Single-shot proton MR spectroscopic inverse imaging

F-H. Lin[1,2], S-Y. Tsai[3], Y-R. Lin[4], R. Otazo[5], G. Wiggins[1], L. Wald[1], J. Belliveau[1], and S. Posse[6,7]

[1]A. A. Martinos Center, Massachusetts General Hospital, Charlestown, MA, United States, [2]Institute of Biomedical Engineering, National Taiwan University, Taipei, Taiwan, [3]Graduate Institute of Biomedical Electronics and Bioinformatics, National Taiwan University, Taipei, Taiwan, [4]Department of Electronic Engineering, National Taiwan University of Science and Technology, Taipei, Taiwan, [5]Electrical and Computer Engineering Department, Univesity of New Mexico, Albuquerque, NM, United States, [6]Department of Psychiatry, Univesity of New Mexico, Albuquerque, NM, United States, [7]Department of Electrical and Computer Engineering, Department of Physics and Astronomy, Univesity of New Mexico, Albuquerque, NM, United States

INTRODUCTION

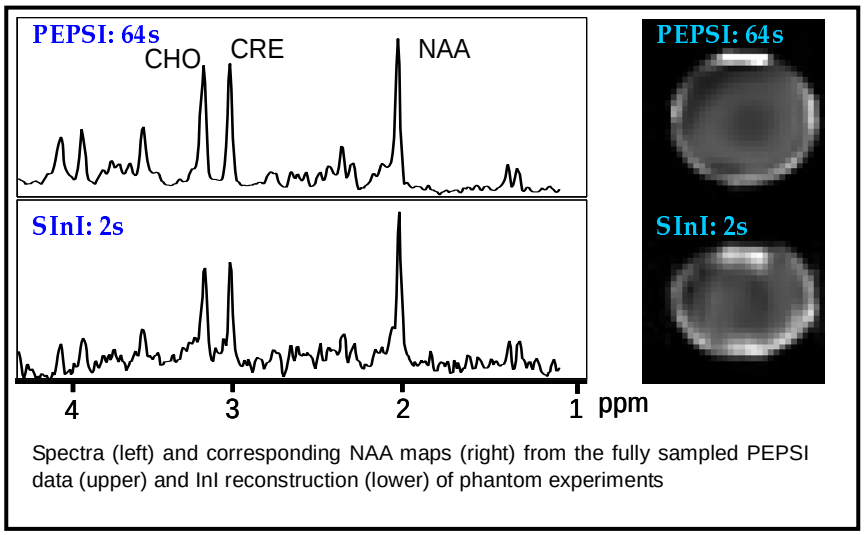
Fast MR spectroscopic imaging can be achieved using EPI [1] or spiral readouts [2]. However, a significant proportion of the acquisition time was spent on the spatial encoding using k-space traversal. Magnetic resonance Inverse Imaging (InI) uses a highly parallel radio-frequency coil array to obtain spatial information by solving an inverse problem in image reconstruction in order to reduce the reliance on the spatial encoding using gradient switching [3]. Previously, we have demonstrated that InI can be applied to dynamic functional imaging of human brain to achieve 3D whole-brain coverage and 100 ms temporal resolution. We propose here MR spectroscopic inverse imaging (SInI) using InI and proton-echo-planar-spectroscopic-imaging (PEPSI) to achieve more than an order-of-magnitude acceleration of MRSI acquisition. Our preliminary 2D MRSI results showed that InI offers sufficient sensitivity to detect N-Acetyl-Acetate (NAA), creatiine (Cre), and choline (Cho) cerebral metabolites using a 32-channel coil array at 3T.

METHODS

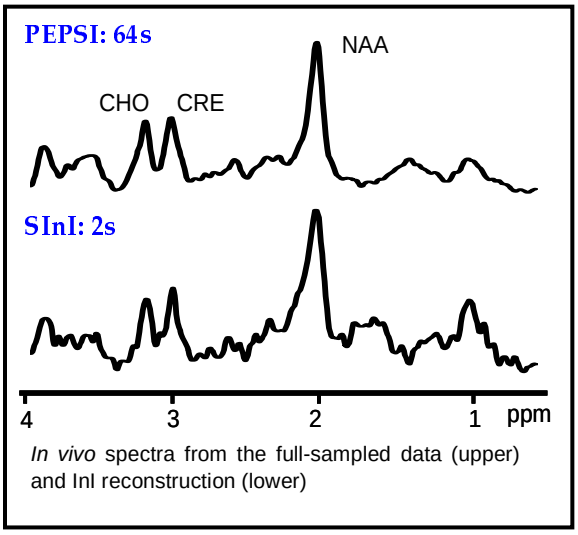
PEPSI [1] was performed on a phantom and healthy volunteers using a 3 T scanner (Tim Trio, SIEMENS Medical Solutions, Erlangen, Germany) and a 32-channel array [4]. PEPSI data were acquired from a para-axial slice at the upper edge of the ventricles with TR 2 s and short TE (15 ms), using a 32x32 image 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. SInI accelerated water-suppressed PEPSI data were simulated by decimating k-space data along the spatial phase encoding direction to keep only the center line, which amounts to 2 s acquisition time. The reference scan (forward solution) required for InI reconstruction were estimated from the water peak of the fully phase encoded non-water suppressed (NWS) data from individual coil element. We used the minimum-norm estimate (MNE) reconstruction algorithm [3] to reconstruct aliased spectral images.

RESULTS

Reconstructed fully sampled PEPSI and SInI phantom data were shown at the left panel. Well discernible NAA, Cre, and Cho peaks with similar shapes and amplitudes were observed in both PEPSI and SInI reconstructions. Spectral projections images were also similar. In vivo results from a single subject were shown at the right panel. Spectra from a selected white matter voxels show NAA, Cre, and Cho metabolite peaks in PEPSI and SInI. Essentially, these results suggest the feasibility of single-shot highly accelerated SInI (32X acceleration compared to fully phase encoding PEPSI).



Spectra (left) and corresponding NAA maps (right) from the fully sampled PEPSI data (upper) and InI reconstruction (lower) of phantom experiments



In vivo spectra from the full-sampled data (upper) and InI reconstruction (lower)

DISCUSSIONS

Single-shot MRSI technique is appealing for hyperpolarized studies with transient high SNR [5], MRSI with moving organs, and diffusion weighted MRSI [6]. This work demonstrates the feasibility of 2D SInI with single-shot RF excitation to detect NAA, Cre, and Cho in 2 seconds. EPI read-out offers spectroscopic and 1D spatial information, while the spatial information in the other dimension was derived from solving an inverse problem using different channels of the coil array. Different from other single-shot MRSI, SInI has high spectral resolution like fully phase-encoded MRSI. To mitigate the limited SNR in MRSI, traditionally a larger image voxel (~1 c.c. and above) is used in the acquisition. This intrinsically relatively low spatial resolution (compared to anatomical or functional studies) supports the choice of MNE as the inverse solution in InI. MNE tends to provide spatially smooth estimates because of the imposed minimal L-2 norm constraint. Regularization embedded in MNE can potentially affect the reconstructed spectra quality and further investigation is on the way. Potentially we can replace MNE with other inverse solutions. In the future we attempt to extend MR SInI for 3D spatial coverage, dynamic imaging on metabolite concentration, and accelerated J-coupled metabolite mappings with phase cycling.

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