Measuring GABA using 1H MR spectroscopy at 3T: A comparison of techniques

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Target audience: Researchers interested in using MR spectroscopy (MRS) to measure GABA in the brain at 3T.

Purpose: To compare optimised PRESS and MEGA-PRESS for measuring GABA at 3T.

Introduction: Measuring GABA levels *in vivo* has been of interest for various different pathologies. Most commonly GABA is measured using a MRS MEGA-PRESS editing sequence[1]. A known limitation of the popular TE=68ms sequence are coedited macro-molecule (MM) signals that give rise to a GABA+MM peak (see Figure 1a). To remove unwanted MM contributions a modified MEGA-PRESS sequence has been proposed that uses a longer TE to apply editing pulses with a narrower bandwidth and symmetrically applied to edit the MM resonances equally in both ON and OFF scans[2]. An alternative approach is using optimised TE and TE1 parameters of a standard PRESS sequence[3] with the potential to reduce scan time and the voxel size compared to MEGA-PRESS. In this study we compare the three techniques in healthy controls (HC).

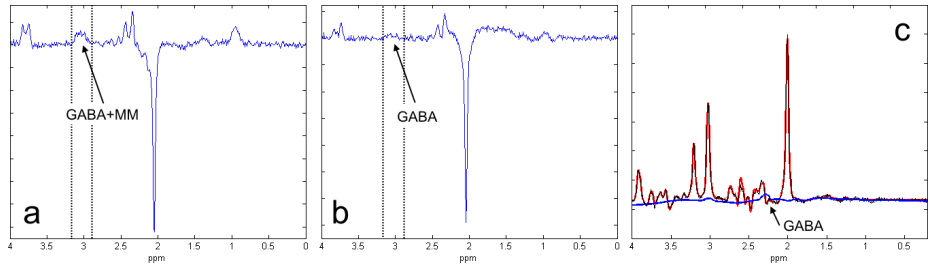

Figure 1: (a) MP68 showing GABA+MM around 3 ppm; (b) MP80 showing low GABA signal around 3 ppm; (c) PRESS105 using optimised TE and TE1 to measure GABA (blue line) using LCModel (LCModel fit – red line, raw spectrum – black line).

Methods: Written informed consent was obtained from 13 HC according to local ethics procedures. All subjects underwent a research scan on our 3T GE MR750 equipped with a 32 channel head coil. Structural MRI was acquired using a 3D T1w sequence with 1 mm isotropic voxels. MRS voxels (35x25x20mm) were placed in grey matter around the anterior cingulate cortex (ACC) in 7 subjects and parietal medial grey matter (PGM) in the remaining 6 subjects. MEGA-PRESS was performed using a TR=1.8s with 128 ON and 128 OFF acquisitions. At TE=68ms (MP68), sinc-weighted Gaussian pulses with a pulse length of 17ms were applied at 7.5ppm and 1.9ppm for editing GABA. At TE=80ms (MP80), editing pulses with a pulse length of 23ms were applied at 1.9ppm and 1.5ppm to symmetrically edit the MM at 1.7ppm [2]. MEGA-PRESS data was processed offline and analysed with TARQUIN[4]. The GABA optimised PRESS sequence (PRESS105) uses a TE/TE1=105ms/15ms, TR=2.5s and 128 averages[3]. PRESS105 data was analysed with LCModel[5] and a simulated basis set[3]. Pearson's correlation coefficient was calculated for GABA across the three sequences using SPSS. To assess the coefficient of variation (CV), the MRS data was corrected for the brain parenchyma fraction by segmenting the T1w MRI into grey matter, white matter and CSF using SPM8[6]. The CVs were calculated separately for the ACC and PGM across the HC as the ratio of the standard deviation to the mean GABA values.

Results: Figure 1 shows example spectra of the three sequences from the same subject and location. Table 1 shows that MP68 correlates significantly with MP80 and PRESS105. After partial volume correction for CSF contribution the CVs for MP68, MP80 and PRESS105 were 7.0%, 16.6% and 10.0% respectively for the ACC and 7.1%, 22.5% and 7.7% for the PGM.

	MP68 vs. MP80	MP68 vs. PRESS105	MP80 vs. PRESS105
r	0.61	0.607	0.434
p	0.027	0.028	0.138

Table 1

Discussion and Conclusion: The correlation of MP68 and MP80 suggests that MM contributions are similar across the healthy subjects used in this study. The reduced GABA signal in the MP80 sequence is due to removal of MM contributions but also increased T2 signal decay and co-editing of GABA, which causes larger quantification errors and an increased CV. This may explain the non-significant correlation in our small dataset between MP80 and PRESS105, both of which are designed to eliminate MM contributions. MP68 still seems the method of choice for measuring GABA, however MM contributions may change when investigating patient groups. PRESS105 offers an alternative while using half the scan time, no macro-molecule contribution and being less susceptible to subject motion.

References: **[1]** Mullins et al. Current practice in the use of MEGA-PRESS spectroscopy for the detection of GABA. Neuroimage 2014; 86, 43-52 **[2]** Edden et al. Macromolecule-suppressed GABA-edited magnetic resonance spectroscopy at 3T. Magn Reson Med. 2012; 68, 657-661 **[3]** Napolitano et al. Reliable gamma aminobutyric acid measurement using optimized PRESS at 3T. Magn Reson Med. 2013; 69, 1528-1533 **[4]** Wilson et al. A constrained least-squares approach to the automated quantitation of in vivo ¹H magnetic resonance spectroscopy data. Magn Reson Med. 2011; 65, 1-12 **[5]** Provencher. Estimation of metabolite concentrations from localized in vivo proton NMR spectra. Magn Reson Med. 1993; 30, 672-679 **[6]** Statistical Parametric Mapping, http://www.fil.ion.ucl.ac.uk/spm/

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