Comparison of TE-averaged with short TE Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) for Mapping Glutamate in Human Brain

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INTRODUCTION

Proton magnetic resonance spectroscopic imaging (1H-MRSI) enables quantification of biomarkers relevant to various neurological and psychiatric disorders. MRSI studies of Glutamate (Glu), an important neurotransmitter have used spectral fitting at short TE [1,2], J-refocused coherence transfer [3], and more recently, 2D J-resolved spectroscopic imaging [4,5]. Spectral editing and 2D J-resolved MRSI techniques enable highly selective mapping of Glu, but they require multi-step encoding that lengthens acquisition times and limits the sensitivity gains at thigh field as metabolite T_2 decreases with field strength. We recently demonstrated the feasibility of measuring J-coupled metabolites in human brain at 3 and 4T including lateral cortex regions using high speed Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) with 1 cc voxel size and measurement time of less than 10 min [6]. However, quantification of Glu using TE-averaged MRSI has not yet been directly compared with short TE MRSI. Here we compare TE-averaged with short TE (15 ms) PEPSI data acquired in human brain at 3T, using identical voxel size (1 cc). In contrast to previous TE-averaged MRSI studies we used a shorter minimum TE of 15 ms to maximize sensitivity for detecting Glu.

METHODS

TE averaged PEPSI data were acquired from axial slices on a Siemens 3T scanner with TR = 2 s, TE stepping in 16 steps (15 ms - 165 ms) with an increment time of 10 ms, spatial matrix: 32x32 pixels, FOV = 256 x 256 mm, slice thickness = 15 mm, spectral width = 1087 Hz, digital spectral resolution: 1 Hz, no. averages = 1, scan time = 17 min. A non-water suppressed (NWS) reference scan was also collected. Short TE data were acquired with TE = 15 ms and 8 averages using identical parameters otherwise, resulting in scan time = 8.5 min. Data processing using LCModel fitting and correction for relaxation and partial volume effects was performed as described previously [4]. Basis sets for 16 metabolites were generated using density matrix simulations [7]. For TE-averaged data the basis sets at different echo times were combined using weights to simulate the T_2 decay. T_2 values were taken from the literature [6]. Two Cramer-Rao lower bound (CRLB) thresholds were used: < 20% = excellent reliability and < 50% = acceptable reliability.

RESULTS

An example of a spectrum from gray matter with superimposed LCModel fit is shown in Fig. 1. As expected, the baseline is flat and the LCModel fit shows a distinct Glu peak at 2.34 ppm. The short TE case exhibits a narrower full width at half maximum (FWHM) and a higher SNR than those of the TE averaged case, as shown in Table 1, averaged across the slice. For the short TE case, the MRI is shown in Fig. 2A, the Glu map (Fig. 2B) shows distinguish contrast from different parts of the brain. Metabolite map for the TE averaged case is shown in Fig. 3.: A) Cho, B), Cr+PCr, C) Glu, and D) NAA/G. Metabolite concentration values with both methods were in a similar range. CRLBs for singlets are smaller with TE averaged method due to longer measurement time. CRLBs of Glu with TE-averaged PEPSI were smaller than with short TE PEPSI, and number of voxels above threshold with TE-averaged PEPSI were significantly smaller than with short TE PEPSI. The singlet line width (FWHM = +/- ppm) of the TE-averaged data was similar to that in the short TE data (FWHM = +/- ppm). The SNR of NAA in the TE-averaged data (+/-) was higher compared to the short TE data (+/-) due to longer measurement time.

DISCUSSION

Our short TE data have higher SNR despite the shorter measurement time and Cramer-Rao lower bounds for Glu are lower compared to the TE-averaged data. Furthermore, the number of voxels above threshold for TE-averaged data is significantly smaller than for short TE data. However, quantification of our short TE data is sensitive to fitting errors due to strong spectral overlap and stronger baseline distortion. On the other hand, it is known that pathological conditions can modify T_2 and fitting of Glu T_2 will be required, which may be challenging due to low SNR at long TEs. Despite these limitations, the concentration estimates for Glu in our healthy volunteer study with both methods are in a similar range. In conclusion, short TE acquisition is advantageous for clinical studies for sensitivity reasons and due to the shorter measurement time. TE-averaged acquisition is complementary to short TE acquisition for positive identification of Glu albeit at lower spatial resolution.

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Table 1 Short TE (8.5 min acquisition) compared to TE averaged (17 min acquisition)

Metabolite	Cho	Cr+PCr	Glu	NAA/G	FWHM	SNR
Short TE	1.5 (0.2)	7.9 (0.5)	10.0 (0.9)	9.4 (0.5)	0.05 (0.04)	7.20 (1.17)
Average TE	1.2 (0.5)	5.6 (1.6)	8.4 (3.3)	12.8 (4.4)	0.06 (0.032)	5.49 (3.17)

Fig. 1

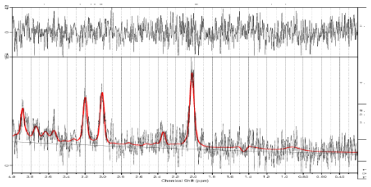

Fig 2a, MRI Fig. 2B TE15 Glu

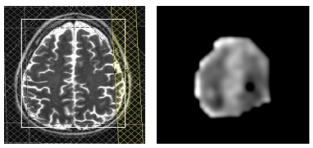

Fig. 3 TE-avg, A) Cho 3B) Cr+PCr 3C) Glu 3D) NAA/G