Proton Echo Planar Spectroscopic Imaging (PEPSI) on liver with parallel imaging

Chun-Tsun Shih[1], Yi-Ru Lin[1], Chih-Ping Liao[1], Bo-Rong Huang[1], and Shang-Yueh Tsai[2,3]

[1]*Department of Electronic and Computer Engineering, National Taiwan University of Science and Technology, Taipei, Taiwan,* [2]*Graduate Institute of Applied Physics, National Chengchi University, Taipei, Taiwan,* [3]*Research Center for Mind, Brain and Learning, National Chengchi University, Taipei, Taiwan*

Introduction

Magnetic Resonance Spectroscopy (MRS) is known to be the most accurate method for the quantification of lipid contents [1]. Previously, we have shown that, proton echo planar spectroscopic imaging (PEPSI) [2], a fast magnetic resonance spectroscopic imaging (MRSI) technique, is able to acquire the spatial distribution of liver fat content (HFC) in single breath hold. As the major concern is the single acquisition time, PEPSI was acquired using 16x32 matrix size, in which the acquisition time is 18 seconds. [3]. For the purpose to further extend the spatial resolution to 32x32 or to decrease the breath hold period for better capability in clinical studies, reduction of single acquisition time for PEPSI is therefore needed. In this study, we combine the PEPSI and parallel imaging methods to reduce the single acquisition time of PEPSI data. Generalized Autocalibrating Partially Parallel Acquisitions (GRAPPA) [4] was enrolled to accelerate PEPSI acquisition. The performance on the quantification of HFC with and without parallel reconstruction is investigated.

Method

PEPSI was performed on a 3 T MR system (Tim, Trio, SIEMENS Medical Solutions, Erlangen, Germany). An abdominal surface array coil along with spine array coil were used to wrap the abdomen region circularly, four coils were selected to cover the whole liver region. Before PEPSI scan, T1-weighted images were acquired for anatomic localization. PEPSI data were acquired from an axial slice without water suppression. Two PEPSI data sets, one with 16x32 matrix size and another with 32x32 matrix size, were acquired with following experiment parameters , FOV=300x400 mm^2, slice thickness = 15 mm, TR=1000ms, and TE=15ms, samplepoint=512. Subject was instructed to hold breath during the period of scan. PEPSI for each resolution were repeated 4 times to observe the reproducibility. Regular reconstruction process was carried out for PEPSI data as described in previous report [2]. GRAPPA accelerated PEPSI data were acquired by decimating k-space data along the phase encoding direction to achieve 2.0-fold accelerations. The GRAPPA weighting coefficients were estimated from fully phase encoded data from individual coil element using Auto-Calibration Signal (ACS) lines. For PEPSI with 16x32 matrix size, we used 4 and 8 ACS lines for the reconstruction of accelerated PEPSI data. For PEPSI with 32x32 matrix size, we used 4, 8 and 16 ACS lines for the reconstruction of accelerated PEPSI data. The standard GRAPPA reconstruction algorithm was implemented to reconstruct the individual aliased spectral images. After GRAPPA reconstruction, lipid peaks at 0.9, 1.3, and 2.0 ppm were quantified using LCModel and HFC was calculated as ratio between lipid content to water content. To compare the performance of GRAPPA reconstruction, root-mean–square (RMS) errors of spectra were calculate between full-sampled PEPSI data and accelerated PEPSI data reconstructed by GRAPPA with different ACS lines. RMS errors were estimated in spectral range of water peak and spectral range of lipid peak. Region of liver were manually selected on the T1 images. To exclude the influence of subcutaneous fat, ROI is chosen to be smaller than boundary of liver.

Result and Discussion

RMS errors were shown in Table 1. As expect, the RMS errors are smaller with increasing ACS line. We can also observe the same tendency on the RMS errors maps (Figure 1 and Figure 2). The RMS errors can be lower to 1.22% for lipid and 2.8% for water for two PEPSI data sets. Representative spectra were selected on 16x32 PEPSI data set (figure 3) and on 32x32 PEPSI data set (Figure 4). Obviously, more ACS lines help in the reconstruction of PEPSI data, yielding superior similarity to the full-sampled spectra. Figure 5 shows the LCModel quantified HFC maps for two PEPSI data sets and the HFC over liver region are summarized in Table 2. The HFCs are 4.91% and 4.92% for 16x32 and 32x32 full-sample data sets. With 8 ACS lines the HFC difference is around 0.38% for 16x32 PEPSI data. With 16 ACS lines, the HFC difference is around 0.19%. The spatial variation of quantified HFC is smaller with more ACS involved in the GRAPPA reconstruction, which is in accordance with previous reports [5]. According to the RMS errors and HFC difference, 16x32 PEPSI with 8 ACS lines are superior in the accuracy for quantification of HFC in lipid region than 32x32 PEPSI using 16 ACS lines. This is reasonable because 16x32 in theory has higher SNR due to larger voxel size.

In conclusion, 2-fold acceleration using GRAPPA reconstruction is feasible to reduce scan time in both 16x32 and 32x32 PEPSI data. With most ACS lines used in the GRAPPA reconstruction, there will be less than 0.38% HFC difference. With the improvement done in this study, compared with 18 seconds of 16x32 matrix size PEPSI scan proposed in the past, the acquisition time can be further reduce to 10 seconds and the spatial resolution can be increase to 32x32 with the same 18 seconds scan time.

References

1.AE Bohte, Eur Radiol, 2011, 21: 87-97

2.SM Mazhar, et al., Clin Gastroenterol Hepatol, 2008,7: 135-140

3.SR Chen, et al., ISMRM, 2011

4.Mark A. Griswold, et al., MR in Medicine, 2002, 47:1202-1210

5.Anagha Deshmane, MEng, et al.,Journal of MRI, 2012, 36:55-72

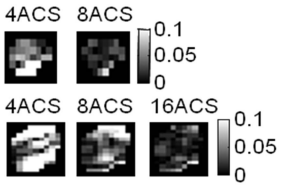

Figure 1

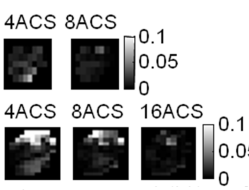

Figure 2

Figure 1 RMS errors in water range for 16x32 data set (Above) and 32x32 data set (below)

Figure 2 RMS errors in lipid range for 16x32 data set (Above) and 32x32 data set (below)

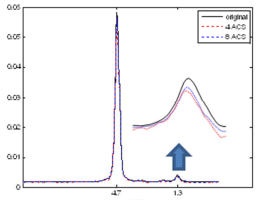

Figure 3 The curve of original and GRAPPA for 16x32

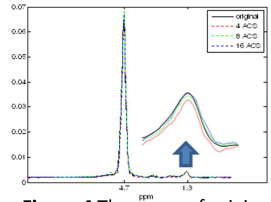

Figure 4 The curve of original and GRAPPA for 32x32

Matrix size	# of ACS line	RMS of water	RMS of lip
16x32	4	0.0876±0.07	0.0229±0.016
	8	0.0279±0.023	0.0122±0.004
32x32	4	0.1533±0.132	0.0758±0.052
	8	0.059±0.054	0.035±0.026
	16	0.0284±0.026	0.0121±0.013

Table 1 The averaged and standard deviation of RMS of difference between original and GRAPPA

Matrix size	# of ACS line	GRAPPA Lip %	Full-sampling Lip%
16x32	4	4.69±0.59	4.91±0.23
	8	4.53±0.44	
32x32	4	5.95±1.49	4.92±0.14
	8	5.34±0.98	
	16	5.11±0.52	

Table 2 The averaged and standard deviation of Fat% between original and GRAPPA

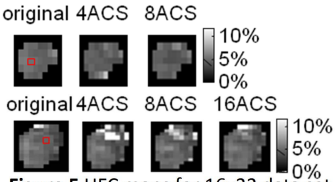

Figure 5 HFC maps for 16x32 data set (Above) and 32x32 data set (below)