

High Resolution GABA Mapping in vivo using a Slice Selective MEGA-MRSI Sequence at 3 Tesla

H. Zhu^{1,2}, R. Ouwerkerk^{1,3}, R. A. Edden^{1,2}, and P. B. Barker^{1,2}

¹Russell H Morgan Department of Radiology and Radiological Science, Johns Hopkins University, Baltimore, MD, United States, ²F.M. Kirby Research Center for Functional Brain Imaging, Kennedy Krieger Institute, Baltimore, MD, United States, ³The National Institute of Diabetes and Digestive and Kidney Diseases, NIH, Bethesda, MD, United States

Introduction:

γ -aminobutyric acid (GABA) [1,2,3] is the most abundant inhibitory neurotransmitter. GABA plays an important role in brain function and is implicated in neurological disorders such as epilepsy, as well as in several psychiatric disorders. MEGA-PRESS [2,3] has gained popularity as a robust single voxel method to acquire GABA spectra in the brain, while a Multiple Quantum (MQ) filtered GABA CSI sequence [4] was implemented to map GABA levels. In this abstract, we demonstrate a high resolution spin-echo based MEGA-MRSI sequence with dualband water and lipid suppression [5] to measure GABA levels in a whole slice.

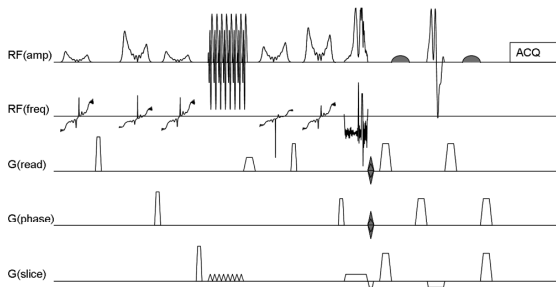


Figure 1. MEGA-MRSI with hypergeometric dualband suppression and OVS

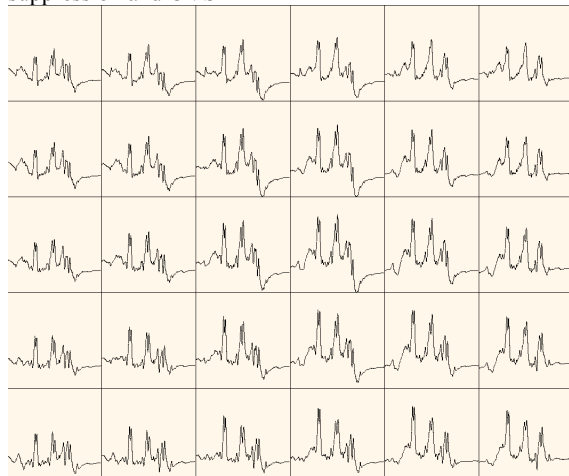


Figure 2. Central 6x5 MRSI grid in one volunteer. The GABA H2 peak (pseudo-doublet) is seen at 3 ppm, and co-edited Glx resonances at 3.7 and 2.2 ppm

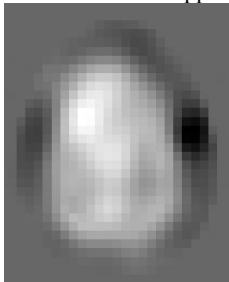


Figure 3. Reconstructed GABA metabolic image in one volunteer. Lower GABA levels can be observed in posterior white matter compared to gray.

al. *NMR Biomed* **11**: 266-272 (1998). [3] Edden et al. *MRM* **58**: 1276-1282 (2007). [4] Choi et al. *NeuroImage* **33**: 85-93 (2006). [5] Zhu et al. *ISMRM* 2009: **5171**. **Acknowledgments:** Supported in part by NIH P41RR015241.

Materials and Methods:

Experiments were performed on 3 normal volunteers on a 3T Achieva system (Philips Healthcare) with a prototype 32-channel phased array coil (Invivo Inc.). 'MEGA' editing pulses (Gaussian, 14 ms, 150 Hz bandwidth) were added to a spin-echo 2D-MRSI sequence with optimized dual-band water and lipid suppression and outer-volume lipid suppression [5] (Figure 1). The passband of the dual-band suppression pulses was 2.3 ppm to 4.1 ppm. The editing pulses were placed on the H3 protons at 1.9 ppm in the *ON* acquisition, and at 0.7 ppm in the *OFF* acquisition. TE/TR was 68ms/2s, and the bandwidths of the slice selective excitation and refocusing pulses were 4.26 kHz and 1.26 kHz, respectively. For 2D-MRSI, the FOV was 21x18 cm², 14x12 acquisition matrix (interpolated to 33x27), 20 mm slice thickness, giving a nominal voxel size of 1.5x1.5x2.0 = 4.5 cm³. 4 averages were performed ([ON+OFF]x2-step phase cycle) resulting in a total scan time with circular phase-encoding of 17 min 38 sec. Multi-channel MRSI data was optimally combined based on receive coil sensitivity profiles determined from MRI. Prior to MRSI data acquisition, a rapid field mapping technique was used to optimize B₀ homogeneity and to determine transmit B₁ level.

Results:

Figure 2 shows the central 6x5 MRSI grid from one subject at the level of the centrum semiovale, showing high SNR spectra from GABA and co-edited glutamate and glutamine (Glx). A metabolic images of GABA is shown in Figure 3. Average GABA SNR measured in central voxel locations over the 3 subjects was 13.6±3.3.

Discussion and Conclusion: The MEGA-MRSI sequence with dualband suppression can acquire edited GABA spectra with excellent SNR within a reasonable scan time. The spatial resolution (4.5 cm³) and coverage of the current scans exceeds by nearly an order of magnitude that of prior single-voxel (MEGA-PRESS) and MQ-filtered CSI experiments. This is the first GABA-MRSI study with high enough resolution to plot meaningful metabolic images with gray matter-white matter contrast. The excellent SNR of the current study can be attributed to (a) the efficiency of the pulse sequence, (b) the 3T field strength, and (c) the 32-channel head coil. Lipid suppression is particularly important since the editing pulse causes co-editing of lipids in the difference spectra. The dualband sequence used here also suppressed the co-edited NAA signal at 2 ppm. The reduced number of 180° pulses (in a spin-echo sequence compared to PRESS) also potentially allows longer (i.e. more selective) MEGA editing pulses to be used for the same TE. Future studies will explore the extension of this methodology to quantitative multi-slice acquisitions, and determine the effects of residual B₀ and B₁ inhomogeneity on the quality of the edited data.

References: [1] Rothman et al. *PNAS* **90**: 5662-5666 (1993) [2] Mescher et