Mapping T2 Relaxation Time of Cerebral Metabolites using Proton-Echo Planar Spectroscopic Imaging (PEPSI)

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Introduction

Estimation of metabolite T2 relaxation time is critical in accurate absolute concentration quantification [1,2]. Using fast MR spectroscopic imaging (MRSI) technique, we can obtain the spatial distributions of metabolites T2s. Proton-Echo-Planar-Spectroscopy-Imaging (PEPSI) uses echo-planar read-out to reduce the 3D spatial-spectral data acquisition time by an order of magnitude [3]. Here we demonstrate the feasibility of using PEPSI sequence to map T2 relaxation times of three cerebral metabolites, N-acetyl aspartate (NAA), creatine (Cre), and choline (Cho), at 3T in less than 30 minutes. Metabolite T2 relaxation times measured using the PEPSI method were consistent with those obtained using conventional PRESS single voxel spectroscopy (SVS).

Methods

Six normal subjects (mean age ± standard deviation, 30 ± 10 years) were enrolled in this study. All experiments were performed on a 3 Tesla MR system (Trio, SIEMENS Medical Solutions, Erlangen, Germany) equipped with a 8-channel head coil array. 2D PEPSI data were acquired from a para-axial slice at the upper edge of the ventricles with voxel size of 0.95 ml (matrix size = 32x32, FOV = 220mm, slice thickness= 20mm). Five PEPSI data sets were collected at TE of 50, 100, 160, 220, 300 ms, using TR of 1200 ms and 8 averages. Complete 8-slice outer volume suppression was applied along the perimeter of the brain to reduce lipid signal contamination. Even- and odd-echo PEPSI data were reconstructed separately using a non-water suppressed reference scan for automatic phasing and frequency shift correction [3]. SVS experiments were performed after the PEPSI scans using the PRESS sequence with 64 repetitions. A white matter voxel and a grey matter voxel located in the same slice as the PEPSI experiment (Figure1A: squares) were selected. The voxel size was 8 ml (2x2x2 cm^3) using the same TE and TR in the PEPSI experiments.

Metabolite signal was quantified by integrating individual spectral peak after polynomial baseline correction. The T2 values were calculated from the slope of semi-logarithmic plot of the metabolite signal versus TE using a least square linear regression. The Pearson's correlation coefficient (R^2) was used to evaluate the goodness of the T2 fit. Regional difference of metabolites T2 between white matter and the gray matter were compared at four ROIs: white matter in the left hemisphere (ROI1), white matter in the right hemisphere (ROI2), gray matter in the frontal lobe (ROI3) and gray matter in the parietal lobe (ROI3) (Figure 1). We compared the T2 values estimated from the PEPSI data and SVS data.

Results

Consistent metabolite T2 values were obtained in the six subjects (Table 1). Significant gray and white matter T2 differences were found for NAA (p<0.01) but not for Cre and Cho (Table 1). Figure 1B shows metabolic T2 maps. Figure 2 shows representative spectra with well-resolved NAA, Cre, and Cho metabolic peaks and minimal baseline distortion after the baseline correction. The averaged difference in T2 values between PEPSI and SVS over six subjects was 4%, 5% and 9% for NAA, Cre and Cho.

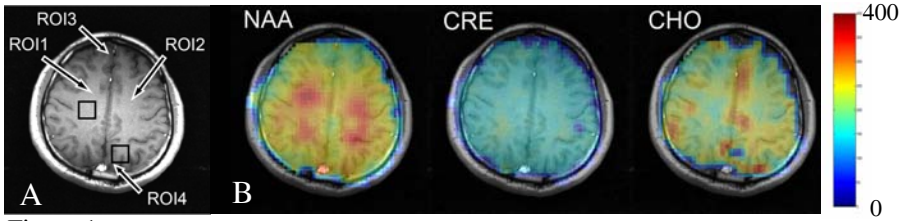

Figure 1

Figure 1. (A)T1 weighted images used as the localization of PEPSI and SVS experiments where ROIs of regional analysis (arrow) and SVS(square) were indicated. (B) The T2 maps of NAA, Cre and Cho (Left to Right) from one subject overlay on the T1 image.

	NAA	CRE	CHO
ROI1	295.5±11.5	156.3±7.2	217.5±16.8
ROI2	287.1±15.7	152.0±5.1	215.5±19.2
ROI3	235.5±17.7	156.5±14.9	228.9±22.6
ROi4	237.8±12.2	155.2±6.8	224.8±25.5
R^2	0.98±0.004	0.97±0.01	0.95±0.01

Table 1

Table 1. List of T2 relaxation time of NAA, Cre and Cho from four ROIs and the whole brain averaged R^2 values. The values shown are the average and standard deviations across six subjects (average ± standard deviation). The R^2s are greater than 0.95 for all metabolites.

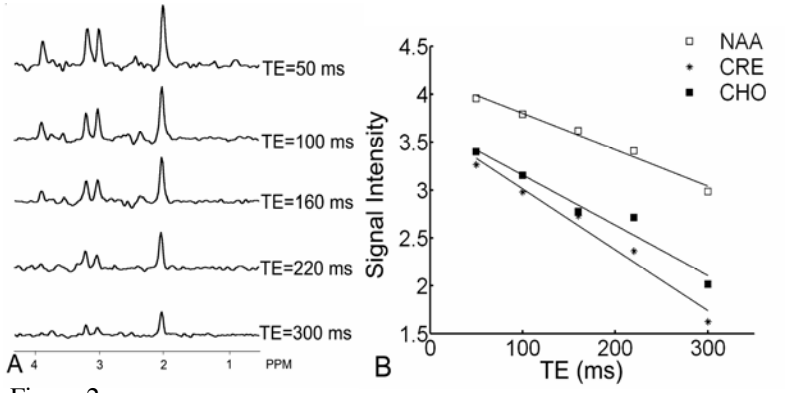

Figure 2

Figure 2. (A) Representative spectra from PEPSI data of different TE and (B) the corresponding semi-logarithmic plot of metabolic signal versus TE. In this case the R^2 is 0.98, 0.97, 0.95 for NAA, Cre and Cho respectively.

Discussion

Our results demonstrate that the proposed high-speed MRSI protocol can quantitatively map T2 relaxations times of three cerebral metabolites within 30 minutes in human brain. Three-dimensional mapping of T2 relaxation times in 8 slices would in principle be feasible within the same acquisition time. Faster data acquisition is possible using fewer signal averages, but at the expense of reduced SNR. The measured gray and white matter differences in NAA T2 are consistent with previous reports using SVS [1,2]. In conclusion, we have successfully developed a method based on PEPSI to rapidly obtain metabolites T2 relaxation time maps to improve absolute quantification of brain metabolite maps. Parametric maps of metabolite relaxation times may also be useful as an adjunct to high resolution T2-weighted images to identify brain pathology in patients with neurodegenerative disease and stroke.

Acknowledgements

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