

In Vivo Metabolite Relaxation Times in Mouse and Rat Brains at 7 Teslas

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Introduction

Accurate T_1 and T_2 relaxation time values are mandatory to determine the absolute concentrations of brain metabolites. An error in their estimates may lead to substantial errors in the metabolite concentration estimates. Several studies have investigated the T_1 and T_2 relaxation times of choline, creatine and N-acetyl aspartate at different field strengths. They demonstrate large variations in T_1 and T_2 values [1, 2].

In the present study, *in vivo* relaxation times of N-acetyl aspartate, creatine and choline in healthy mouse and rat brains are estimated at 7 teslas.

Method

All experiments were performed on a 7T Biospec BRUKER system, using a PRESS sequence (spectral bandwidth of 4 kHz, 4096 data points, 128 averages). The maximum available amplitude field gradient was 400mT/m.

In vivo mouse and rat brain signals were acquired using a bird cage coil (72 mm inner diameter) for excitation and a surface coil (15 or 25 mm diameter depending on animal) for signal reception. The voxel size was 3.5x3.5x3.5 mm³ for rat brain and 3.5x2x3.5 mm³ for mouse brain. Four healthy mice (Swiss, 25-30g in weight, 3 month old) and eight healthy rats (Sprague-Dawley, 320g in weight, 3 month old) were examined. For *in vivo* T_1 and T_2 relaxation time estimation, time series of five/seven signals were acquired using increasing repetition times/echo times respectively (TR=3, 4, 5, 6, 7s; TE=20ms) and (TE=20, 40, 60, 80,100,150, 200ms; TR=4s). First and second order shim terms were adjusted using a FASTMAP sequence. We used VAPOR for water suppression and three outer volume suppression (OVS) blocks.

Using the jMRUI software [3-4], the *in vivo* MRS time-series signals were processed in the time-domain. Removal of residual water components was achieved using the Hankel-Lanczos singular value decomposition algorithm (HLSVD). The signals were then fitted using AMARES [5] (Figure 1). For each signal of the time-series, 14 Lorentzian spectral components were selected to fit the major contributions of the metabolites, the zero-order phase was estimated and the first-order phase was fixed to zero. The individual phases relative to the zero-order phase were fixed to zero. To minimize the influence of the large broad baseline components (macromolecules), the first 20 data points of the *in vivo* signal were weighted with a quarter-sine wave. The time evolution of estimated amplitudes of NAA (2.02ppm), creatine (3.03ppm) and choline (3.22ppm) singlets were then fitted using a non-linear least squares algorithm based on a mono-exponential model function.

Results

In vivo T_1 and T_2 relaxation times of NAA, creatine and choline in mouse and rat brain were investigated. The relaxation time estimates and the corresponding standard deviations are reported in the tables below. For comparison, *in vitro* estimates of T_1 and T_2 relaxation times of NAA, creatine and choline [6] are also displayed.

$T_1 \pm$ sd (s)	NAA	Creatine	Choline
Mouse brain	1.70 \pm 0.36	2.35 \pm 0.41	1.94 \pm 0.22
Rat brain	2.10 \pm 0.30	1.98 \pm 0.38	2.16 \pm 0.40
<i>In vitro</i>	1.72 \pm 0.04	2.16 \pm 0.16	2.36 \pm 0.25

$T_2 \pm$ sd (s)	NAA	Creatine	Choline
Mouse brain	0.12 \pm 0.03	0.11 \pm 0.01	0.12 \pm 0.02
Rat brain	0.14 \pm 0.03	0.126 \pm 0.015	0.18 \pm 0.03
<i>In vitro</i>	0.42 \pm 0.02	0.42 \pm 0.05	0.40 \pm 0.02

Table: *In vivo* T_1 and T_2 relaxation time estimates at 7 teslas and corresponding standard deviations for NAA, creatine and choline in mouse and rat brains. For comparison, *in vitro* T_1 and T_2 values are also reported.

Conclusion

As the longitudinal/transverse relaxation times of brain metabolites exhibit a direct/inverse proportionality with the field strength and a decrease compared with *in vitro* values [1-2], our T_1 and T_2 estimates are in good agreement with the values reported in the literature. Investigated T_1 and T_2 relaxation times in mouse brains are not significantly different from those obtained in rat brains.

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References

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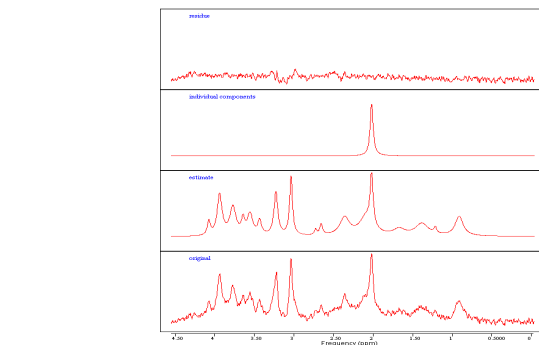


Figure 1: jMRUI quantitation result window. From bottom to top, raw *in vivo* spectrum of a rat brain, estimated spectrum using AMARES (14 Lorentzian spectral components in the fitting procedure), estimated NAA singlet (2.02ppm), residue.

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