

## Comparing MEGA-SPECIAL to MEGA-STEAM for Pure GABA Detection at 7T

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### Introduction:

$\gamma$ -aminobutyric acid (GABA) [1,2,3] is the most abundant inhibitory neurotransmitter. In vivo detection of GABA with Magnetic Resonance Spectroscopy (MRS) is a major topic in clinical neuroscience research. MEGA editing [2,3] has been demonstrated as a reliable MRS method for observing GABA in single voxel spectroscopy using PRESS or STEAM localization. Unfortunately, the GABA signal acquired by the majority of MEGA-PRESS studies at 3T is contaminated by co-edited signals of macromolecules (MM), resulting in the notation of “GABA+”. In vivo MRS at ultrahigh field (7T) presents two advantages for GABA detection without MM contamination. First, wider spectral separation at 7T more than doubles the selectivity of RF pulses compared to 3T. Second, as the amount of MM contamination can be as high as 40%[4], observing pure GABA signal requires higher sensitivity naturally provided at 7T. In this abstract, we implement MEGA editing with SPECIAL[5] localization on a whole body 7T scanner for pure GABA detection in the brain.

### Materials and Methods:

Experiments were performed on a phantom (3mM GABA, 10mM Cr, 3mM Cho, 12.5mM NAA and 12.5mM Glu), and 3 normal volunteers on a 7T Achieva system (Philips Healthcare) with a 32-channel phased array coil (NOVA Inc.). ‘MEGA’ editing pulses (truncated sinc, 22ms, 190Hz BW) were added to a single voxel SPECIAL sequence with a 1D ISIS inversion and 2D bar-selective spin echo excitation (Fig.1). The 1D ISIS inversion was achieved with an adiabatic inversion pulse interleaved into a 7T version of the dualband water and lipid suppression pre-saturation sequence[6]. Two MEGA editing pulses were inserted into the spin echo sequence in the same fashion as MEGA-MRSI [7]. The editing pulses were placed on the H3 protons at 1.9 ppm in the *ON* acquisition, and at 1.5 ppm in the *OFF* acquisition[4]. TE/TR was 68ms/3s, and the BW of the inversion pulse and spin echo excitation and refocusing pulses were 8.0kHz, 4.26kHz and 1.26kHz, respectively. Voxel size was 40mm<sup>3</sup>. 4 averages were performed for each phase cycling step (MEGA [ON+OFF]  $\times$  ISIS [ON+OFF]). 16-step phase cycling and 192 averages were used for each voxel, resulting in a scan time of 9.6 minutes. To validate the efficiency of MEGA-SPECIAL, a MEGA-STEAM acquisition with identical editing scheme and runtime was included. To investigate the amount of MM contamination, the MEGA-SPECIAL sequence was also repeated with editing pulses placed at 1.9ppm and 8ppm.

### Results:

Figure 2 shows phantom spectrum of MEGA-SPECIAL as well as the frequency profiles of the editing pulses at 1.9ppm and 1.5ppm. The editing pulse at 1.5ppm does not affect the GABA H3 protons at 1.9ppm because of its half BW of 0.32ppm. In vivo results (Fig. 3) show that MEGA-SPECIAL(blue) produced  $1.7 \pm 0.4$  times the signal of MEGA-STEAM (black). The ratio of the signals from two MEGA-SPECIAL acquisitions (blue/red) was  $58 \pm 10\%$ , implying MM contamination of 42%. For quantification, the ratio of the integrals of the GABA signal to unsuppressed water was  $1.3 \pm 0.5 \times 10^{-5}$ .

### Discussion and Conclusion:

The SPECIAL sequence is a unique localization method for ultra high field (7T) because it combines STEAM’s shorter echo time and PRESS’s full signal acquisition. When implemented in an editing sequence with fixed echo time (68ms for GABA), SPECIAL’s spin echo configuration permits longer editing pulses compared to PRESS. Recently, the same spin echo based MEGA editing configuration was implemented successfully at 3T for slice selective spectroscopic imaging of GABA[6]. This method resulted in an order of magnitude increase in sensitivity compared to MEGA-PRESS. In the 3T MEGA-MRSI sequence, two 20ms Gaussian editing pulses were used. At 7T, 20 msec Gaussian pulses were found experimentally to lead to decreased editing efficiency, presumably because they are too frequency-selective. Therefore, two truncated sinc pulses were chosen for 7T MEGA editing because they have a more favorable frequency profiles than Gaussian pulses of the same duration. Additionally, the adiabatic inversion pulse of SPECIAL was interleaved into a 7T version of dualband water and lipid suppression sequence, between the 2<sup>nd</sup> and 3<sup>rd</sup> suppression pulses. This efficient scheme combines spatial localization with both water and lipid suppression into a relative short module (186 msec) prior to signal excitation. In conclusion, a MEGA-SPECIAL sequence was implemented and compared to MEGA-STEAM on a 7T whole body scanner to acquire edited GABA spectra without macromolecule contamination. This technique has good sensitivity and can be used to reliably measure GABA at 7T free from macromolecular contamination.

**References:** [1] Rothman et al. *PNAS* **90**: 5662-5666 (1993) [2] Mescher et al. *NMR Biomed* **11**: 266-272 (1998). [3] Edden et al. *MRM* **58**: 1276-1282 (2007). [4] Henry et al. *MRM* **45**: 517-520 (2001) [5] Mlynarik et al. *MRM* **56**:965-970 (2006). [6] Zhu et al. *MRM* **63**: 1486-1492 (2010) [7] Zhu et al *MRM* (in press 2011). **Acknowledgments:** Supported in part by NIH P41RR015241.

