2D and 3D RINEPT {^{1}H}-^{31}P-MRSI in the human brain and its possible application to schizophrenia

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Introduction

An altered metabolism of membrane phospholipids has been hypothesized in schizophrenia and various ^{31}P MRS studies have been undertaken to explore possible changes in the detectable phosphomonoesters (PME) and phosphodiesters (PDE) signals which are intermediates of membrane phospholipid turnover. The most consistent finding of previous ^{31}P MRS studies in schizophrenia is an increase of the PDE signal (considered predominantly an GPC increase) [1-7]. In general, broad macromolecular contributions underlying the PME and PDE resonances complicate the determination of metabolite concentrations. In addition, the large chemical shifts of most ^{31}P metabolites naturally prohibit the application of slice selection pulses or single voxel techniques. However, the actual chemical shift range of an edited RINEPT [8-11] spectrum is only 5 ppm compared to 30 ppm for the full ^{31}P brain spectrum. Here a 2D slice selective and a 3D pure phase encoding ^{31}P MRSI sequence utilizing RINEPT editing are compared with respect to time demand, spatial resolution and applicability to psychiatric patients.

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 and a second independent transmit channel operating at the proton frequency. Figure 1 shows an RINEPT edited ^{31}P spectrum of the human brain. The PME and PDE resonances can be well resolved into the phosphoethanolamine (PE), phosphocholine (PC), glycerophosphoethanolamine (GPE) and glycerophosphocholine (GPC) resonances while broad macromolecular contributions are strongly suppressed. Echo times were set to TE_1=40 ms and TE_2=32 ms [9]; the repetition time was optimized in vivo to 1350 ms. 3D spatial localization (8 x 8 x 8 encoding) is obtained by phase encoding gradient pulses which are free from chemical shift displacement errors. Additionally, using the advantage of a reduced chemical shift range of the edited RINEPT spectra, a 2D 8 x 8 encoding sequence was recently developed. Spherical encoding is used in both sequences to reduce scan time [11]. The encoding schemes incorporate warp sampling in order to minimize patient motion artifacts. Both sequences can be combined with proton decoupling using a WALTZ-4 pulse train. Reconstruction of the MRSI data set is performed as a postprocessing step with a custom-made software on the MR console.

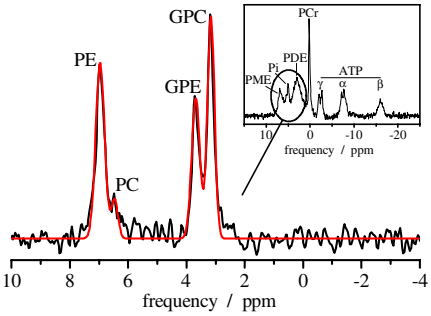

Figure 1: RINEPT edited spectrum of the human brain.

Results

The time demand for a 3D RINEPT scan is 37 minutes with 8 x 8 x 8 encoding for adequate S/N. Alternatively, a 2D slice with sufficient S/N can be acquired in the same time with 48 ml voxels (12 ml interpolated) using 8 x 8 encoding. In both measurements full proton decoupling can be employed. Spherical encoding reduces measurement time by 45% and 19% in 3D and 2D respectively in contrast to standard encoding. This is accompanied by a tolerable degradation of spatial localization by a broadening of the point-spread function. Both 2D and 3D sequence provide excellent ^{31}P spectra of the PME/PDE metabolites. The 3D sequence is advantageous if several key regions are to be examined in one study. However, if a single key region, or regions that can simply be placed within one slice are in the center of interest, the 2D MRSI provides better S/N which can be used to increase spatial resolution or reduce total measurement time. The latter might be the crucial factor when examining schizophrenic patients. The results convincingly show that both sequences are useful in clinical routine ^{31}P MRS protocols for the study of a possibly altered membrane phospholipid metabolism in schizophrenia even at the low field strength of 1.5 T.

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