Sensitivity Encoded Proton Echo Planar Spectroscopic Imaging (PEPSI) in Human Brain at 7 Tesla

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Introduction

Using parallel MRI, it is possible to reduce the long data acquisition time of MR spectroscopic imaging (MRSI) experiments at the cost of reduced SNR. Recently, we have demonstrated the feasibility of combining parallel imaging (SENSE, GRAPPA) and Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) at 3T and 4T to accelerate MRSI data acquisition [1-3]. The increase of the signal-to-noise ratio and the increase in spatial information of the RF coil sensitivity profiles with field strength [4,5] promise considerable gains in the performance of SENSE accelerated PEPSI at 7 T. In this study we demonstrate feasibility of 2-fold acceleration of SENSE-PEPSI at 7T in human brain using an 8-channel coil array.

Methods

Measurements were performed on a metabolite phantom and on healthy subjects using a 7 T scanner (Siemens Medical Solution, Erlangen, Germany) equipped with a home-made 8-channel head array coil and head gradient insert (80 mT/m, 600 mT/m/ms slew rate). In vivo PEPSI data were collected using TR: 2s, TE: 30 ms, pixel size: 5.6 mm, image matrix: 32x32, voxel size: 0.63 cc, acquisition time 8.5 min using 8 averages. The reconstructed spectral width after even-odd echo editing was 1560 Hz (5.2 ppm) with 2.6 Hz digital spectral resolution using a 320 us trapezoidal readout gradient. Complete 8-slice outer volume suppression was applied along the perimeter of the brain. For comparison, measurements with 8-channel array coils of similar design were performed at 3 and 4 T. Even- and odd-echo data were reconstructed separately using a non-water suppressed reference scan for automatic phasing and frequency shift correction as described previously [1]. SENSE reconstructions were simulated by decimating k-space data along the phase encoding direction at 2.0, 3.0 and 4.0 acceleration rate. The coil sensitivity maps were estimated for each individual coil separately using the non-water suppressed reference scan. Standard SENSE reconstruction algorithm [6] was implemented to unfold the individual aliased spectral images in one spatial dimension at 2.0, 3.0 and 4.0 fold accelerations. Lipid deconvolution using k-space extrapolation and the Papoulis-Gerchberg algorithm [7] was used for 7 Tesla data to reduce contamination from peripheral lipids. Metabolite maps were obtained with LCModel fitting of 15 model spectra. Cramer-Rao-Lower bounds (CRLB) for NAA, cho, cr, glu and ino were averaged across the slice.

Results

Phantom experiments demonstrate consistent SENSE reconstruction performance for up to 4-fold acceleration at 7 T (**Fig.1**) with average g-factors of 3.1 (SD: 2.6), in contrast to results at 3 and 4 T that show increasing degradation of reconstruction performance at 4-fold acceleration with much increased g-factors. In vivo data acquired at 7 Tesla showed show excellent spectral resolution and nearly linear increase in the signal-to-noise-ratio (SNR) of NAA as compared to 1.5, 3 and 4 T [4], but reduced sensitivity in peripheral areas due to increased B1-inhomogeneity (**Figs.2,3**). 2-fold acceleration of in vivo metabolite maps was feasible with only minor degradation of the metabolite maps (**Fig.4**). The SNR of NAA in central brain regions at 7 T without acceleration was 25 $cm^{-3}min^{-1/2}$. Mean CRLBs increased more than 50 % with 2-fold acceleration. SENSE reconstruction was mostly limited by unfolding errors due to residual lipid signals from peripheral regions, which are more difficult to suppress at high field due to increased B1-inhomogeneity and which are predominantly encoded in high k-space regions that are susceptible to SENSE unfolding errors.

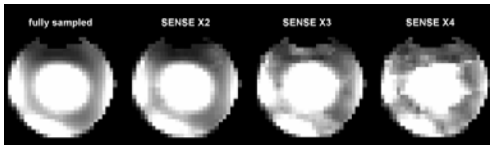

Fig.1 Non-water-suppressed PEPSI maps on phantom at 7 T show good reconstruction performance for up to 4-fold acceleration

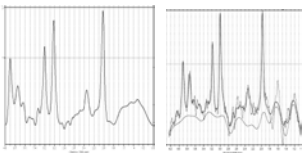

Fig.2 Un-accelerated (L) and 2-fold accelerated (R) in vivo spectra from central gray matter with clearly demarcated glutamate peak and LCmodel fit.

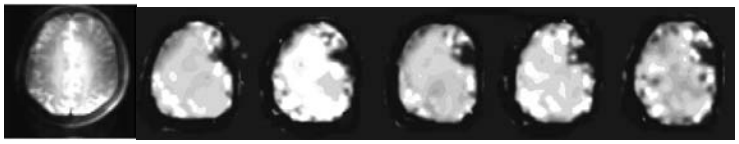

Fig.3 Fully sampled PEPSI maps of non-suppressed water (64x64 matrix) and metabolite maps of NAA, creatine, choline, glutamate and inositol (32x32 matrix), acquired in 8.5 min with 0.63 cc voxel size.

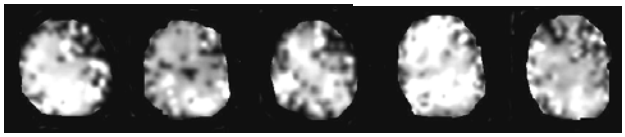

Fig.4 Corresponding PEPSI metabolite maps of NAA, creatine, choline, glutamate and inositol (32x32 matrix) with 2-fold SENSE acceleration.

Discussion

These preliminary data demonstrate feasibility of accelerating short TE high-speed spectroscopic imaging at 7 T using the SENSE methodology. The high SNR and improved multiplet resolution at this field strength in combination with the 32-channel RF system that is currently under development will enable 2D metabolite mapping in just a few seconds and 3D encoding in just a minute. The advantages of this leap in imaging technology include much reduced motion sensitivity and increased patient comfort. However, limitations in RF pulse performance and RF inhomogeneity at high field need to overcome to develop a clinically robust high-speed MRSI technique. Recent advances in SENSE reconstruction using prior information [8] will be adapted for SENSE-PEPSI to further stabilize reconstruction performance.

Acknowledgements

Supported by NIDA 1 R01 DA14178-0, NIH R01 HD040712, NIH R01 NS037462, NIH P41 RR14075 and MIND Institute.

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