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 (B_0). Short echo time (TE) acquisition benefits from the reduced T_2 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 (mI) in human brain at 7T.

METHODS

PRESS echo time dependences of Glu, Gln, NAA, GSH, GABA, NAAG and mI have been investigated for subecho times TE_1 and TE_2 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 (TE_1, TE_2) = (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 mm^3 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, NAA_{Asp}, GSH_{Glu}, GABA, $NAAG_{Asp}$, mI and creatine (Cr) at a concentration ratio of 10:3:10:1:1:1:5:8 at 7T, for the optimized PRESS, a short-TE STEAM and a optimized STEAM [2] sequences. Spectra are scaled incorporating T_2 = 130 ms, a mean value of Cr and NAA singlet T_2 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 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 NAA_{Asp} 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 T_2 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 T_2 between gray and white matter. In addition, the PRESS sequence gives a well defined mI multiplet between 3.5 and 3.65 ppm. In conclusion, PRESS (TE_1, TE_2) = (37, 63) ms provides enhanced resolution and signal intensity for Glu, Gln and mI at 7T. Further *in vivo* studies are currently underway for quantification of these metabolites in human brain.

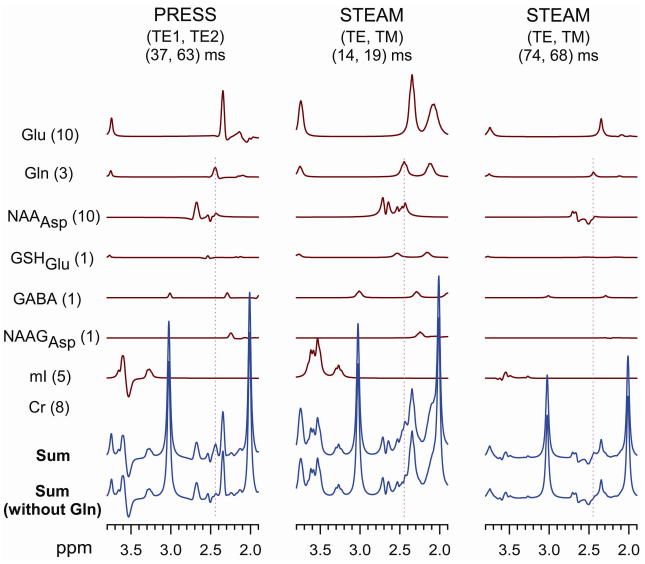

FIG. 1. Numerically-calculated spectra of Glu, Gln, NAA, GSH, GABA, NAAG, mI and Cr at a concentration ratio of 10:3:10:1:1:1:5:8, at 7T, for optimized PRESS and short-TE and optimized [2] STEAM, are shown. Spectral difference due to the presence and absence of Gln is most noticeable in the optimized-PRESS spectra. The spectra are scaled incorporating T_2 = 130 ms. Spectra are broadened to 0.04 ppm (12 Hz).

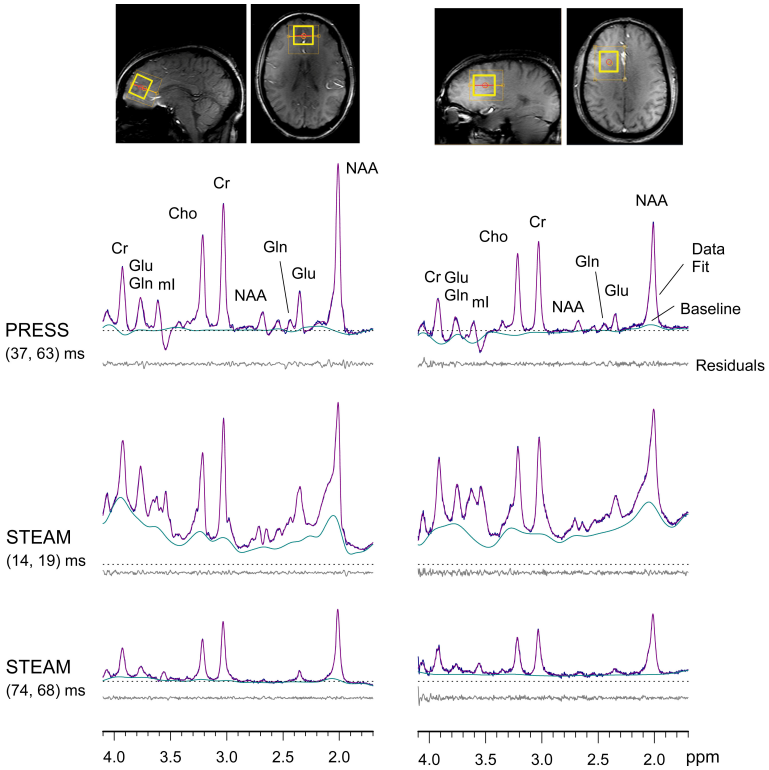

FIG. 2. LC model analysis results of *in vivo* brain spectra from the prefrontal and left frontal lobes obtained with optimized PRESS, short-TE STEAM and optimized STEAM [2]. Spectra are normalized with respect to the brain water signal at TE = 14 ms. The voxel size was 25×30×30 mm^3. TR = 2.5 s. NEX = 64. Horizontal dotted lines indicate the zero of the axes.

REFERENCES

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