Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) on the Human Brain Using a 32-channel Coil Array and GRAPPA reconstructions at 3T

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Introduction

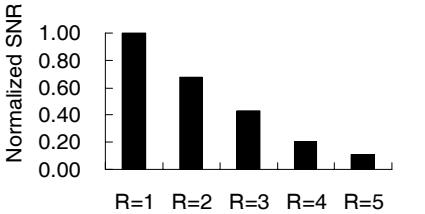
The combination of fast spatiospectral encoding using Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) [1] and parallel imaging with an RF coil array [2] has been demonstrated to achieve accelerated MR spectroscopic (MRSI) data acquisition at the cost of reduced SNR. Here we reported an *in vivo* experiment utilizing the 32-channel head RF coil array at 3T to investigate the feasibility of up to 4-fold GRAPPA acceleration along the phase encoding direction in single-average PEPSI experiment. The intrinsic SNR improvement at higher field and better coil geometry are used to shorten the 2D MRSI data acquisition time to 16 seconds with satisfactory spectral quality.

Methods

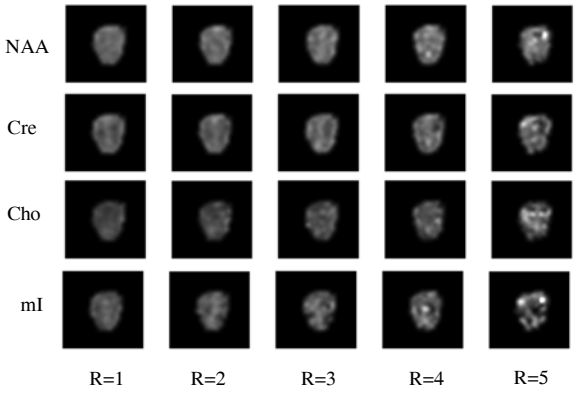
Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) [1] was performed on a phantom and healthy volunteers using a 3 T scanner (Tim Trio, SIEMENS Medical Solutions, Erlangen, Germany). The 32-channel array was tiled from circular coils of 8.5 cm and 6 cm diameter using the combination of hexagonal and pentagonal symmetry with overlapping between nearest neighbors to minimize mutual inductance [3]. Our previous study showed that, compared to traditional head coils, significant 3- to 6-fold gains in SNR were obtained in the array, particularly in the cerebral cortex [3]. PEPSI data were acquired from a para-axial slice at the upper edge of the ventricles with TR 2 s and short TE (15 ms), using a 32x32 image matrix. Complete 8-slice outer volume suppression was applied along the perimeter of the brain to suppress lipid signal. Even- and odd-echo data were reconstructed separately using a non-water suppressed reference scan for automatic phasing and frequency shift correction [1]. The total scan time was 64 second for a fully phase encoded 2D MRSI data set. GRAPPA accelerated water-suppressed PEPSI data were acquired by decimating k-space data along the phase encoding direction to achieve 2.0-, 3.0-, 4.0- and 5.0-fold accelerations with imaging time of 32, 22, 16, and 12 seconds, respectively. The GRAPPA weighting coefficients were estimated from fully phase encoded non-water suppressed (NWS) data from individual coil element. The standard GRAPPA reconstruction algorithm [2] was implemented to reconstruct the individual aliased spectral images. After GRAPPA reconstruction, metabolites of N-acetyl-aspartate(NAA), Creatine(Cre), Choline(Cho) and myo-Inositol(mI) were quantified using LCModel fitting [4]. Cramer-Rao Lower Bounds (CRLB) from LCModel were employed to compare the performance for the different accelerations.

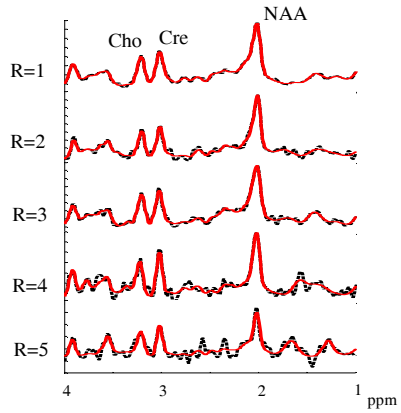
Results

GRAPPA reconstruction metabolites maps were successful at 2-,3-, and 4-fold accelerations. We observed homogeneous metabolite concentrations in the brain parenchyma. Spectra at 2- and 3-fold accelerations were virtually identical the full-sampled spectra with similar spectral widths and shapes. Increased noise level was found at 4-fold acceleration but three major metabolite peaks can be still identified. At 5-fold acceleration, quantification of metabolic peaks was limited by increased noise level. Quantitatively, CRLBs also showed Good reconstructed spectra up to 4-fold acceleration were in agreement with the finding in the phantom data. Significant SNR loss at 5-fold acceleration indicated the limitation of the array. The quantification of mI is limited to 2-fold acceleration, due to the lower intensity of the mI multiplet pattern..



	R=1	R=2	R=3	R=4	R=5
NAA	5.6	7.5	8.1	10.7	17.1
CRE	4.9	6.5	7.7	10.0	15.5
CHO	5.2	7.0	8.1	16.1	18.2
mI	7.5	12.0	15.7	20.0	47.6





Left Upper: Normalized SNR of phantom NAA spectra. Better coil geometry of 32 channel coils over 23 channel coils reduce the SNR loss due to geometry factor at higher acceleration. **Middle**: LCModel quantified metabolite concentration maps of NAA, CRE, Cho and mI from full-sampled PEPSI data and 2-, 3-, 4-, and 5-fold accelerated GRAPPA reconstructions. **Right**: The representative spectra. Fully sampled and 2-, 3-, 4-fold accelerated data show well resolved major metabolite peaks, while a lower SNR at 5-fold acceleration reduces the resolvability of metabolite peaks. **Left Lower:** List of whole brain averaged CRLBs. The CRLBs increase as the acceleration rate.

Discussion

This work demonstrates that the increase in spatial information of coil elements and the increase in the SNR with the 32-channel array can further accelerate a single-average PEPSI with acceptable reconstructed images and spectra. This increase in the temporal resolution enables observation of transient metabolic responses during physiological challenges, and reduces motion artifacts in studies on patients who can't hold still during experiments. The application of parallel imaging is particularly important in reducing the long scan time of 3D MRSI experiments. Further acceleration may be achieved using a 2-dimensional acceleration in 3D PEPSI experiments. The limit of acceleration using parallel MRI is naturally upper-bounded by the ultimate intrinsic SNR [5,6]. However, in this 3T 32-channel study, the results indicate that we are still below such a limit using 4-fold acceleration. In addition, further improvement of GRAPPA reconstruction can be achieved by using regularization[7] or optimal kernel estimation[8] to reduce the noise amplification during reconstruction.

Acknowledgements

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References

[1]. Posse, S., et al., Magn Reson Med, 1995. 33: 34-40 [2]. Griswold, M.A., et al., Magn Reson Med, 2002, 47: 1002-10 [3]. Wiggins, G.C., et al. Magn Reson Med, 2006. 56: 22-26 [4]. Provencher, S.W., et al., Magn Reson Med, 1993, 30: 672-79 [5]. Ohliger, M. A., et al. Magn Reson Med, 2003. 50: 1018-1030 [6]. Wiesinger, F., et al., Magn Reson Med, 2004, 52: 376-390. [7]. Lin, F.H., ISMRM, 2006, p3656. [8] Rueckert, M., et al., ISMRM, 2006, p296