

# Accelerating TE-Averaged 2D Magnetic Resonance Spectroscopic Imaging Using Data-Sharing

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## Introduction

Glutamate (Glu) is one of the primary excitatory neurotransmitters of the central nervous system. However, on the <sup>1</sup>H MR spectrum Glu at 2.35 ppm is hard to identify because it is strongly overlapped with glutamine (Gln) and N-acetyl-aspartate (NAA). Previously Hurd et al. [1] has proposed a TE-averaged technique using single voxel spectroscopy, in which spectra acquired at TEs ranging from 35 to 185 ms are averaged to optimize the quantification of Glu. To maintain reasonable total measurement time, fast 2D MR spectroscopic imaging (MRSI) such as proton echo planar spectroscopic imaging (PEPSI) need to be used for data acquisition [2]. Last year we have shown that PEPSI [3] with radial acquisition (rPEPSI) provides comparable spectra with regular PEPSI [4]. In this preliminary study we further investigate the data-sharing property inherently in radial acquisition by varying the TE at each radial line (or view) in a single acquisition. The reconstructed spectra are expected to have similar TE-averaged property on the Glu resonance. This data-sharing radial PEPSI (dsrPEPSI) sequence can be used to further reduce the required scan time of TE-averaged technique.

## Methods

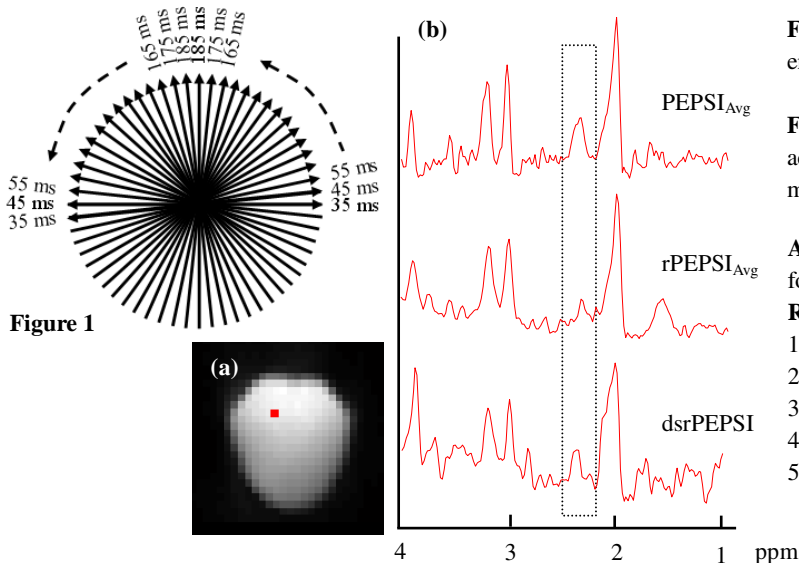
The experiments data were acquired on a 3T MR system (Trio, Siemens Medical Solutions, Erlangen, Germany) using a 8-channels array-coil. rPEPSI data were acquired with 16 different TEs ranging from 35 to 185 ms. rPEPSI data were collected in the range  $0 \leq \phi < \pi$  with 32 views and  $6^\circ$  for each step. The experiment parameters are TR = 1500 ms, readout point = 32, FOV = 240 mm, slice thickness = 20 mm, NEX = 1. Complete 8-slice outer volume suppression was applied along the perimeter of the brain to suppress the extra cranial signal especially lipid. For comparison, regular PEPSI data using Cartesian scheme at the same slice with identical experiment parameters (32x32 matrix size). dsrPEPSI were simulated using rPEPSI data at different TE by sequentially incorporating radial lines from different TE into one radial k-space. To minimize the difference between adjacent radial lines, the sequential order of TEs varies from 35 ms to 185 ms with 10 ms step in the first quarter cycle ( $0^\circ \sim 90^\circ$ ) and decrease from 185 ms to 35 ms in the latter quarter cycle ( $90^\circ \sim 180^\circ$ ). The complete diagram of dsrPEPSI is depicted in Figure 1. For the reconstruction rPEPSI and dsrPEPSI were first re-sampled into Cartesian grid using Kaiser-Bessel kernel [5]. Then even- and odd-echo of PEPSI, rPEPSI and dsrPEPSI data were reconstructed separately using same procedure described in the previous study [3]. Finally, for PEPSI and rPEPSI TE-averaged spectrum were acquired by averaging spectra at 16 different TEs.

## Results

Figure 2 shows the representative TE-averaged spectra from PEPSI (PEPSI<sub>Avg</sub>), rPEPSI (rPEPSI<sub>Avg</sub>), and dsrPEPSI. We can see that PEPSI and rPEPSI provided similar spectrum quality. Glutamate at 2.35 ppm can be clearly seen on both PEPSI<sub>Avg</sub> and rPEPSI<sub>Avg</sub>. Since dsrPEPSI is derived from single k-space data, on the other hand PEPSI<sub>Avg</sub> and rPEPSI<sub>Avg</sub> are averaged from 16 data; SNR in dsrPEPSI is relatively lower than PEPSI<sub>Avg</sub> or rPEPSI<sub>Avg</sub> as expected. Nevertheless Glu is still visible on the dsrPEPSI.

## Discussion

Although TE-averaged technique can easily detect glutamate resonance from the strongly overlapping [1], TE-averaged spectroscopic imaging is strictly limited for the lengthy acquisition time. Our study shows the feasibility to combine rPEPSI acquisition and TE-averaged technique to reduce the scan time from 13 min to 48 sec. SNR limitation for dsrPEPSI and quantification of metabolite maps will need further investigation.



**Figure 1.** Trajectories and the k-space of radial phase encoding line. Each k-space lines have different TEs.

**Figure 2.** (a) Non-water suppressed image using rPEPSI acquisition (b) The representative spectra of 4 acquisition methods. Voxel location was marked in figure (a) as red.

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## References

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