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

H. Ho[1], S. Tsai[1], Y. Lin[2], S. Posse[3,4], and F. Lin[5,6]

[1]Electrical Engineering, Chang Gung University, Tao Yuan, Taiwan, [2]Electronic Engineering, National Taiwan University of Science and Technology, Taipei, Taiwan, [3]Neurology, University of New Mexico School of Medicine, Albuquerque, NM, United States, [4]Electrical and Computer Engineering, University of New Mexico, Albuquerque, NM, United States, [5]Biomedical Engineering, National Taiwan University, Taipei, Taiwan, [6]6 MGH-HST Athinoula A. Martinos Center for Biomedical Imaging, Charlestown, MA, United States

Introduction

T2 relaxation times of cerebral metabolites are important for the estimation of quantification of metabolite concentrations [1]. T2 values have also been suggested as pathological index for neurological disorders [2]. Measurement of T2 values conducted by collecting multiple spectra from different echo time has been presented using single-voxel spectroscopy (SVS) in specific region [3] and spectroscopic imaging (SI) for better spatial coverage [1,4]. Here we propose to acquire 3-dimensional distribution of three cerebral metabolites N-acetyl aspartate (NAA), creatine (Cre), and choline (Cho), at 3T using Proton Echo Planar Spectroscopy imaging (PEPSI) with the total acquisition time less than 20 minutes.

Material and Method

Six normal subjects were enrolled in this study. All experiments were performed on a 3 Tesla MR system (Trio, SIEMENS Medical Solutions, Erlangen, Germany) equipped with 32-channel head coil array. 3D PEPSI were used with experiment parameters: slab size = 240*240*60, Matrix size: 32*32*6. After removing 2 oversampling slices located at the upper and lower of the slab SI were acquired in four slices with the voxel size of 7.5x7.5x10 mm^3. Five PEPSI data sets were collected at TE of 50, 100, 160, 220 ms, using TR of 1400 ms and single average yielding total acquisition time of 18 minutes.

Regular post processing procedures were applied as previous report for PEPSI data [1]. After simple baseline correction signal of NAA, Cre, Cho were calculated by area under each peak. The T2 values were calculated from the slope of semi-logarthmic plot of metabolite signal versus TE using least square linear regression. Regional difference of metabolites T2 between white matter (WM) and the gray matter (GM) were compared at ROIs defined from masks selected on anatomic T1 images for each slice respectively. The Pearson's correlation coefficient (R^2) was used to evaluate the goodness of the T2 fit. For the analysis voxels with $R^2 < 0.7$ were excluded.

Result

Consistent metabolite T2 values were obtained in the six subjects (Table 1). Significant gray and white matter T2 differences were found for NAA (p<0.05) but not for Cre and Cho (Table 1), which is in accordance with previous reports [1]. Figure 1(a,b) shows representative spectra from voxel located at different slice. Well-resolved NAA, Cre, and Cho metabolic peaks with minimal baseline distortion can be found, which may suggest reliable metabolite signal with acceptable linear regression as shown in Figure 1(c,d). Overall the R^2 is higher than 0.9 except the NAA in lowest slice.

T_2 (ms)	WB	WM	GM
NAA	261±16	284±32	211±12
Cre	146±5	153±7	119±4
Cho	220±14	213±17	181±9

Table 1 List of mean value with standard deviation of ROIs defined in whole brain (WB), WM and GM.

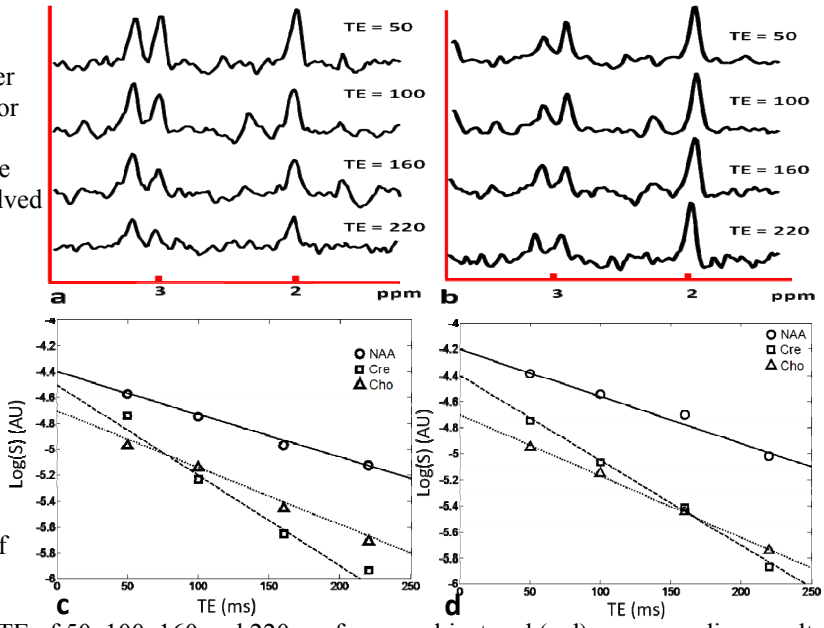

Figure 1 (a,b) Two representative spectra acquired at TE of 50, 100, 160 and 220 ms from a subject and (c,d) corresponding results of linear regression. Voxels were selected from (a,c) WM in slice 2 and (b,d) GM in slice 3. Note that the R^2 are all above 0.95.

Discussion

In this study, we have demonstrated the potential to map the 3-dimensional distribution of T2 relaxation times of NAA, Cre and Cho in less than 20 minutes. The measured T2 values and GM/WM differences in NAA T2 are consistent with previous reports [1,3]. Compared with method proposed in [2] we use four echo times instead of two echoes which enables the linear regression process for the estimation of T2 values. In conclusion, we have successfully developed a method based on 3D PEPSI to rapidly obtain metabolites T2 relaxation time maps in four slices to improve absolute quantification of brain metabolite maps. In the following study we will compare the variation of T2 values between slice and subject in detail especially for the lowest slice. In addition the current protocol can be extended to acquire metabolite information from six slices which is under further investigation.

Acknowledgements

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Reference

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