Three-dimensional, J-resolved H-1 MRSI of volunteers and patients with brain tumors at 3 T

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Introduction

Two-dimensional J-resolved spectroscopy has been implemented and evaluated using whole body MR scanners. This technique enables the separation of J-coupling information from chemical shift by encoding J-coupling in the t1 dimension of a 2D spectrum using different echo times. The addition of the second frequency dimension also allows the separation of Lac from Lip (1). Recent studies have used this sequence in conjunction with a averaging across the different echo times in the t1 domain to offer unobstructed detection of Glu at 3 T, called TE-averaged PRESS (2). Since data are acquired at multiple echo times, it also enables measurement of T_2 relaxation times of singlets, such as Cho, Cr and NAA, which are important for accurate quantification in glioma studies (3). The goal of this study is to design a new acquisition within a clinically feasible scan time and post-processing methods for interpretation of 2D J-resolved PRESS MRSI data with three spatial dimensions and develop strategies for improving the quantification of metabolites from these spectra by using prior information concerning the J-coupling of metabolites such as Glu, mI and Lac, as well as obtaining the relaxation times of metabolites whenever possible.

Methods

PRESS spectra of Glu and Gln with TE starting at 35 ms in 6 steps of 40 ms, respectively, were simulated using GAMMA software. A 4-Hz Lorentzian apodization, zero filling and Fourier Transform were applied and the spectra were averaged in the t_1 domain. All the empirical studies were performed using an 8-channel phased array coil on a 3 T GE Signa scanner running Excite software (GE Healthcare Technologies, Waukesha, WI). In order to show the reliability of the relative position of metabolites, a single-voxel 2D J-resolved acquisition was performed in the metabolite phantoms. The initial echo time was 35 ms. In the t1 dimension, 6 increments were acquired over a 25 Hz spectral bandwidth to yield an F1 resolution of 4.17 Hz per point. The 3D J-resolved MRSI acquisition was incorporated with the flyback echo planar gradient trajectory (4) in the right/left direction with 16 encodes. The spectral data was collected with 712 dwell points and 988 Hz sweepwidth, which provides ~1.39 Hz spectral resolution per point in the F2 dimension. The 3D spectral array size was 16x12x8 (RL x AP x SI) and the spatial resolution was 1 cc. With a TR of 1.2 s and a NEX of 2, the total acquisition time for 2D J-resolved 3D MRSI was 23 min. An MRS phantom, six healthy volunteers and four patients with different kinds of gliomas were examined in the study. To test the reproducibility of such data, the phantom and the two of the volunteers were scanned twice. Postprocessing was performed on a SunBlade 1500 Workstation (Sun Microsystems, Santa Clara, CA). The raw data from each channel were apodized and first-point phased individually, and then were combined using in-house developed software that weights the data by their coil sensitivity. The data were averaged in the t1 domain and then quantified using LcModel (5). The 2D spectra were generated by applying two FFTs in both the t1 and t2 domain with a 45º rotation. Metabolic T_2 relaxation times were calculated from a single exponential fit using the peak heights of Cho (3.22 ppm), Cr (3.02 ppm) and NAA (2.02 ppm) from the spectra. The coefficient of variance (CV) for reproducibility was calculated using the normalized peak height based on voxel, and CV for the T_2 measurement was calculated by the standard deviation divided by the mean.

Results

The TE-averaged spectra of GAMMA simulations and phantoms are shown in **Figure 1**. The C4 protons of Glu were separated from Gln with the chemical difference of 0.1 ppm. **Figure 2** shows the 2D spectra recorded from the lactate phantoms within two different locations. The J cross-peaks caused by the methyl group of lactate were separated from the overlapping lipid peaks (bacon), which were compared with the 1D TE-averaged spectra extracted from J = 0.0 Hz of the 2D spectrum. *In vivo* TE-averaged MRSI data were obtained with good quality and SNR (**Figure 3**). The SNR values of Cho, Cr, NAA, and Glu in volunteers was 17.0±4.9, 15.8±4.5, 33.4±11.5 and 4.3±2.0, respectively. The CVs for the reproducibility were 4% (Cho), 5% (Cr), 6% (NAA) and 9% (Glu) in the phantom, compared with 15%, 16%, 12% and 35% *in vivo*. The Glu/Cr and mI/Cr ratios were in 1.8±0.7 and 1.6±0.6 in segmented white matter, while they were 1.9±0.8 and 1.4±0.5 in grey matter. **Figure 4** illustrates the TE-averaged spectra and the 2D J-resolved spectrum within the Lac region from a glioma patient, and the metabolic maps of Glu/Cr and mI/Cr are plotted with the same scale as in the figure 3. The Lac cross-peaks were clearly visualized in the 2D spectrum. The Glu/Cr and mI/Cr in the T_2 hyperintensities lesions of patients were 1.6±0.6 and 1.7±0.8. The T_2 values of Cho, Cr and NAA in the head phantoms were 194±14 ms (CV, 7%), 296±26 ms (9%) and 550±72 ms (13%), respectively. The T_2 values of Cho, Cr and NAA in the segmented white matter from the volunteers were 209±62 ms, 161±45 ms and 284±82 ms, respectively, and 264±71 ms, 150±27 ms and 225±40 ms in grey matter, while they were 241±74 ms, 181±57 ms and 261±82 ms in T_2 hyperintensities lesions of patients.

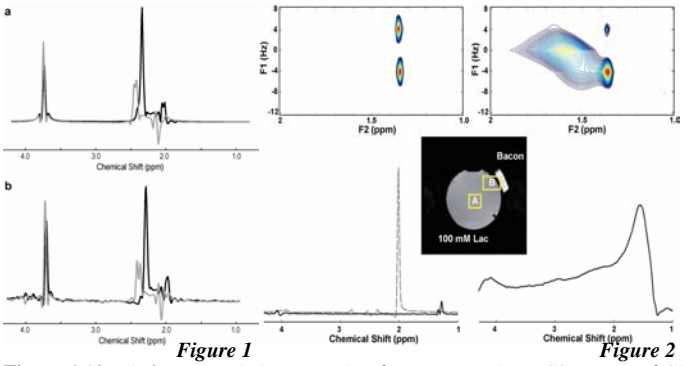

Figure 1

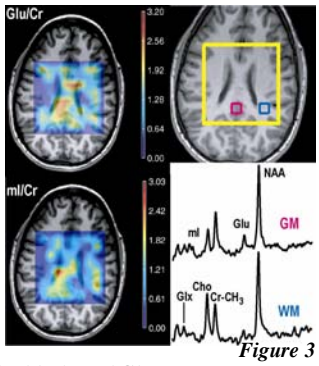

Figure 2

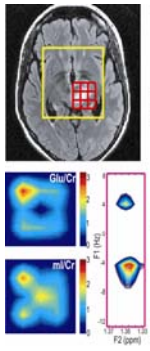

Figure 3

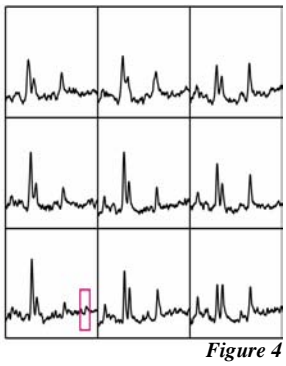

Figure 4

Figure 1 Simulation (a) and phantoms (b) of TE-averaged PRESS spectra of Glu (black) and Gln (grey).
Figure 2 Single voxel 2D J-resolved spectra from a 100 mM lactate phantom with two localizations (voxel A and voxel B). The 2D spectrum and the corresponding 1D spectrum were plotted. The TE-averaged spectra from 50 mM NAA phantom (dotted line) were coplotted with the Lac spectra.
Figure 3 Metabolic maps of Glu/Cr and mI/Cr, TE-averaged spectra in grey matter and white matter from a healthy volunteer.
Figure 4 TE-averaged spectra along with the 2D spectrum of the labeled region and the metabolic maps corresponding to the location from a glioma patient.

Discussion

This study has demonstrated a clinically feasible technique for simultaneous detection of Cho, Cr, NAA, Glu, mI and Lac at 3 T. It also allows the evaluation of the T_2 values of singlets, Cho, Cr and NAA. Compared to short echo MRSI data, the TE-averaged spectra have less macromolecules contamination and also offer unobstructed Glu for more accurate quantification. Lactate could also be quantified from the spectra extracted from the 2D spectra at J = ±4.17 Hz. The next step will be to incorporate this technique into the protocol being used to evaluate patients with gliomas.

References

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