

# 3D High Spatial Resolution Short TE Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) at 3T in Clinically Feasible Measurement Times

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## INTRODUCTION

The development of 3D short TE MRSI has been an elusive target due to lipid contamination as a result of low spatial resolution and long acquisition times [1]. However, recent advances in high-field MR scanner technology, head array RF coils and short-TE high-speed MRSI techniques led to considerable sensitivity enhancements and improvement in spectral quality. In this multi-center study we present initial results of 3D Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) at short-TE (11 ms) in healthy subjects with measurement times as short as 7 min and a spatial resolution as small as 0.14 cc. The purpose of this study is to demonstrate improved quantification of metabolite concentrations, especially in gray matter [2], using high spatial resolution to reduce contamination from peripheral lipid resonances and to minimize the effects of magnetic field inhomogeneity, enabling the visualization of cortical brain structures in metabolite maps.

## METHOD.

Data from 7 healthy volunteers were obtained on 3T TIM Trio scanners (Siemens Medical Solutions, Inc.) at VB15 equipped with 8, 12 and 32 channel Siemens head array RF coils and Avanto gradient system located at the 7 partnering MRI research centers. Water suppressed data (WS) were acquired from the slab location shown in Fig.1 using a 3D PEPSI sequence with 8 slices, outer volume suppression along the perimeter of the brain [4] and circular k-space sampling (TR: 2 s, TE: 11 ms, spatial matrix: 32x32x8 or 64x64x8, voxel size ranging from 0.14 to 0.34 cc, spectral width after even/odd echo sorting: 1087 Hz, digital spectral resolution 1 or 2 Hz, acquisition time ranging from 4:40 to 11 min). Data reconstruction with even/odd echo sorting, echo summation and hamming spatial filtering (100% window) was implemented in the Integrated Computing Environment (ICE, Siemens Medical Solutions). Offline spectral analysis using an automated pipeline was performed in reference to a non-WS (NWS) scan using LCMoDel with simulated basis sets of 18 metabolites [4] and partial volume and relaxation correction based on segmented MPRAGE scans.

## RESULTS

Metabolite maps of 5 selected metabolites in 4 slices within the volume of interest (VOI) present consistent spectral quality within the VOI with narrow line width (FWHM < 0.1 ppm) and SNR > 4 for all the voxel sizes (Fig.1, Table 1). Excellent spectral fits were obtained throughout the entire 3D PEPSI slab with only minor lipid contamination. Metabolite ratio quantification of 4 metabolites (Ins, NAA/G, Glx and Cho) and 2 macromolecules (MM09 and MM20) in comparison with Cr+PCr was possible with CRLB of less than 20% (table 1) for voxel sizes of more than 0.2 cc. and less than 30% for voxel sizes of less than 0.15 cc. The concentration ratios were in the ranges reported by previous studies [1, 4]. Anatomical structure, such as sulci in lateral cortex, are visible in the Glu+Gln maps.

## DISCUSSION AND CONCLUSION

The short acquisition times of less than 10 min and the feasibility of mapping both singlet and multiplet resonances with maximum sensitivity makes this methodology attractive for clinical studies. Absolute quantification of metabolite concentrations in different tissue compartments in reference to the NWS scan is in progress. Expansion of the MRSI VOI using automated placement of up to 16 OVS slices is being evaluated.

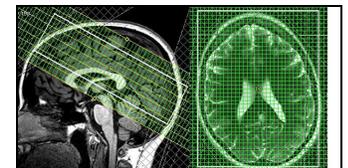


Fig. 1: MRSI localization.

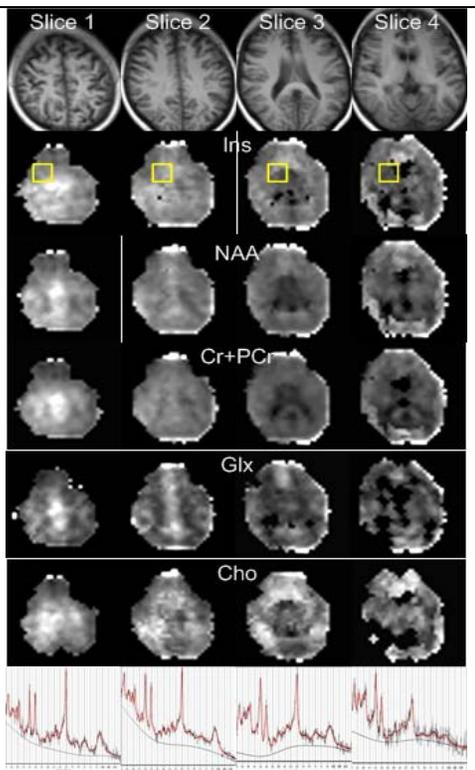


Fig.2: 3D PEPSI with 0.2 cc voxel size obtained in 11 min. Averaged high-resolution MRI, metabolite maps and example spectra (yellow box) of slices inside the VOI (slice 1, 2 and 3) and a slice at the edge of the VOI that shows chemical shift related attenuation of NAA (slice 4).

Table 1 (Volume Average)	Voxel size					
	4.47x4.47x6.88mm <sup>3</sup> (0.137 cc)		4.47x4.47x10 mm <sup>3</sup> (0.200 cc)		7.06x7.06x6.88 mm <sup>3</sup> (0.343 cc)	
	Metabolite/Cr+PCr	CRLB (%)	Metabolite/Cr+PCr	CRLB	Metabolite/Cr+PCr	CRLB
Ins	1.29±0.24	24.1±3.45	1.18±0.22	10.15±2.94	1.13±0.23	9.65±4.56
NAA/G	1.42±0.42	22.25±3.65	1.36±0.35	7.92±3.29	1.4±0.43	8.02±4.65
Cr+PCr	1±0	23.45±3.30	1±0	8.27±2.8	1±0	9.18±5.51
Glx	2.29±0.56	25.57±2.86	1.36±0.44	16.65±5.46	1.33±0.37	15.88±5.3
Cho	0.34±0.08	25.64±2.68	0.33±0.11	11.23±3.4	0.33±0.26	11.01±5.73
MM09	2.22±0.89	24.49±3.90	2.3±1.21	14.95±2.65	1.41±0.69	16.75±4.63
MM20	3.63±0.9	27.27±1.88	3.78±1.34	15.82±2.27	2.38±1	19.46±5.42
SNR	4.34±7.45		16.38±26.95		27.13±46.21	
FWHM	0.1±0.04 ppm		0.08±0.04 ppm		0.08±0.04 ppm	
	32 channel coil, 7 min		32 channel coil, 11 min		8 channel coil, 4:40 min	
	(Mean +/- SD).					

**References:**[1] Maudsley et al. Magn Reson Med 2009, Mar;61:548-559, [2] Noworolowski 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.