Volumetrically Resolved TE-Averaged Spectroscopic Imaging

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Introduction

Spiral readout based MRSI (Magnetic Resonance Spectroscopic Imaging) offers greatly reduced minimally required scan time compared to conventional phase encoded approaches. This additional scan time available can be subsequently used to gather other useful information such as resolving J-coupling. It has been shown that the glutamate resonance can be isolated using TE-averaging at 3T [1]. Extensions of this approach to multi-voxel spatial coverage have been made by incorporating oscillating readouts or at the expense of increased scan time [2,3,4]. However, these extensions have been limited to 2D slice spatial coverage, which can be limiting for certain clinical applications. In this study, we demonstrate TE-averaging over a 3D spatial coverage within reasonable scan time. Our overall clinical goal is to determine NAA or glutamate metabolite distributions over volumetric regions providing increased sensitivity to regional changes which can be useful in numerous neurodegenerative diseases or psychiatric disorders.

Methods

In vivo data were acquired at 3T scanner. The TE-averaging approach was combined with spiral readout MRSI. The PRESS excitation scheme was used. Nine different echo times were chosen for TE-averaging. As noted in [1], the number of steps is relatively unimportant for detecting glutamate. The echo times were chosen to maximize glutamate detection while preserving the TE-averaging feature. Specifically, the echo times chosen for this study were 40-50-65-85-110-140-170-200-220 ms. This sampling density of the echo time steps is proportional to the amplitude of the C4 2.35 ppm proton peak of the glutamate metabolite. The spectroscopic imaging parameters were as follows; 16x16x8 spatial coverage over a 16x16x12 cm FOV, 1.7 second TR, 2 nex, CHESS water suppression, 1000 Hz spectral bandwidth, 16:30 minute scan time, 8 channel phased array head receiver coil. Data reconstruction consisted of 1.summing all echo time acquisitions in the Fourier domain which reduces the recon time, 2. gridding and FFT, 3. phasing of individual coil data sets, and 4. data combination from each set of coil by weighting them according to the remaining water signal amplitude to maximize for SNR. Repeatability study was also performed to evaluate the potential for usage in clinical applications.

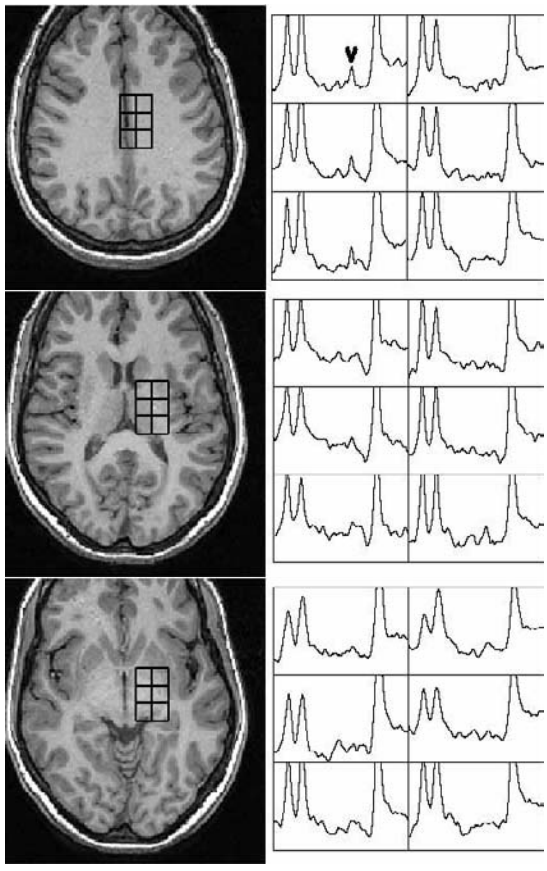
Results and Conclusion

The figure shows representative TE-averaged spectra for several slices from an in vivo data. The location of the glutamate peak is marked with the 'v' sign on the most superior slice. Increased glutamate levels can be seen in the gray matter regions in agreement with literature. Repeatability study performed resulted in CV (coefficient of variation) for NAA to be approximately 7%.

Additional optimization to reduce lipid ringing artifacts during the short echo acquisitions are needed to by fully incorporated into the clinical settings. Although our protocol used very selective saturation (VSS) pulses to exclude and lipid contamination, the resulting spectra still have baseline contributions from the remnant lipids.

In this preliminary study, we demonstrated a protocol to perform in vivo TE-averaged 3D spectroscopic imaging of NAA, Cr, Cho, and glutamate. The whole spectroscopic imaging study can be performed within a reasonable scan time of approximately 16:30 minutes.

The procedure can be readily combined with other J-coupling acquisition techniques such as CT-PRESS for homonuclear detection [5]. In addition, desired echo timing steps can be readily prescribed on the scanner when maximizing for other metabolite detection such as glutamine or GABA [6].



References

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