# High Spatial Resolution Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) in Human Brain at 3 Tesla using 32-Channel RF Coil Array

**A. E. Yoshimoto[1], A. van der Kouwe[2], A. Caprihan[3], F-H. Lin[2], L. L. Wald[2], and S. Posse[4]**

[1]Electrical and Computer Engineering, U. New Mexico, Albuquerque, NM, United States, [2]MGH-HMS-MIT Athinoula A. Martinos Center for Biomedical Imaging, Charlestown, MA, United States, [3]The MIND Research Network, Albuquerque, NM, United States, [4]Neurology, U. New Mexico, Albuquerque, NM, United States

## Introduction

The feasibility of measuring metabolites in human brain with a spatial resolution high enough to delineate anatomical structures has been an elusive goal in clinical MRSI. Low spatial resolution makes MRSI sensitive to errors in partial volume correction as a result of errors in image segmentation [1]. Increasing spatial resolution at the expense of SNR has the potential to significantly improve quantification of metabolite concentration in gray matter [2] and to reduce spectral contamination from peripheral lipid resonances. It also reduces the effects of magnetic field inhomogeneity [3]. The introduction of clinical high field MR scanners, recent advances in large-scale head array RF coils and the development of short TE high-speed MRSI provide the sensitivity increase necessary for improving spatial resolution in MRSI. Here we demonstrate the feasibility of mapping J-coupled metabolites in human brain, including lateral cortex, with 4.5 mm spatial resolution using short TE Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) [4].

## Methods

Data in 3 healthy volunteers were obtained on a 3 T TIM Trio scanner (Siemens Medical Solutions, Inc.) equipped with 32 channel Siemens head array RF coil and Avanto gradient system. High resolution multi-slice T2-weighted turbo spin-echo data were obtained for placement of the outer volume saturation bands and for spatial coregistration. Water suppressed data (WS) were acquired from a supraventricular axial slice using the PEPSI sequence with 8-slice outer volume suppression along the perimeter of the brain [4] (TR: 2 s, TE: 15 ms, spatial matrix: 64x64, FOV: 286x286 $mm^2$, slice thickness: 15 mm, spectral width after even/odd echo sorting: 1087 Hz, digital spectral resolution 1 Hz, number of averages: 16, acquisition time: 34 min). Data were reconstructed as described previously [4] using only very mild spatial apodization (Fermi filter: R= 0.9, D=0.1) to preserve spatial resolution. Constrained spectral fitting in reference to a non-WS (NWS) scan was performed using LCModel 6.2-0R with simulated basis sets of 16 metabolites [4]. Correction for relaxation attenuation and partial-volume effects was performed using tissue segmentation of $T_1$-weighted Magnetization Prepared Rapid Gradient Echo (MP-RAGE) scans with SPM5.

## Results

Excellent spectral quality (Figs.1&2) with narrow line width (slice mean: 0.046 +/- 0.024 ppm) and adequate SNR (slice mean: 7.5 +/- 1.6) was obtained throughout the entire PEPSI slice with only minor lipid contamination, Quantification of 5 metabolites (Ino, Cho, Cr+PCr, Glu+Gln, NAA+NAAG) was possible with mean Cramer Rao lower bounds (CRLBs) less than 30 % and 5 metabolite resonances, including Macromolecules, were quantified with mean CRLBs less than 40 %. The concentration values of the metabolites (table 1) were in the ranges reported in our previous studies using 1 cc voxel size [4]. Considerable anatomical detail is visible in metabolite maps, including cortical structures that are seen as signal voids in Cho images and high intensity areas in Glu+Gln images. Relaxation and partial-volume correction increase gray/white matter contrast.

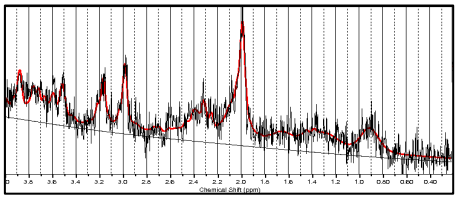

**Fig.1**:Selected central gray matter spectrum with overlaid LCModel fit (red).

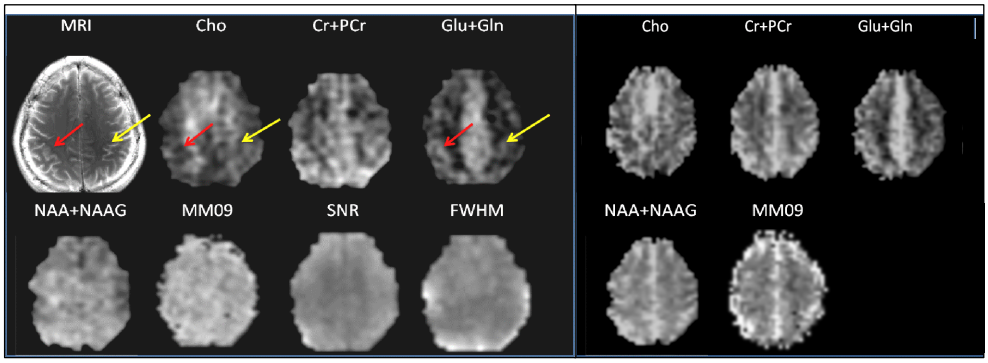


**Fig.2**: TSE-MRI scan (averaged across the 15 mm PEPSI slice) and metabolic images of mI, Cho, Cr+PCr, Glu+Gln, NAA+NAAG and macromolecules at 0.9 ppm (MM09) measured with 0.25 cc spatial resolution, (left) before and (right) after partial volume and relaxation correction. Cho, Cr+PCr and Glu+Gln maps show strong GM/WM contrast and considerable anatomical detail, including sulcal structure (see red and yellow arrows).

**Table 1**: Spectral quantification with relaxation and partial volume correction (slice average)

| | Ins | Cho | Cr+PCr | Glu+Gln | NAA+NAAG |
|---|---|---|---|---|---|
| Conc. [mmol] | 4.69 (4.04) | 1.39 (1.15) | 6.56 (2.65) | 10.44 (6.00) | 10.33 (3.10) |
| CRLB [%] | 25.57 (11.96) | 13.5 (4.52) | 7.28 (1.49) | 14.6 (6.61) | 5.57 (0.91) |

**Discussion** The Fast High Spatial Resolution MRS provides detailed information of the metabolites concentration and it also can provide the compartments distribution inside the brain with a short acquisition time in comparison with lower resolution studies. With further refinement in spectral modeling to improve the depiction of GM/WM metabolite differences we expect that these data can be acquired in 16 minutes, which is a clinically acceptable measurement time. We anticipate that high spatial resolution short TE MRSI will improve quantification of metabolic abnormalities in cortical Multiple Sclerosis lesions, facilitate characterization of metabolic correlates of Glutamatergic excitotoxicity in cortical regions of Schizophrenic patients, and increase acceptance of MRSI by radiologists.

**References**: [1] Gasparovic C et al. Magn Reson Med 2006, Jun;55(6):1219-26, [2] Noworoloski S et al. Magn Reson Med 1999;41: 21-29 [3] Ebel A et al. Magn Reson Imag 2002;21: 113-120 [4] Posse S et al. Magn Reson Med 2007;58: 236-244 [5] Hetherington HP et al. Magn Reson Med 1996;36: 21-29. *Supported by the MIND Research Network.*