HIGH RESOLUTION 2D CTPRESS WITH 2D SPIRAL ENCODING

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INTRODUCTION: J-coupling causes spectral splitting and complicated signal modulation that limit the detection of important brain metabolites such as glutamate (Glu) and glutamine (Gln) in proton spectroscopic imaging. Glu is an important excitatory neurotransmitter in the brain and changes in Glu and Gln are an indication for metabolic ailments such as hepatic encephalopathy [1, 2] and Rett's syndrome [3]. While 2D spectroscopy, e.g. CTPRESS [4], has been demonstrated to successfully improve signal detection of coupled spins, it carries a heavy penalty in scan time over conventional chemical shift spectroscopy. To mitigate the scan time constraints, Mayer et al [5] exploited the diagonal feature of 2D CTPRESS spectra to achieve eight-fold spectral undersampling with a 17-step 2D MRS experiment and demonstrated the method for a voxel size of 4.5cc at 3T with a quadrature birdcage head coil within a total scan time of 4:40min for two averages with fast spiral spectroscopic image encoding.

32-element receive coil arrays offer significant SNR gains over birdcage coils [6], which can be traded for faster scans of improved spatial resolution. Here we demonstrate in vivo 2D CTPRESS on a 3T Siemens Tim Trio with spiral encoding at a spatial resolution of 0.85cc with minimum scan time of 5:16min. Four averages were taken for improved SNR, resulting in a total scan time of 20:32min.

METHODS: The pulse sequence for the 17-step CTPRESS experiment shown in Fig. 1 was implemented and applied in vivo on two human subjects on a 3.0 T MRI scanner (Siemens AG, Erlangen, Germany) using a 32 channel head coil. The last refocusing pulse of the PRESS selection module was shifted in increments of $\Delta t_1/2 = 6.4$ ms corresponding to a spectral bandwidth of 78.125Hz in f_1 . For optimal SNR from Glu, the average TE of the 17-step CTPRESS experiment was chosen to be 151 ms [5]. The bandwidth in the f_2 dimension was 1.2 kHz.



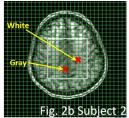


Fig 2a and b. MPRAGE images of two subjects. White rectangle marks excitation volume. Red labels identify voxels with predominantly gray or white matter.

FOV was 24 cm x 24 cm with voxel size of 0.92cm x 0.92cm x 1cm = 0.85cc. As shown in Fig. 2a and b, an 8 x 8 x 2 cm³ excitation volume was selected for both human subjects. With four averages, total scan time was 20:32 min. For comparison with prior

RF
Gx
Gy
Gz

Signature

Acquisition

Fig. 1. Pulse sequence disgram for a (2i+1) star

Fig 1. Pulse sequence diagram for a (2i+1)-step CTPRESS experiment

work, a lower-resolution 2D CTPRESS experiment was also implemented with two temporal and two angular spiral interleaves on the same spatial FOV of 24 cm x 24 cm for a voxel size of 1.5cm x 1.5cm x 20 cm = 4.5cc. Total scan time for this lower resolution scan was 4:40min. The t_1 and t_2 dimensions were apodized with a tapered cosine function and diagonal spectra from the 2D CTPRESS experiments were obtained by integrating the magnitude spectra along t_2 within ± 13 Hz along the 2D spectrum diagonal.

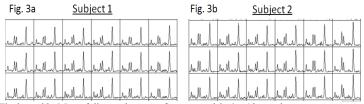


Fig 3a and b. Map of diagonal spectra from central 3x6 = 18 voxels.

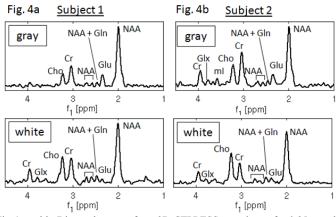


Fig 4a and b. Diagonal spectra from 2D CTPRESS experiment for 0.85cc and total scan-time of 20:32 min. Spectra from predominantly gray matter (top row) and white matter (bottom row) voxels corresponds to red labels in Fig. 2a and b. Glu, Gln and NAA peaks are clearly separated

RESULTS: SNR of the 0.85cc and 4.5cc 2D CTPRESS experiments were calculated from the NAA peaks centered at 2.01ppm and averaged over the excitation volume. The reduction in SNR by a factor of approximately 2.5 of the 0.85cc experiment is consistent with a 5.29 factor decrease in voxel size and a 4.64 factor increase in acquisition time. Fig. 3a and b is a map of the central 3x6 = 18 voxels of the excitation volume, demonstrating successful reduction of line splitting for the multiplets of NAA, Glu, and Gln. Fig 4a and b show the 1D diagonal spectra for the 0.85cc 2D CTPRESS experiment from voxels

with predominant gray matter and white matter, corresponding to the red crosses in Fig. 2a and 2b. Glu and Gln signal that are typically obscured in 1D spectroscopic imaging manifest as peaks between 2.25ppm-2.50ppm and 3.50-3.80ppm. Relative metabolite amplitudes in gray-matter and whitematter voxels demonstrate signal pattern variations similar to [5].

CONCLUSION & DISCUSSION: We have demonstrated the application of a spatially-resolved 2D CTPRESS acquisition at a resolution of 0.85cc. Peaks from Glu, Gln, mI and NAA are well distinguished and can be reliably measured at this resolution. An immediate extension is to enable 3D spectroscopic imaging by incorporating phase-encoding in k_z space. Without scan time penalty or SNR tradeoffs, four slices can be encoded within a 4-cm thick slab for the same voxel size of 0.85cc.

References: [1] Chamuleau et al; NMR Biomed. 1991; 4:103-108 [2] Kreis et al; NMR Biomed. 1991; 4:109-116 [3] Pan et al; MRM 1996; 36: 7-12 [4] Dreher et al; MRI 1999; 17:141-150 [5] Mayer D et al; MRM 2005; 54:439–442 [6] Wiggins et al; MRM 2006; 56(1):216-223

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