A Novel Approach for Reducing Chemical Shift Registration Error at 3T: Short TE CPRESS

N. Sailasuta[1], R. E. Hurd[1], C. Cunningham[2], D. Vigneron[3], S. Nelson[3], J. Pauly[2]

[1]GE Medical Systems, Menlo Park, CA, United States, [2]Electrical Engineering, Stanford, Stanford, CA, United States, [3]Radiology, UCSF, San Francisco, CA, United States

Introduction

Proton MRS at high field ($\geq$ 3T) has gained wide acceptance in the past several years as evidenced by clinical and research sites moving toward high field systems for their diagnostics and research studies. However larger chemical shift registration errors are a problem, which can negate the larger chemical shift dispersion advantage for MRS at high field. In a PRESS pulse train, having large, matched 90- and 180-degree RF pulse bandwidths, is key to reducing chemical shift errors. However a high bandwidth 180-RF pulse usually requires high peak B1, which is limited on whole body high field systems. In this abstract, we describe an approach, in pulse sequence design, to address this problem and still maintain short effective echo times for detection of strongly coupled metabolites with moderate-to-short T2 relaxation times.

Methods

Data were acquired on a GE 3T Signa scanner (Milwaukee WI), using a volume head coil. Studies were performed on a standard GE MRS HD phantom, and on normal volunteers. A modification of the conventional PRESS pulse sequence -(Figure 1) was used. A Carr-Purcell RF pulse train approach CPRESS (1) was used, where the slice selective 180 RF pulses in a double spin echo pulse scheme, PRESS, are replaced by a pair of, linear-phase, high-bandwidth 180 RF pulses. The timing of the sequence is 90-t1-180-tcp-180-tcp-180-tcp-180-t2-acq, where t1 is kept at a minimum of 3.8ms, tcp = TE/4 and t2 = (tcp –t1). The bandwidths for the 3.6ms 90 RF pulse is 2366 Hz and the bandwidth for the 2ms 180 RF pulse was 2479 Hz. This compares with a 6.5ms linear phase 180 used in conventional PRESS at an effective bandwidth of only 1100 Hz. The CPRESS echo time is 45ms and TR is 3sec for volunteer scans. Spectra were also obtained for basis set solutions for LCModel analysis. A voxel size of 8cc is used for both volunteers and basis set solution scans.

Results and Discussion

A normal volunteer PRESS at TE 35ms, and basis set spectra for NAA, glutamate, glutamine and myo-inositol are shown in Figure 2. In addition to the overlapping signals from small metabolites, such as NAA, glutamate, glutamine and myo-inositol, a significant contribution from macromolecules is evident. A representative spectrum from volunteer gray matter acquired with CPRESS sequence is shown in Figure 3 together with NAA, glutamate, glutamine and myo-inositol phantom spectra, acquired with the same acquisition parameters. Metabolite peak intensities, NAA, creatine and choline, are maintained even at this echo time of 45ms, but with less contribution from macromolecules (Note baseline changes in Figure 4). Also some of the strongly coupled spin systems show less modulation, as expected (2). Note that myoinositol peak height at 3.61 ppm is equal to that of choline peak. LCModel fit of TE 45ms for CPRESS spectrum gives similar, Cramer-Rao lower bounds (%SD) to those from a short echo time PRESS.

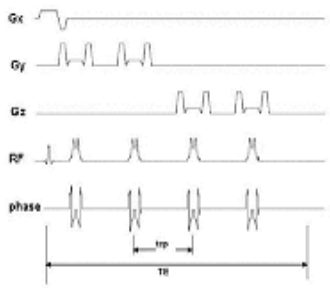

Figure 1

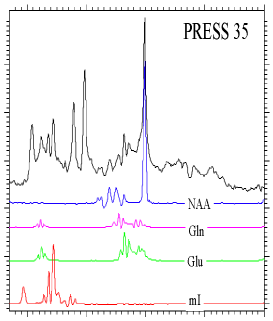

Figure 2

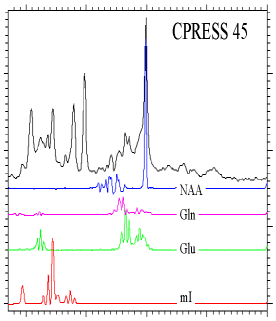

Figure 3

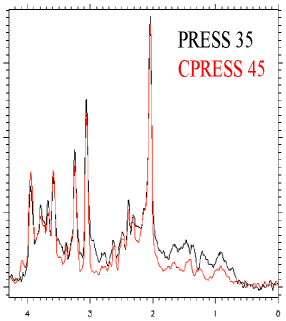

Figure 4

Conclusions

Our preliminary data demonstrate that with CPRESS there is no significant loss in metabolite signal intensities of NAA, creatine and choline at TE 45ms compared to TE 35ms PRESS. Replacing linear 180's in PRESS with pairs of high-bandwidth non-linear phase 180's, chemical shift misregistration is reduced, thus making this approach suitable for general high field proton MRS applications. In addition, an increase in peak intensity of the strongly coupled system of myoinositol should make quantification of this metabolite more reliable.

References

1. Hennig. J, et al, MRM, 37, 816-820 (1997).
2. Allerhand A, J. Chem. Phys, 44, 1-9 (1966).