Resolution Enhancement of Brain Glutamate, Glutamine and myo-Inositol by PRESS (TE1, TE2) = (37, 63) ms at 7T

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INTRODUCTION

At high fields, although the resolution between singlets may remain the same, the selectivity of coupled resonances is enhanced because the coupling strength which governs the overall linewidth of the multiplet is independent of field strength (B0). Short echo time (TE) acquisition benefits from the reduced T2 signal loss, but the increased macromolecule (MM) baseline signals complicate the spectral analysis. Alternatively, long TE acquisition can be employed with an advantage that TE optimization provides improved selectivity of target metabolites and suppresses the MM signals to noise level. Given that PRESS (point-resolved spectroscopy) and STEAM (stimulated-echo acquisition mode) sequences are readily available in most of the clinical MR scanners, a strategy for selectivity enhancement of experimentally-challenging metabolites using these methods would be valuable. Here, we report PRESS echo time optimization for precise detection of glutamate (Glu), glutamine (Gln) and myo-inositol (ml) in human brain at 7T.

METHODS

PRESS echo time dependences of Glu, Gln, NAA, GSH, GABA, NAAG and ml have been investigated for subecho times TE1 and TE2, between 20 and 150 ms with 1 ms increments, using density matrix simulation incorporating the volume selective shaped radio-frequency (RF) and gradient pulses. The published chemical shift and coupling constants [1] were used in the simulation. Spatial localization was obtained with an 8.8- ms 90° RF pulse (BW = 4.7 kHz) and two 11.9-ms 180° RF pulses (BW = 1.4 kHz). The simulation indicated that the Glu and Gln C4-proton multiplets can be completely resolved from each other and from the NAA multiplet at ~2.5 ppm using PRESS (TE1, TE2) = (37, 63) ms at 7T. Preliminary in vivo tests were conducted on two healthy subjects at 7T (Philips Medical Systems, Cleveland, OH, USA). A 25×30×30 mm3 voxel was positioned in the medial prefrontal and left frontal cortices (see Fig. 2). Data were obtained with the optimized PRESS sequence, together with short-TE STEAM ((TE, TM) = (14, 19) ms) and the recently-reported optimized STEAM sequence timings ((TE, TM) = (74, 68) ms [2]). A quadrature birdcage head RF coil with 16 reception channels was used for RF transmission and reception. LC model software [3] was used for spectral analysis.

RESULTS and DISCUSSION

Fig. 1 presents numerically-calculated spectra of Glu, Gln, NAAas, GSHas, GABA, NAAGas, ml and creatine (Cr) at a concentration ratio of 10:3:1:1:1:5:8 at 7T, for the optimized PRESS, a short-TE STEAM and a optimized STEAM [2] sequences. Spectra are scaled incorporating T2 = 130 ms, a mean value of Cr and NAA singlet T2 values (110 and 150 ms, respectively), as measured from the prefrontal brain (using TE = 100 and 200 ms). The simulation indicates that Glu and Gln C4-proton multiplet resonances (at 2.35 and 2.45 ppm, respectively) are best resolved from the optimized PRESS due to the narrowing of the Glu peak and the reduced NAAas multiplet.

Fig. 2 presents in vivo brain spectra from the prefrontal (PF) and left frontal (LF) lobes, obtained with the three methods. Spectra are normalized with respect to the brain water signal at TE = 14 ms. In vivo spectral patterns are in good agreement with calculation. Despite the increased T2 signal loss at 7T, the PRESS at TE = 100 ms gives greater signals than the short-TE STEAM. The PRESS spectra exhibit a well-defined small Gln peak at 2.45 ppm on a clean background, for both PF and LF. Elevated Glu and Cr levels are seen in PF spectra consistently, most likely due to the high content of gray matter in PF. The NAA signal is observed to be smaller in LF than in PF, especially in the PRESS spectra. This may imply a difference in NAA T2 between gray and white matter. In addition, the PRESS sequence gives a well defined ml multiplet between 3.5 and 3.65 ppm. In conclusion, PRESS (TE1, TE2) = (37, 63) ms provides enhanced resolution and signal intensity for Glu, Gln and ml at 7T. Further in vivo studies are currently underway for quantification of these metabolites in human brain.

REFERENCES