2D Spectroscopic Imaging of Glutamate at 3T using TE-Averaged PRESS

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Introduction

Glutamate and Glutamine are important neurotransmitters in the central nervous system. The neurotoxic properties of excess glutamate have been associated with several neurodegenerative and psychiatric diseases. Glutamate cannot be isolated using conventional one-dimensional spectroscopic techniques because of strong J-coupling of the resonances. Two dimensional constant time PRESS (CT-PRESS) [1] and 2D J-resolved [2] methods have been developed to increase the spectral resolution by measurement of an additional spectral dimension. These have been implemented both as localized single voxel and spectroscopic imaging [3] techniques. Recently it was shown [4] that the zeroth component of a 2D-J resolved spectrum resulted in an unobstructed detection of Glutamate at 2.35 ppm that was separated from Glutamine. This technique called TE-Averaged PRESS has been implemented as a single voxel technique [5]. In this study we extended the TE averaged scheme for two-dimensional (2D) MR spectroscopic imaging (MRSI). To ensure that the TE averaged scheme could be implemented in a reasonable amount of time for clinical applications, a fast encoding trajectory (Flyback MRSI) [6] was used which enabled the rapid acquisition of MRSI spatial arrays spectra with good spectral bandwidth and resolution. Since this fast spectroscopic imaging technique simultaneously encoded one spatial and spectral dimension, the scan time for a 2D MRSI TE-Averaged acquisition was equivalent to a one-dimensional acquisition.

Methods

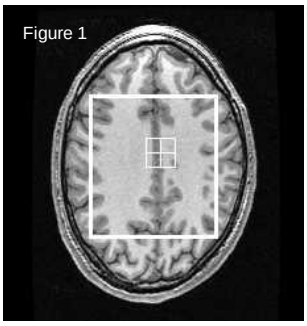
In-vivo data were acquired on a 3T GE Signa scanner on an EXCITE platform using an 8-channel phased array coil (Medical Advances). The single voxel PRESS J-resolved sequence [4] was modified to implement the two dimensional (2D) J resolved spectroscopic imaging by using the Flyback trajectory [6] to collect data simultaneously along one spatial and spectral dimension. In the design chosen for this study conventional phase encoding was used in the readout right-left direction and the flyback trajectory was used in the orthogonal anterior-posterior direction. For J resolved spectroscopy 64 echo time steps were implemented starting at TE = 35ms with an echo time increment of 2.5ms. The spatial data were acquired with a spatial resolution of 16 x 16 pixels over a 16 cm field of view from a two dimensional region of thickness of 1.5 cm over the supra tentorial brain. The excited region of interest was approximately 130 cc. The 2D spectral data had a spectral bandwidth of 976 Hz in the chemical shift direction with 512 points resulting in a ~ 2 hz spectral resolution. The scan time for this 2D TE-Averaged acquisition was ~ 17 minutes. To verify that the 2D and single voxel J-resolved techniques gave similar results, we scanned a single voxel within the 2D excitation region. All data was sent to a SUN Ultra 10 workstation for post-processing, using programs developed in our laboratory. The first step in the reconstruction of flyback MRSI data is to sort the data points so that the dataset resembles a conventional two-dimensional (2D) spectroscopic dataset. The spectra were then spatially transformed without transforming the spectral domain, combined and corrected for coil intensity [7] and then presented to LCmodel for spectral quantification.

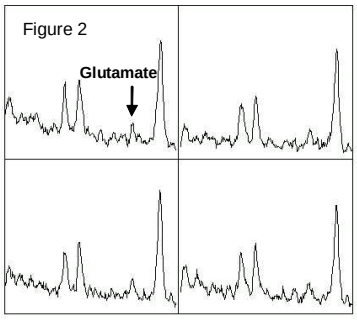
Results

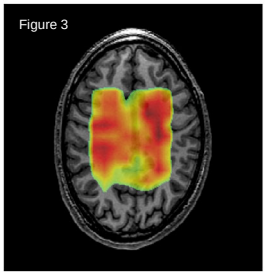
Figure 1 shows the 2-dimensional excitation region. The TE-averaged spectra from the region of interest are shown in **Figure 2** with the glutamate peak indicated. The SNR of Glutamate in the 2D CSI acquisition and single voxel acquisition was ~ 6.8 and 13.6 respectively. Given that a single voxel resolution is ~ 8cc and takes ~ 5.0 minutes and the CSI voxel resolution is ~1.5cc and takes ~17.0 minutes, the observed ~1/2 reduction in SNR of the CSI acquisitions relative to single voxel technique is slightly worse than the predicted 1/3rd reduction in SNR. This is likely due to the use of an encoding trajectory in which all spectral points sampled are not used, unlike conventional phase encoding. The flyback trajectory used for spatial encoding samples data along a rectilinear grid and can be reconstructed without extensive re-gridding or density corrections. It was possible to reconstruct the data offline within few minutes after data acquisition. **Table 1** shows the comparison of the metabolite concentration ratios obtained from a similar region in the CSI grid as the single voxel. While the results are comparable the CSI metabolite ratios are somewhat lower than the single voxel technique. **Figure 3** and **Figure 4** display the 2D map of NAA/Creatine and Glutamate/Creatine respectively.

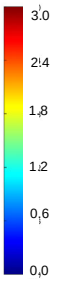
Table1:Comparison of metabolite concentration ratios obtained from a single voxel and 2D CSI TE-Averaged PRESS technique. Four CSI voxels of resolution [1x1x1.5cc] each were averaged to compare to a single 8cc voxel [2x2x2]

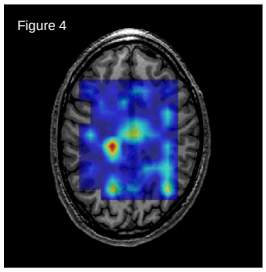
	NAA/Cr	Glu/Cr	Gln/Cr
Single Voxel	2.3	1.4	2.8
2D csi	1.9	1.1	2.7











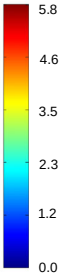


Figure 1:The slice showing the excited region. **Figure 2**: The spectra from the region of interest shown in Figure 1. The voxels shown had quantification error estimates within 25% in LCModel. **Figure 3**: NAA/Creatine concentration ratio map. **Figure 4**: Glutamate/Creatine concentration ratio map. .

Conclusions

This study has demonstrated the successful implementation of the TE-averaged PRESS scheme for detection of Glutamate within a 2D region of interest. Use of a fast imaging technique resulted in 16-fold reduction in scan time for a 16x16 matrix relative to a conventional acquisition making 2D TE-averaged PRESS a viable technique for clinical applications. It was verified that the metabolite concentration ratios obtained with the 2D TE averaged spectroscopic scheme with 64 echo times were similar to the single voxel acquisition. These preliminary studies validate the method and further optimization studies will be performed and subsequently used for clinical studies.

References

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