Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) acquired using radial trajectory (rPEPSI)

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Introduction

Motion during the lengthy 3-dimensional spatial-spectral data acquisition time of MR spectroscopy imaging (MRSI) will degrade the quality of spectrum. Previously Proton Echo Planar Spectroscopic Imaging (PEPSI) has been developed to reduce the scan time for a 2-dimensional MRSI to the order of minutes [1]. However subjects such as the patients with Parkinson disease or children can not hold still even if the acquisition can be finished in several minutes. Radial acquisition is known to be less sensitive to the motion artifacts compared with the regular Cartesian sampling scheme, where the motion artifacts presented as blurring is particularly suitable for low resolution images such as MRSI [2]. In this preliminary report, a radial PEPSI (rPEPSI) sequence [3] is implemented and compared with the regular PEPSI.

Methods

All experiments were performed on healthy subjects at a 3T MR system (Trio, Siemens Medical Solutions, Erlangen, Germany) using a circularly polarized head coil. rPEPSI data were collected in the range $0 \le \phi < \pi$ with 36 views and 5º for each step. The imaging parameters are TE/TR = 30/2000 ms, readout point = 32, FOV = 240mm, slice thickness= 20mm, NEX = 8. Complete 8-slice outer volume suppression was applied along the perimeter of the brain to reduce lipid signal contamination. For comparison regular PEPSI data using Cartesian scheme were collected at the same slice with identical imaging parameters (32x32 matrix size). rPEPSI is first re-sampled into Cartesian grid using Kaiser-Bessel kernel [4]. Then even- and odd-echo of PEPSI and rPEPSI data were reconstructed separately using a non-water suppressed reference scan for automatic phasing and frequency shift correction [1]. After reconstruction, all the spectra were quantified with LCModel [5]. Metabolites concentrations of N-acetyl-aspartate (NAA), Creatine (CRE), Choline (CHO) and myo-Inositol (mI) were obtained using water scaling method.

Results and Discussion

Qualitatively, spectra and metabolite maps quantified from rPEPSI and PEPSI are comparable (Figure 1 and Figure 2). We did not observe significant artifact caused by the radial reconstruction on the metabolite maps. Quantitatively the averaged concentrations of rPEPSI and PEPSI over the slice are at similar level, which is in good agreement with values reported previously [6]. LCModel quantified fitting errors (CRLBs) are lower than 6% for NAA, CRE and CHO and 18% for mI for both rPEPSI and PEPSI, which indicate acceptable spectral fitting (< 20%) as suggested by the LCModel software package [5]. In this preliminary report, we demonstrate the feasibility to combine radial acquisition and PEPSI technique. The inherent capability for motion correction using radial trajectory and issues such as point spread function resulting from non-uniform sampling and selection of rotation angle and number of views is under further investigation.

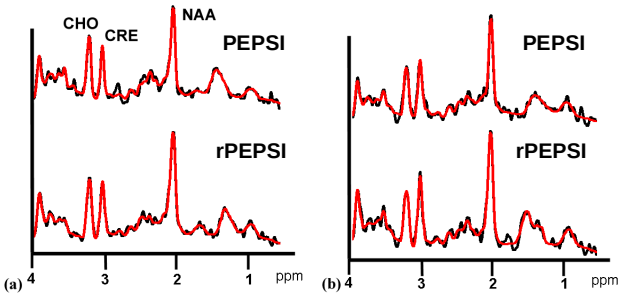

Figure 1

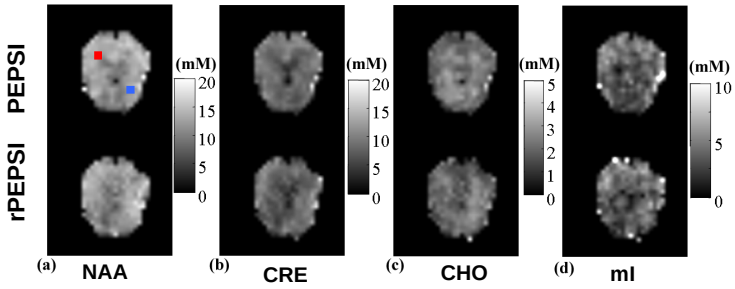

Figure 2

Figure 1. The representative spectra from 2 voxels of 2 acquisition methods. Voxel locations were marked in figure 2 as red (a) and blue (b). Both PEPSI and rEPPSI show well resolved major metabolite peaks

Figure 2. Metabolite concentration maps of (a) NAA (b) CRE (c) CHO and (d) mI from regular PEPSI and rPEPSI

Conc.(mM)	NAA	CRE	CHO	mI
PEPSI	12.67±1.88	8.65±1.38	2.40±0.46	3.90±1.39
rPEPSI	12.06±2.24	8.14±1.73	2.15±0.49	4.07±1.46
CRLB (%)	NAA	CRE	CHO	mI
PEPSI	5.01±1.70	4.97±0.89	5.90±1.53	17.73±8.09
rPEPSI	4.89±2.01	4.77±0.94	5.86±1.84	15.16±7.05

Table 1

Table 1. List of whole brain averaged concentrations and CRLBs

Acknowledgement The authors thank 3T MRI lab in NTUH for technical support

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