

Single Echo Time Glutamate Editing at 3 Tesla

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Introduction

Glutamate plays an important role in normal brain function and in brain disorders. Recently, MRS measurement of total glutamate concentration has been applied to studying several neurological and psychiatric disorders. Short-TE single voxel MRS methods cannot separate glutamate from overlapping resonances at field strengths accessible to most clinical studies. As a result, spectral editing methods have been developed to isolate the γ -H₂ glutamate signal at 2.35 ppm from overlapping resonances (1-4). For example, a TE-averaged PRESS-based strategy using 32 different echo times has been developed for single voxel detection of glutamate (3). Adding the robust 2D conventional phase encoding to this method for spectroscopic imaging of glutamate is not practical because of the excessive scan time required. Single echo time spectrally semi-selective homonuclear polarization transfer method for glutamate imaging at 4 Tesla has also been developed (4). We propose a new strategy for imaging glutamate using a single echo time without employing any spectrally selective pulses at 3 Tesla. The advantage of this strategy is that i) 2D conventional phase encoding can be completed with acceptable scan time; ii) because no spectrally selective pulses are used the glutamate editing process is basically independent of B₀ inhomogeneity, allowing greater coverage of the brain.

Methods

At 3 Tesla, the γ -H₂ of glutamate and overlapping resonances are strongly coupled with their respective neighboring resonances. The intensity and phase of strongly coupled spins are significantly influenced by spectrally nonselective pulses. Therefore, there exists an interesting possibility of isolating the glutamate γ -H₂ signal by the use of one more refocusing pulse in the PRESS sequence. The four pulse PRESS sequence was shown in Fig.1. The total and individual echo times ($TE_1+TE_3=TE_2+TE_4=TE/2$) were optimized using numerical simulation of the four-pulse PRESS sequence to find the best condition for resolving the glutamate γ -H₂ signal from overlapping glutamine γ -H₂ signal and signals from the aspartate moiety of NAA. The concentration ratios of NAA, glutamate and glutamine used in the simulation were 1:1:0.3 based on MRS measurements reported in literature.

Results

The optimal echo times were $TE_1 = 14$ ms, $TE_2 = 13$ ms, $TE_3 = 33$ ms and $TE_4 = 32$ ms ($TE = 94$ ms). The simulated spectra were shown in Fig.2. The top trace represents the summed spectra. The glutamate peaks at 2.35 ppm appear as a pseudo singlet. Spectra of the glutamate, glutamine and the aspartate moiety of NAA were shown in the 2nd, 3rd, and 4th trace, respectively. Note that the integrated contributions from glutamine and the aspartate moiety of NAA are close to zero. An in vivo spectrum from a $2.5 \times 3 \times 3 \text{ cm}^3$ voxel in the frontal lobe of a healthy volunteer was shown in Fig. 3. The spectrum was acquired using a 3T scanner (GE Excite), with TR = 2 s and NS = 32. The spectral feature of the in vivo spectrum is a very similar to the top trace in Fig. 2 around the 2.35 ppm spectral region, indicating that the four-pulse PRESS method is feasible for measurement of glutamate in vivo at 3T using a single echo time (94 ms) and without using any spectrally selective or semi-selective pulse.

Discussion

The use of four-pulse PRESS and optimized echo times provides a method for spectrally nonselective glutamate editing using a single echo time. It is expected that this method may be converted into a spectroscopic imaging method for mapping glutamate distribution in the human brain at 3 Tesla with improved tolerance to B₀ inhomogeneity.

References

1) Thompson, et al. MRM 1998;39:762-771. 2) Mayer, et al. MRM 2005;54:439-442. 3) Hurd et al, MRM, 51:435, 2004. 4) Pan et al, MRM, 36:7, 1996.

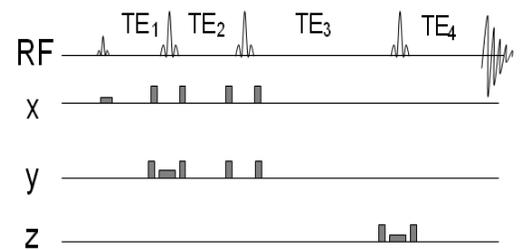


Fig. 1 Pulse sequence of modified PRESS using four RF pulses for glutamate editing pulses.

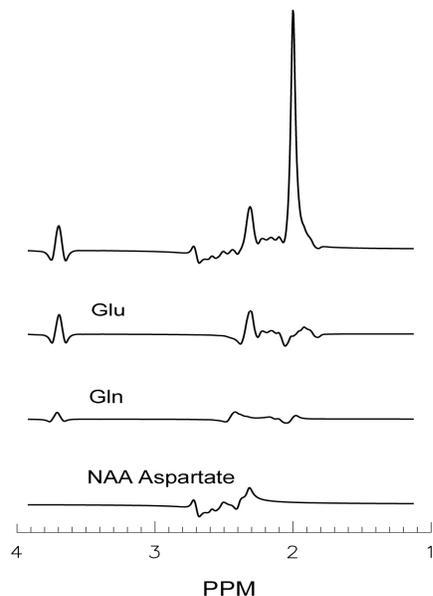


Fig.2. Simulated four-pulse PRESS spectra of NAA, glutamate and glutamine. TE = 94 ms, $TE_1 = 14$ ms, $TE_2 = 15$ ms, $TE_3 = 33$ ms, $TE_4 = 32$ ms. 1st trace: summed spectrum; 2nd trace: glutamate; 3rd spectrum: glutamine; 4th spectrum: aspartate moiety of NAA.

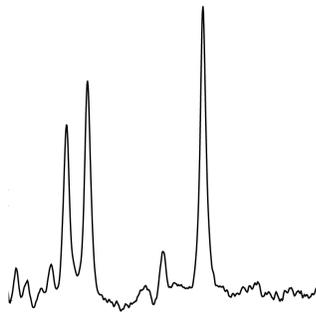


Fig.3. In vivo demonstration; the spectrum collected in a voxel of $2.5 \times 3 \times 3 \text{ cm}^3$ in frontal lobe.