semi-LASER ^{1}H MR Spectroscopy at 7T in Human Brain: Metabolite Quantification Incorporating Subject-Specific Macromolecule Removal

Jacob Penner[1,2] and Robert Bartha[1,2]

[1]*Centre for Functional and Metabolic Mapping, Robarts Research Institute, London, Ontario, Canada,* [2]*Medical Biophysics, Western University, London, Ontario, Canada*

Target Audience: Scientists interested in measuring absolute metabolite levels in neuropathological conditions using short echo time ^{1}H spectroscopy at 7 Tesla.

Purpose: Metabolite levels measured by short echo time ^{1}H MRS may provide indicators of disease status and progression in various neuropathological conditions. The use of high magnetic fields increases signal to noise ratio (SNR) and spectral dispersion leading to improved metabolite quantification. The purpose of this study was to develop an *in vivo* ^{1}H short-echo-time magnetic resonance spectroscopy protocol at 7T incorporating macromolecule removal and yielding absolute metabolite concentrations.

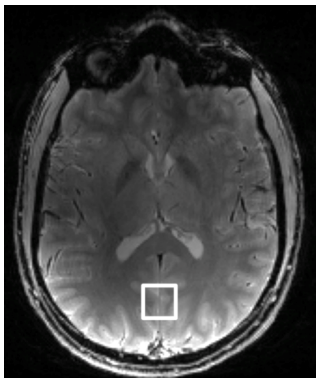

Figure 1: Axial T_2-weighted MRI image with MRS voxel shown

Methods: A 7T Agilent/Siemens MRI system with a 16-channel transmit and receive head coil (built in-house) was used to acquire single-voxel short-echo-time ^{1}H MR spectra as previously described.[1] Data were acquired from a 2x2x2 cm^3 volume of interest in the bilateral parietal-occipital region (Figure 1) of five young healthy volunteers (mean age 28.0 ± 2.7 years). T_2-weighted 2D FLASH images (TR = 1000 ms, TE = 6.5 ms, $\alpha = 30°$, 1x1x2 mm^3 resolution) were used for voxel placement (Figure 1). Water (8 averages), water suppressed (full - 128 averages), and water and metabolite suppressed (macromolecule - 128 averages) spectra were collected in each subject. A conventional localization by adiabatic selective refocusing (LASER) sequence[2] was modified as described by Scheenen *et. al.*[3]. Briefly, the sequence consisted of a 2 ms slice-selective 90° excitation pulse followed by two pairs (one pair for each remaining orthogonal dimension) of slice-selective adiabatic full-passage pulses (hyperbolic secant, R10, 3.5 ms) (TR/TE = 3700/38 ms). Eight global 5 ms Gaussian pulses were used for variable pulse power and optimized relaxation delays (VAPOR) water suppression.[4] Two inversion pulses (non-selective 5 ms adiabatic full-passage pulses) were used to null the metabolite signal when acquiring the macromolecule spectra. The macromolecule spectrum was subtracted from the full spectrum. Resulting metabolite spectra were fitted in the time domain using the fitMAN software,[5] incorporating prior knowledge from sixteen metabolite lineshapes. The decay rate of the water signal was also measured by acquiring unsuppressed water spectra at TEs ranging from 38 ms to 2000 ms and used to determine the fractions of cerebral spinal fluid (CSF) and tissue water within the MRS voxel. Absolute metabolite concentrations were calculated using water as an internal reference standard and correcting for signal relaxation and tissue partial volume.

Results: Figure 2 shows a representative spectrum following macromolecule removal with superimposed fit, the residual difference between the data and the fit, and the individual metabolite components below. The absolute concentrations of *N*-acetylaspartate (NAA), glutamate (Glu), glutamine (Gln), γ-aminobutyric acid (GABA), glutathione (Glth), aspartate (Asp), creatine (Cr), phosphocreatine (PCr), phosphorylcholine (PC), glycerophosphorylcholine (GPC), taurine (Tau), phosphorylethanolamine (PEth), *scyllo*-inositol (sI), glucose (Glc), and *myo*-inositol (mI) were determined. Table 1 lists the average levels of NAA, Gln, Cr + PCr, PC + GPC, and mI, all within ~1 mM of the only two previous studies that reported mM levels at 7T in healthy human brain,[6,7] and Glu that was approximately 3 mM higher. The average spectral SNR was 48 ± 6, calculated as the NAA peak area divided by the standard deviation of the baseline.

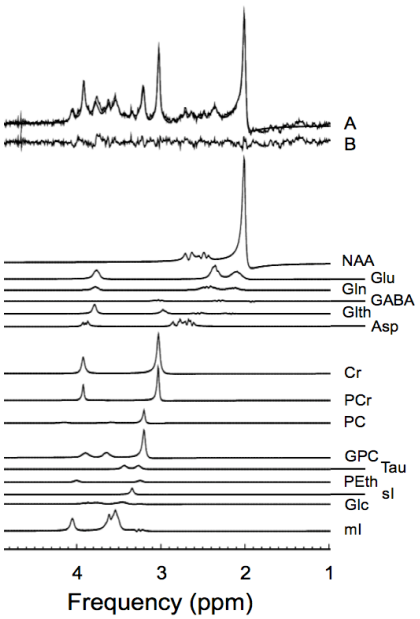

Figure 2: (A) Representative spectrum with superimposed fit, (B) residual difference, and individual metabolite components

Discussion and Conclusion: A 7T short-TE semi-LASER MRS protocol incorporating subject-specific macromolecule removal is demonstrated and yielded metabolite levels in good agreement with previous studies that report metabolite concentrations in healthy brain measured at 7T.[6,7] This protocol produced high quality metabolite spectra ideal for measuring metabolic changes in neuropathological conditions.

Metabolite	Average ± SD
NAA	13.14 ± 0.97
Glu	12.83 ± 1.89
Gln	3.06 ± 0.58
Cr + PCr	8.81 ± 0.54
mI	6.06 ± 0.35
PC + GPC	1.88 ± 0.16

Table 1: Average concentrations (mM)

References:

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