of J modulation of signal. For resonances of coupled spin systems, the J modulation strongly affects both the spectral area (signal intensity) and the spectral lineshape of the metabolite resonances. Thus, to fit the spectral shape of coupled spin resonances at TE >> 0, it was necessary to take into account the J modulation of the lineshapes [3] by quantum mechanics simulations [4], using published values of coupling constants J and chemical shifts δ [5]. Spectra at each TE were analyzed with LCModel [6] software using TE-specific basis sets.

*Experiments.* $T_2$ measurements were performed on an actively-shielded 9.4T/31cm magnet (Varian/Magnex). In vivo spectra were acquired at eleven echo times (TE = 2.8, 20, 40, 60, 80, 110, 130, 150, 170, 200, and 300 ms) in five rats from a VOI located in the hippocampus, using a novel pulse sequence (SPECIAL) that retains full signal sensitivity [7]. Shimming was done with FASTMAP.



Chemical shift (ppm)
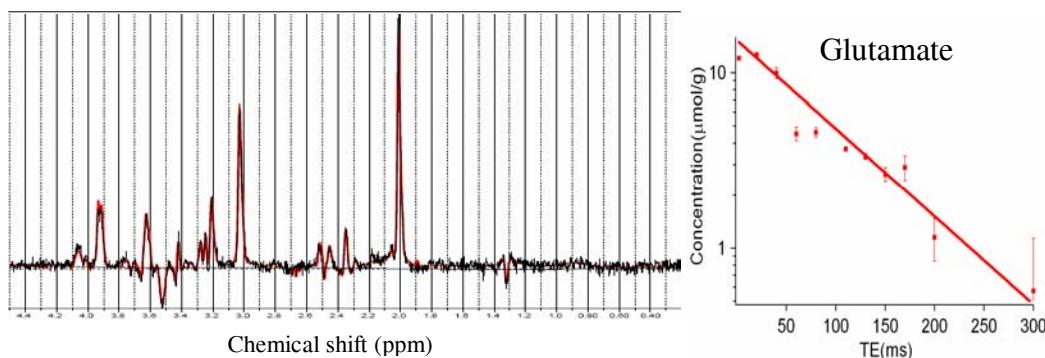
**Figure 1. Left.** Water-suppressed 1H MR spectrum (black line) and LCModel fit (overlayed red line) at TE = 80 ms. **Right.** The signal intensity of the glutamate plotted as a semilog function of TE. Fit to exponential decay function yielded $T_2 = 88 \pm 16$ ms ($R^2 = 0.944$).

## Results

The J-modulation of the signal of cerebral metabolites at 9.4 Tesla was adequately mimicked by spin simulations , as demonstrated by the good agreement between the fit and the experimental results at all echo times (Figure 1, left, TE = 80 ms). The resulting signal (expressed in concentration units) showed an exponential decay, as shown for glutamate (Figure 1, right). The $T_2$ relaxation time of the singlet resonances ranged from $113 \pm 21$ms (creatine) to $193 \pm 31$ms (NAA), in excellent agreement with literature values [1, 2]. In the Table, the average value ± standard deviation (n=5) of the $T_2$ relaxation time for the coupled resonances of the major brain metabolites are given. The values of $T_2$ for the coupled metabolite ranged from 86 ms (glutamate) to 141 ms (inositol).

## Discussion

In this study, the $T_2$ relaxation time of a number of coupled spin resonances has been investigated at 9.4 T, in the rat brain in vivo. The high spectral resolution and SNR afforded at 9.4 T allowed the detection of a neurochemical profile (13 metabolites) at TE = 110 ms with CRBs < 20%. Most reliably determined $T_2$s fall in the range of those measured for the singlets, thus validating previous assumptions in spectral editing (GSH, GABA) techniques. Quantification of less well represented metabolites at lower field strengths may be difficult due to increased overlap and lower SNR. The present results suggest that a good working assumption is that $T_2$s and linewidths are similar to creatine.

| Metabolite | T2 (ms) |
|------------|---------|
| Glu | 86 ± 10 |
| Tau | 96 ± 13 |
| GABA | 114 ± 18 |
| Gln | 123 ± 28 |
| GSH | 130 ± 38 |
| Ins | 141 ± 26 |

## References

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