GABA Fitting for MEGA-PRESS Sequences with Different Selective Inversion Frequencies

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Introduction

GABA detection faces the problem of contamination from co-edited macromolecule signal at 3.0 ppm (MM30) when using the MEGA-PRESS technique [1]. Therefore, direct quantification of GABA by LCModel software [2] yields the sum of GABA and MM30. One of the proposed methods to eliminate MM30 is to alternate the editing pulse between 1.9 ppm and 1.5 ppm, the latter a position symmetric to 1.9 ppm with respect to the J-coupled MM resonance at 1.7 ppm [3]. New MM basis have also been introduced into LCModel analysis [4], and a soft constraint has been applied to better quantify GABA [5]. In this study, we compare three LCModel fitting approaches for both the original MEGA-PRESS and the modified "MM-symmetric" sequence which has the editing pulse alternating between 1.9 ppm and 1.5 ppm.

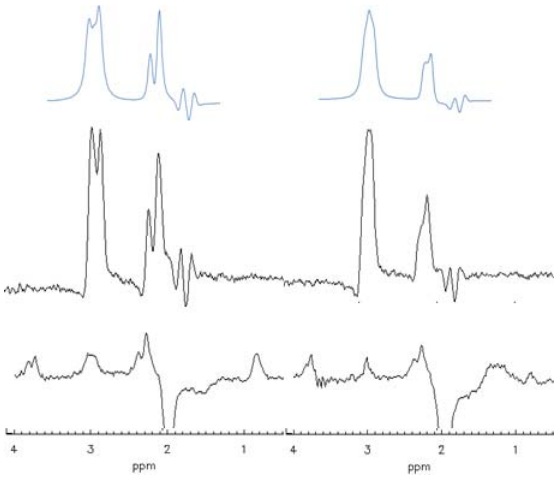
Materials and Methods

Phantom and *in vivo* experiments were carried out on a 3T Siemens Tim Trio scanner (Siemens Healthcare, Erlangen, Germany), equipped with a 32-channel head coil. Six subjects (n=6, three male) were recruited for our study and written informed consent forms were obtained from all subjects prior to the study. Voxels were placed in basal ganglia (18.75 ml). 196 averages were acquired with the editing pulse centered at 1.9 ppm and 196 averages with the pulse centered at 7.5 ppm in an interleaved fashion using the original MEGA-PRESS (TR=1500ms, TE=68ms). For the MM-symmetric sequence, 196 averages were acquired with the editing pulse centered at 1.9 ppm and 196 averages with the pulse centered at 1.5 ppm. A spherical phantom containing a saline solution of 10mM GABA was prepared for *in vitro* study, and spectra were collected using the procedures described above (VOI=27ml, number of averages=128). Data processing and quantification of all spectra were performed with LCModel using basis sets generated from density matrix simulations of both MEGA-PRESS sequences with an exact treatment of evolution during the two frequency-selective MEGA inversion pulses. Three LCModel fitting techniques were compared: **A**: direct quantification, assuming that the flexible baseline of LCModel plus a built-in default macromolecular peak ("MM20") with a contribution at 3.0 ppm would fill MM30; **B**: an extra Gaussian peak at 3.0 ppm was added to the LCModel calculation to explicitly fit MM30 [4]; **C**: a soft constraint was applied to the ratio of MM30 and MM09 (MM30/MM09 = 0.667±0.1) based on results from technique B [5].

Results

Figure 1 shows simulated, *in vitro* and *in vivo* spectra obtained with both editing sequences: original (left) and MM-symmetric (right). The mean Cramer-Rao Lower Bounds (CRLB) of *in vivo* GABA values were 12.5%, 32.6% and 20.8% using fitting techniques A, B, and C respectively with the original MEGA-PRESS sequence, and 17.7%, 37.3% and 23.5% using A, B, and C with the MM-symmetric sequence. Average GABA values from the three LCModel fitting techniques are compared in Table 1 (mean±SE). LCModel technique A fits of *in vivo* spectra using both editing schemes are shown in Figure 2.

Figure 1: Simulated, *in vitro* and *in vivo* GABA-edited spectra from top to bottom, using the original MEGA-PRESS (left) and the MM-symmetric sequence (right).



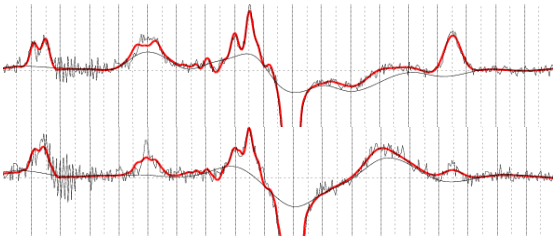
Discussion

Fitting technique A generates the highest GABA concentrations with small CRLB values, but the concentrations are probably overestimated since MM30 is not explicitly included in the fit. Technique B yields the lowest GABA concentrations with largest CRLB. The MM-symmetric editing scheme should eliminate the MM30 contamination, so technique A should be used for direct quantification of GABA. Technique C with the original editing scheme seems to provide the closest value to technique A with the MM-symmetric scheme, which suggests C should be a good approach for the original sequence. GABA levels may deviate considerably if an inappropriate fitting approach is chosen for a specific editing scheme.

	Pulse at 1.9 and 7.5 ppm	Pulse at 1.9 and 1.5 ppm
Technique A	187.56±35.75	134.00±26.85
Technique B	101.16±22.66	93.57±15.89
Technique C	118.87±19.10	114.91±24.33

Table 1: GABA values from the three LCModel fitting techniques for the original and MM-symmetric MEGA-PRESS editing sequences

Figure 2: LCModel fitting of in vivo MEGA-PRESS spectra using the original (top) and adapted (bottom) editing scheme by technique A



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