An Investigation of the Acceleration Factor in TE-averaged Data-Sharing Radial Proton Echo Planar Spectroscopic Imaging (dsrPEPSI)

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Introduction

TE-averaged technique is a general application to measure Glutamate (Glu) [1], one primary excitatory neurotransmitter of the central nervous system on the ^{1}H MR spectrum at 2.35 ppm. For obtaining TE-averaged MRSI data sets using multiple TEs was time consuming. Previous study had shown that radial proton echo planar spectroscopic imaging (rPEPSI) [2] and data-sharing radial PEPSI (dsrPEPSI) [3] were feasible to measure Glu, and the scan time could be reduced from 16 minutes to 1 minute by dsrPEPSI. However, the reduced scan time will decrease both SNR and spectrum quality. This study was conducted to investigate and optimize the spectral quality versus scan time.

Material and Methods

The experiment was performed at 3T MR system using 32-channels array head coil (Trio, Siemens Medical Solutions, Erlangen, Germany). rPEPSI were collected in the range of $0 \le \phi < \pi$ with 32 views and 5.7° rotation angle. The imaging parameters are TR = 2000ms, readout point = 32 with over-sampling, FOV = 224mm, slice thickness = 15mm, NEX = 1. Complete 8-slice outer volume suppression was applied along the border of brain to reduce the extra cranial signal especially lipid. For TE-averaging, data were acquired with rPEPSI and 16 different TEs ranging from 15ms to 165ms. dsrPEPSI were simulated from full-sampled rPEPSI. A equally distributed subset of K-space lines were chose from full-sampled data for each TE, and the information of empty K-space lines was covered by data from other TEs. Figure 1 shows the diagram of radial trajectory of a 4-fold dsrPEPSI. The reconstruction of rPEPSI and dsrPEPSI were re-sampled into Cartesian grid using Kaiser-Bessel kernel [4] following with spectra post processing.

Results and discussion

The result was showed in Figure2. Glu at 2.35 ppm can be clearly seen in the TE-averaged rPEPSI data. When the acceleration factor was small, such as 2-fold dsrPEPSI, there was no obvious difference between the accelerated spectrum and the original one. But when the acceleration factor exceeds 4, SNR lost will affect the visibility and quantization of Glu. The baseline drift also increased as the acceleration factor increased, which may be resulted from the extra cranial lipid signal. From our result, 4-fold dsrPEPSI is feasible to acquire Glu at a 3T system while maintaining spectral quality. And the scan time can be reduced to 4 minutes, which is a reasonable length for clinical use.

References

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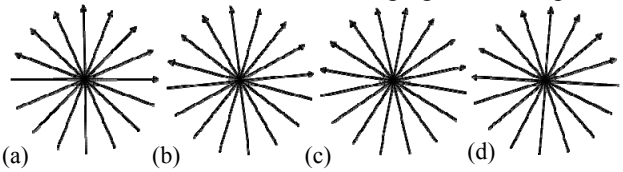

Figure 1. The K-space trajectory of dsrPEPSI for (a) TE=15ms, (b) TE=25ms, (c) TE=35ms, (d) TE=45ms and so on. For a 4-fold dsrPEPSI, 8 K-space lines were used for each TE, and the required total scan time is 4 minutes.

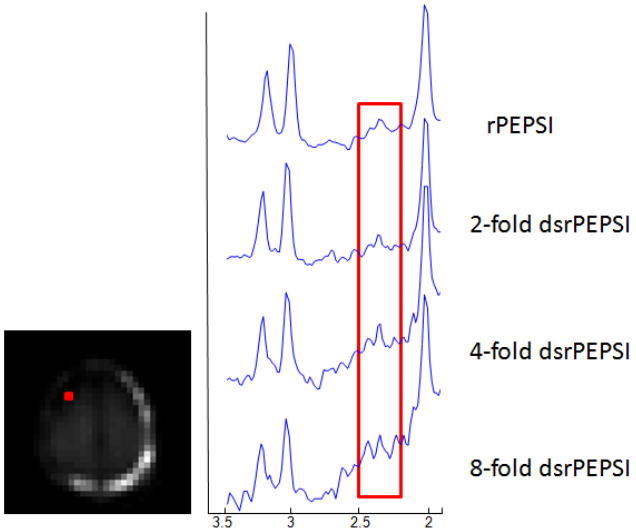

Figure 2. Comparison of spectrum of TE-average rPEPSI and dsrPEPSI