J-Resolved 1H Spectroscopic Imaging of Human Brain

A. Gonenc[1], S. Sheriff[1], V. Govind[1], and A. A. Maudsley[1]
[1]Department of Radiology, University of Miami, Miami, FL, United States

Introduction:

There is an increasing interest in MRS measurement of glutamate (Glu) and glutamine (Gln) in the human brain as altered concentrations are linked to several neurodegenerative diseases [1,2]. However, accurate spectral quantitation using standard spatially localized acquisition sequences is challenging due to their low concentrations, complex multiplet resonance patterns and overlapping resonances. The main goal of this work was to develop a 2D J-resolved MRSI data acquisition method for mapping the spatial distributions of Glu, Gln, and myo-Inositol (mI), and to examine the age, gender, and tissue dependencies of these metabolites and their T2 relaxation times.

Methods and Materials:

Twenty-four subjects in two age groups, 18 to 28 and 40 to 67, were scanned using an 8-channel phased-array head coil at 3T (Siemens Trio). The MR protocol consisted of a high-resolution T1-weighted MPRAGE (TR/TE= 2150/4.43 ms) and a 2D J-resolved MRSI acquisition with spin-echo excitation, 25x25 k-space points, 18-mm slice thickness, outer volume suppression, and TE values from 26 to 186 ms in equal steps of 10 ms. MRSI data were processed as previously described [3]. Prior spectral information was generated by computer simulation [4] and used for a time-domain spectral analysis using a constrained Simulated Annealing optimization method written in Python. The influence of the spectral baseline on the metabolite fitting was minimized by excluding a few initial sample points from the metabolite model. Metabolite and T2 values corresponding to 100% grey-matter (GM) and 100% white-matter (WM) were obtained by regression of each parameter against the tissue content determined from the segmentation images.

Results and Discussion:

Sample images for Glu and Gln are shown in Fig. 1 and tissue regressions in Fig. 2. Decreased of Glu and Gln with age was observed in GM, which is consistent with previous reports of healthy aging [5,6], and a slight, but non-significant change in WM. The ratio of Glu/Gln was 4.8 in GM and 6.1 in WM. No significant differences with gender were detected. The T2 values obtained for the younger age group were Glu=106 ms, Gln=116 ms, mI= 158 ms, NAA= 200 ms, Cre=102 ms, and Cho= 191 ms. The 2D J-resolved MRSI method with the full 2D parametric spectral model was shown to provide more reliable spectral fitting and improved image quality for mapping of Glu and Gln in comparison to conventional MRS methods, and in addition to provide T2 information. The multi-voxel spin echo imaging method with outer volume suppression enables separation of WM and GM metabolite values in a single measurement.

Acknowledgements:

This work was supported by NIH grant EB000730.

References:

[1] Griffith et al., NMR Biomed. 2008; 21: 381–387
[2] Hattori et al., NeuroReport 2002; 13:183-186
[3] Maudsley et al., NMR Biomed 2006;19:492-503
[4] Soher et al., J Magn Reson. 2007;185(2):291-9
[5] Sailasuta et al., Magn Reson Img. 2008;26(5):667-75
[6] Kaiser et al., Neurobiol Aging 2005;26(5):665-72

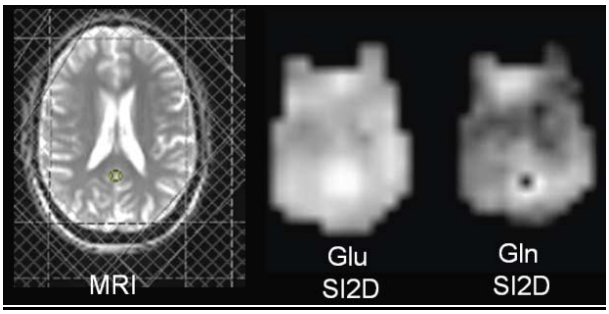

Figure 1: MRI with overlaid outer volume suppression slices and metabolite images.

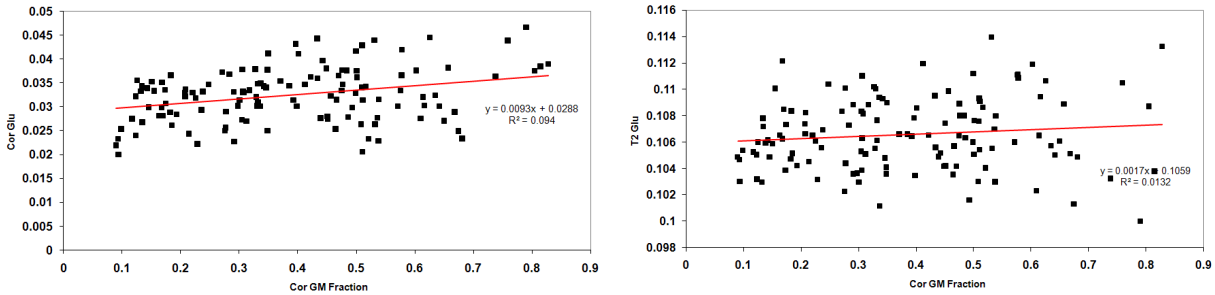

Figure 2: Example results for the regression of CSF corrected Glu (left) and Glu T2 (right) as a function of the tissue content determined by segmentation.