Multiple Spin Echo Spectroscopic Imaging of Glutamate and Glutamine (Glx)

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Introduction

The collective levels of glutamate (Glu) and glutamine (Gln), known as Glx, are relevant in the study of a number of diseases and disorders. The spin echo MRSI sequence [1] has been used to measure Glx levels [2]. The advantage of the spin echo MRSI sequence is that signal from more than one slice can be acquired without an increase in scan time [1]. The acquisition time can be further reduced when targeting non-coupled spins by acquiring more than one echo, each with a different phase encode, after every excitation [3]. Multiple spin echo spectroscopic imaging, also known as turbo spectroscopic imaging (TSI), has proven to be useful for observing uncoupled protons; however, its application to coupled spins is difficult because the J-modulation as a function of echo time, TE, can lead to spatial misregistration [4]. The objective of this paper is to demonstrate how the TSI sequence can be altered to enable the detection of spins that are solely involved in weak coupling interactions such as the C_2 protons of Glx. The technique involves rewinding the J-coupling evolution of the C_2 protons in the slice of interest by turning the chemical shift displacement effect to advantage by employing TSI refocusing pulses that have a bandwidth less than the chemical shift difference between the C_2 protons and the C_3 protons to which they are weakly-coupled. This ensures that only the C_2 protons of Glx experience the refocusing pulse in the desired slice, thereby rewinding their J-evolution no matter what TE or echo spacing is employed.

Methods

All experiments were carried out with a 3 T Philips Intera scanner and a transmit/receive birdcage head coil. Two spin echo spectroscopic imaging sequences were used; in one an 870 Hz bandwidth refocusing pulse was employed, while in the other the refocusing pulse was replaced by one with a bandwidth of 175 Hz. For the TSI sequence an additional 175 Hz bandwidth refocusing pulse was added to the latter sequence speeding up acquisition by a factor of two. The frequency of all pulses was set to 3.75 ppm. For phantom experiments, the FOV was 80 mm and 8×8 phase encodes were carried out. For *in-vivo* scans the FOV was set to 240 mm and 20×20 phase encodes were executed. The slice thickness was 15 mm for all experiments yielding a nominal voxel size of 1.2×1.2×1.5 mm^3 *in vivo*. The data was collected as 256 complex points sampled at 2000 Hz, and the repetition time was set to 3 s. The sequence was preceded by an outer volume suppression module to suppress signal from outside the volume of interest and from the skull regions. The echoes were not collected symmetrically about the echo time, but rather acquisition began immediately after application of the refocusing pulse. The abrupt truncation of the FIDs resulted in ringing in the real spectra and therefore all spectra are displayed in magnitude mode.

Results

Figure 1 shows spectra obtained from a 10 mM Cr/50 mM Glu phantom. A TE of 100 ms was used, and for the TSI experiment, the echo spacing was 200 ms. It can be seen that the Glu signal increases by about 30% when employing the narrow bandwidth refocusing pulse. The quality of the spectrum is maintained when using the TSI sequence. It was experimentally found that a TE of 170 ms minimized signal from myo-inositol (mI) in the Glx spectral region. This can be seen in Fig. 2 where a short-TE, spin echo MRSI spectrum (TE = 30 ms) obtained from a phantom containing a mixture of Cr, Glx, and mI is compared to a TSI spectrum (TE = 170 ms, echo spacing = 160 ms) of the same voxel. The TSI spectrum shows a Glx peak that is well resolved from Cr and mI. The efficacy of the narrow bandwidth TSI sequence *in vivo* is demonstrated in Fig. 3, where spectra from four different voxels from a slice that cut through the frontal and parietal lobes are shown. The Glx and Cr peaks are well resolved while the signal from mI is minimized. Furthermore, the relatively long TE allowed the macromolecule baseline signal to decay. Because of the limited bandwidth of the refocusing pulses, the 3 ppm Cr peak suffers from chemical shift displacement; therefore the 3.9 ppm Cr peak serves as a better internal reference.

Conclusion

We have shown how a TSI sequence can be modified to allow the observation of high signal from the C_2 protons of Glx with minimal contamination from mI. TSI data sets with a nominal voxel size of 1.2×1.2×1.5 mm^3 were acquired from the human brain within a clinically acceptable time of 10 minutes. The technique demonstrates that weakly coupled spins can also be candidates for detection by the relatively fast spectroscopic imaging sequence.

References

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4. R.V. Mulkern et al. *Ann. N. Y. Acad. Sci.,* **820**, 820, 1997.

Figures

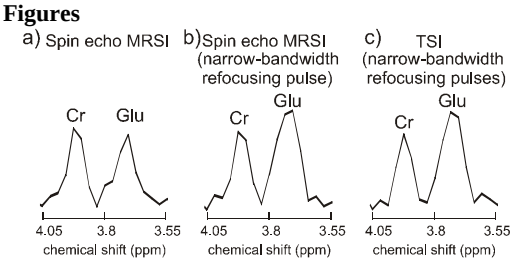

Figure 1: Spectra from a central voxel of MRSI acquisitions of a 10 mM Cr/ 50 mM Glu phantom. TE = 100 ms and TSI echo spacing = 200 ms.

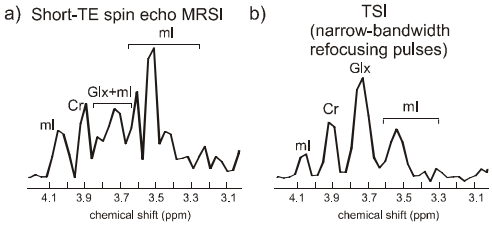

Figure 2: Spectra from a central voxel of a 10 mM Cr/50 mM Glu/24 mM Gln/31 mM mI phantom. The TSI sequence with the optimized TE of 170 ms yields a Glx peak that is resolved from Cr and mI and in half the scan time.

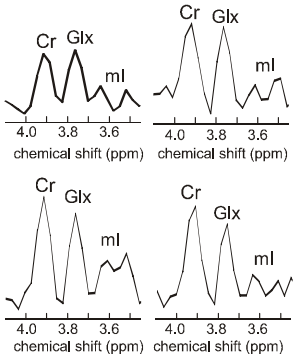

Figure 3: Spectra from four different voxels of a TSI acquisition grid from the brain of a normal volunteer (TE = 170 ms, echo spacing = 160 ms).