3D RINEPT {^{1}H}-^{31}P-CSI: A feasible approach for the study of membrane turnover in the human brain

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Introduction

Phosphomonoesters (PME) and Phosphodiesters (PDE) are intermediates of membrane phospholipid turnover and thus phosphorous MRS studies of the human brain gain in importance in many brain diseases that involve membrane defects. The application of multinuclear techniques known from high-resolution MR spectroscopy are constricted by the low S/N at field strengths available for clinical routine (3 T or less) which lead to long measurement times and / or low spatial resolution. In addition, broad macromolecular contributions underlying the PME and PDE resonances complicate the determination of metabolite concentrations. The large chemical shifts of most ^{31}P metabolites prohibit the application of slice selection pulses or single voxel techniqes. Here a 3D spherical k-space encoding ^{31}P-CSI sequence is presented which incorporates heteronuclear polarization transfer editing (RINEPT) [1]. RINEPT has been previously proposed for in vivo brain studies [2,3]. However, yet no spatial localization was obtained [2] or measurement times were extremely long [3].

Methods

All measurements were performed on a Siemens Magnetom Vision 1.5 T full-body clinical scanner with a double-tuned ^{1}H-^{31}P circularly polarized head coil [4] and a second independent transmit channel operating at the proton frequency. Signal enhancement and spectral editing of the phosphorous spectra is obtained through RINEPT [1]. Echo times were optimized with phantom measurements and numerical simulations to TE_1=40 ms and TE_2=32 ms [2]. 3D spatial localization is obtained by 0.9 ms long triangular phase encoding gradient pulses which are free from chemical shift displacement errors. Spherical (keyhole) encoding is used which reduces scan times particularly in 3D sequences. Two versions using 8 x 8 x 8 and 6 x 6 x 6 encoding were implemented. The encoding scheme incorporates warp sampling, i. e. the center of k-space is sampled first, which minimizes patient motion artefacts. The sequence can be combined with proton decoupling using a WALTZ-4 pulse train on the second channel. Reconstruction of the CSI data set is performed as a postprocessing step with a custom-made software on the MR console.

Results

The polarization transfer with RINEPT depends on the scalar coupling of protons and phosphorous nuclei. Therefore, all metabolite signals of non J-coupled ^{31}P nuclei are strongly suppressed, see figure 1. In particular the broad macromolecular contributions are completely eliminated. This makes quantification of metabolite concentrations more reliable and reproducible. The PME and PDE resonances can be well resolved into the Phosphoethanolamine (PE), Phosphocholine (PC), Glycerophosphoethanolamine (GPE) and Glycerophosphocholine (GPC) resonances.

Figure 2 shows exemplary localized spectra from 125 ml voxels in a transversal slice through the temporal lobe including the hippocampus of a healthy male volunteer. The S/N is adequate for precise quantification. The time demand for such a 3D RINEPT scan with TR=1.8 s is 37 minutes with 8^3 encoding and 17 minutes with 6^3 encoding respectively (each with NEX=4 and full decoupling). These short scan times are compliant with clinical routine protocols, which is a major improvement compared to [3]. Spherical encoding reduces measurement time by 45% (8^3 encoding) and 37% (6^3 encoding) respectively compared to standard cubic encoding. This is accompanied by a tolerable degradation of spatial localization by a broadening of the point-spread function (PSF). Numerical calculations show that the PSF is bleeding into adjacent voxels with an intensity of 14.9% exhibiting almost perfect spherical symmetry with very little ringing. The knowledge of the PSF is indispensable if automatic tissue segmentation is employed for cerebrospinal fluid (CSF) correction [5].

The results convincingly show that the sequence is useful in clinical routine ^{31}P MRS protocols and provides excellent spectra for the study of membrane defects in the human brain even at the low field strength of 1.5 T.

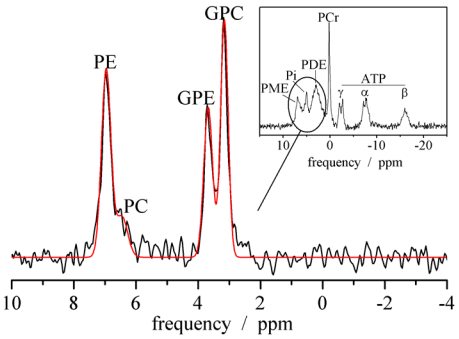

Figure 1: Non-localized ^{31}P RINEPT spectrum of the human brain with full decoupling (TR=1.9 s, NEX=128). The inset shows the pulse-and-acquire spectrum for comparison (TR=5 s, NEX=32, no decoupling).

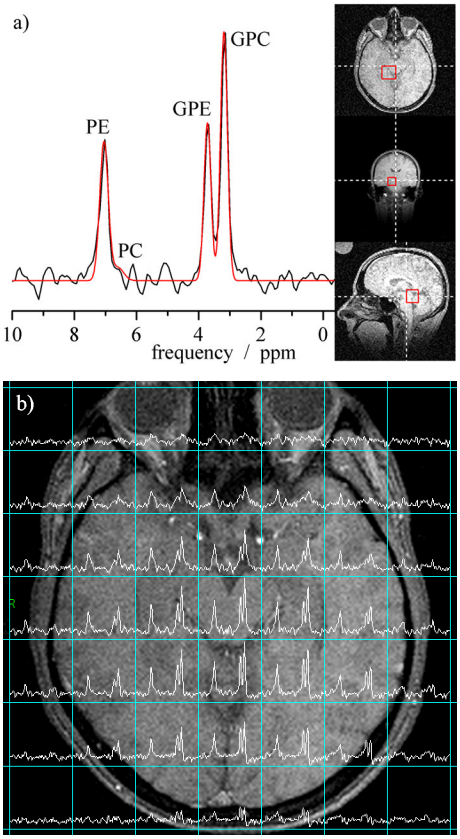

Figure 2: Localized RINEPT spectra, 8 x 8 x 8 encoding, FOV=400 mm, NEX=4, TR=1.8 s, k-space zero filling to 16^3, 125 ml voxel (15.6 ml interpolated), 128 ms spectral Gauss apodization, zero filling from 512 to 1024 data points, phase and baseline correction. a) exemplary voxel: $(S/N)_{GPC} \sim 35$. b) spectral plot on a transverse slice through temporal lobe and hippocampus.

References

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