2D J-Resolved Spectroscopy at 7T

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Introduction: Initial 7T human proton MR spectroscopy studies have shown significant increases in SNR and spectral resolution as compared to lower magnetic fields [1]. However, these studies have focused on short TE acquisitions and have not investigated changes in T2 relaxation times. Accurate quantitative metabolite T2 measurements not only enable direct assessment of health of the tissue changes, but are also necessary for T2 relaxation time correction in other quantitative analyses. In this project, we applied 2D J-Resolved PRESS acquisition method [2] to quantify T2 values as well as to obtain TE-averaged spectra in both gray and white matter.

Methods: PRESS spectra of glutamate (Glu) and glutamine (Gln) with TE starting at 35 ms in 48 steps of 5 ms, respectively, were simulated using GAMMA software [3]. The simulated data were processed with apodization and Fourier Transformation, and the spectra were averaged in the t1 domain. All in vivo studies were performed on a 7T GE MR scanner (GE Healthcare Technologies, Waukesha, WI) equipped with a commercial volume excite coil and 8-channel phased array reception (Nova Medical, Wilmington, MA). Higher order shimming was performed using a gradient echo based phase-mapping method [4]. Data in 6 volunteers with informed consent was acquired in 3.3 minutes using a custom single-voxel 8cc PRESS-MRSI sequence with a TR=2s, starting TE=35ms, 5ms increment, 48 steps, NEX=2, with 2048 pts, 5000Hz bandwidth, and CHESS water suppression. One voxel was placed in occipital gray matter, and another in occipital white matter. Specially designed, low power, high bandwidth, very selective saturation (VSS) pulses were employed to sharpen the volume selection profile and combined with over-prescribed volume excitation to reduce chemical shift misregistration effects. The signals from the different phased-array coil elements were combined using previously described methods [5]. The data presented below was processed with a 4Hz Gaussian apodization and baseline corrected. Peak heights were fitted to a single exponential function.

Results:

Due to variable quality of the shimming, only 4 sets of white matter data and 3 sets of gray matter data were usable. Overall, the goodness of fit for the T2 values were acceptable (shown in the Table) and the T2 relaxation times are listed below. In vivo spectra at multiple TE (Fig 1 left) and TE-averaged spectrum (Fig. 1 right) are shown below. Simulated spectra are shown in Figure 2.

Metabolite	WM T2 (ms)	GM T2 (ms)
Cho	120±8.4	136±56
Cr	113±26	107±12
NAA	168±25	140±28

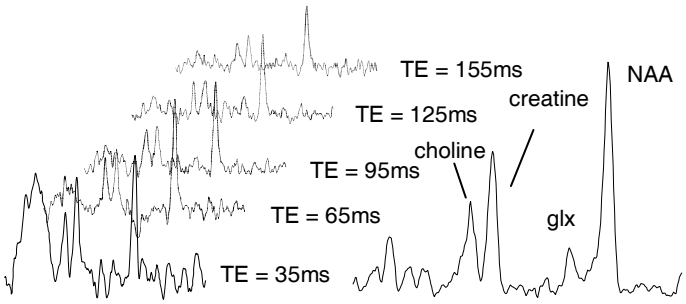

Figure 1. Representative spectra at selected TEs from occipital WM of a volunteer are shown on the left. On the right is the TE-averaged spectrum from TE=35ms through TE=275ms (48 steps from 35ms at 5ms increments) from occipital GM of a volunteer is shown on the right. Similar to what is shown in simulation, the Glx resonance can be observed as a distinct peak in the TE averaged spectra.

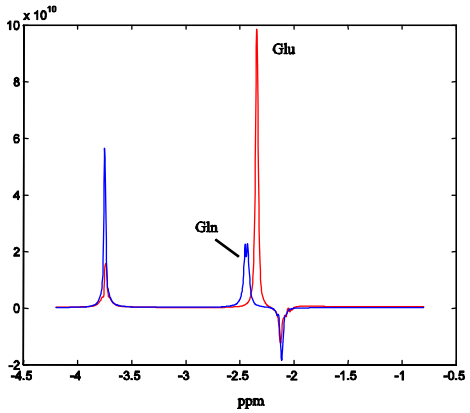

Figure 2. Simulated TE-averaged Glu and Gln spectra at 7T using GAMMA.

Discussion: As demonstrated above, consistent metabolite T2 values at 7T were measured. The higher variability in T2 values reported for choline in the gray matter can be attributed to exact placement of the voxel and partial volume with amount of CSF. At 7T, measured T2 values are substantially shorter than those reported at 3T [6]. This may be due to the larger effects of T2* contribution, caused by increased field inhomogeneity. SNR and spectral quality of the summed spectra demonstrate the possibility of using the TE-averaged method for the detection and quantification of glutamate (as demonstrated, the glutamine contribution is small) at 7T in 3 minutes.

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References:

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