Proton T₁ relaxation times of metabolites in human occipital white matter and grey matter at 7T

Lijing Xin¹, Benoit Schaller², Vladimir Mlynarik², Huanxiang Lu³, and Rolf Gruetter^{1,2}

¹Department of Radiology, University of Lausanne, Lausanne, Switzerland, ²Laboratory of functional and metabolic imaging, École Polytechnique Fédérale de Lausanne, Lausanne, Switzerland, ³Institute of Surgical Technologies and Biomechanics, University of Bern, Switzerland

Introduction Knowledge of longitudinal relaxation times of metabolites is essential for optimization of measurement parameters, for the quantification of metabolites in single voxel MR spectroscopy and spectroscopic imaging and for investigating cell microenvironment changes induced by physiological and pathological processes. Previous studies have reported T₁ values for N-acetylaspartate (NAA) singlet, total creatine CH₂ and CH₃ group, total choline at 3.22ppm, myo-inositol at 3.57ppm and 3.65ppm and glutamate/glutamine at 3.75ppm in human occipital white matter (WM) and grey matter (GM) at 3T [1,2], however, no values have been yet reported at 7T. The aim of this study is to measure T₁ relaxations of ¹H resonances (singlets and J-coupled peaks) of brain metabolites in occipital WM and GM at 7T.

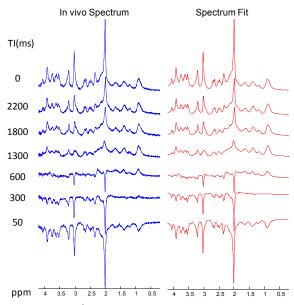


Fig. 1. In vivo ¹H inversion recovery MR spectra acquired using semi-adiabatic SPECIAL (TE/TR=12/7500ms, NA=32) at different TIs in occipital WM of a healthy volunteer and the corresponding LCModel fits.

Methods MRS Sequence: SPECIAL[3,4] sequence achieves the localization based on applying a slice-selective adiabatic full-passage pulse on alternate scans (1D ISIS scheme) followed by a spin echo sequence. To minimize the chemical shift displacement introduced by the narrow-band refocusing pulse at 7T, a semi-adiabatic SPECIAL sequence was implemented by replacing the Mao refocusing pulse (BW=1.8kHz, T_{pulse} =3.2ms, $\gamma B_1/2\pi$ =1.7kHz) by two broadband adiabatic pulses (HS4, R=28, BW= 7.4kHz, T_{pulse} =3.5ms, $\gamma B_1/2\pi$ =1.6kHz) with an optimized TE of 12 ms. To determine T_1 relaxation times, a non-selective adiabatic full passage was inserted and interleaved with OVS and VAPOR prior to the localization sequence.

Protocol: Ten volunteers (8 male, 2 female, 20-28 years old) were recruited and given informed consent prior to the study. MRS experiments were performed on a 7T/68cm MR scanner (Siemens Medical Solutions, Erlangen, Germany) with a home-built ¹H quadrature surface coil (10cm diameter). Anatomical images acquired using MP2RAGE[5] (TE/TR=3.37/5000ms, TI1/TI2=700/2200ms, slice thickness=1mm, FOV=176×256mm², matrix size=176×256) were used to place the VOI and to determine the tissue content of the voxel[6]. B₀ field inhomogeneity was optimized in the occipital WM (VOI=20×15×20mm³, 60±2% white matter tissue) and GM (VOI=15×20×20mm³, 75±5% grey matter tissue) using first- and second-order shimming with FASTMAP, which results in water linewidth of 12.8 ± 0.6 Hz. Six TI (50, 300, 600, 1300, 1800, 2200ms) were chosen and equilibrium signals were obtained from spectra acquired without inversion (TE/TR=12/7500ms, T_{acq}=512ms, NA=2×16 blocks/TI). Spectra acquired without water suppression were used to calculate T₁s of water.

Data Analysis: Metabolite concentrations at each TI were determined by LCModel[7] and fitted by a three-parameter exponential function in Matlab.

Results and Discussion A representative series of spectra acquired in occipital WM at different TI (Fig. 1) demonstrated high spectral quality obtained using the proposed MR sequence at 7T. The macromolecule signal was nulled at TI=300ms, indicating its T_1 is about 440ms, which was confirmed by the measured T_1 value (Fig.2). At TI=600ms, metabolite and macromolecule resonances showed opposite phase, thus reflecting longer T_1 s of metabolites compared to that of macromolecules. LCModel fits of spectra at individual TI demonstrated a good agreement with the in vivo data (Fig.1). T_1 values of metabolites ranged from 900-2100ms. Similar to observations in rodent brain, taurine had the longest T_1 , followed by NAA singlet and tCr resonances at 3.03ppm (Fig.2). In this study, T_1 s of GSH, scyllo-Ins, Tau and NAAG were reported for the first time in human brain at any field. T_1 of water in WM was much shorter compared to GM, reflecting the high localization of myelinated axons in WM. Surprisingly, T_1 s at 7T reported in this study show an increase compared to the values measured in the same regions at T_1 . Note that T_1 of tCho and NAAG are statistically shorter in WM than GM, while that of NAA and Glu show contradictory pattern.

In summary, T_1 relaxation times of metabolites in human brain were measured at 7T. The values for GSH, scyllo-Ins, Tau and NAAG were determined for the first time. T_1 s of NAA, tCho, Glu and NAAG were significantly different in WM and GM. The reported values will be useful for the quantification of metabolites by MR spectroscopy at 7T.

References [1] Mlynarik V et al., NMR in Biomed. 2001. [2] Ethofer T et al., Magn Reson Med. 2003. [3] Mlynarik V et al., Magn Reson Med. 2006. [4] Mekle R et al., Magn Reson Med. 2009. [5] Marques JP et al., Neuroimage. 2010. [6] Van Leemput K et al., IEEE transactions on medical imaging, Vol.18. No.10, 1999. [7] Provencher SW, Magn Reson Med 1993.

<u>Acknowledgements</u> Supported by Centre d'Imagerie BioMédicale (CIBM) of the UNIL, UNIGE, HUG, CHUV, EPFL and the Leenaards and Jeantet Foundations.

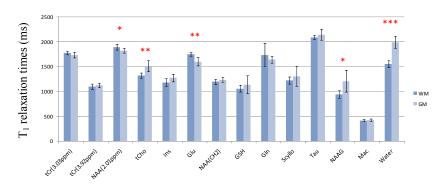


Fig. 2. T_1 relaxation times (mean \pm sd, n=6) of 12 metabolite peaks, macromolecule and water signals in occipital WM and GM at 7T. p<0.05*, p<0.01**, p<0.001***(Student's t-test).