Combining tissue segmentation with quantitative 31P and 1H MRSI can resolve the distribution of three trimethylamine components in gray and white matter.

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Introduction

Alterations in phospholipid and high-energy phosphate metabolism are frequently observed in neuropsychiatric disorders (e.g. Alzheimer's disease (Pettegrew, 1997, Ann.N.Y.Acad.Sci.)). A combination of quantitative ^{31}P and ^{1}H MR spectroscopy (MRS) provides more detailed information on these metabolic pathways than the single modalities. However, a voxelwise coregistration in spectroscopic imaging is hampered by the rather large voxel size and the poor point-spread-function (PSF) of ^{31}P MRSI data. The problem can be addressed by minimizing the partial volume effects using image segmentation and linear regresson analysis as described previously for ^{31}P (Mason, 1998, MRM.) and ^{1}H (Gasparovic, 2006, MRM). In this study, the approach was evaluated to determine concentration differences between gray and white matter for the three components of the trimethylamine (tCho) signal at 3.2 ppm in ^{1}H MRSI.

Material and Methods

The study required accumulation of an anatomical dataset for segmentation, and both spectroscopic imaging modalities. To be applicable to patients a protocol was designed which did not to exceed 40 min examination time. In the presented pilot study, which was performed on 4 healthy volunteers, an additional 3D 1H CSI was acquired. Phantom measurements were performed to map the B1 field inhomogeneity and estimate their impact.

MR data acquisition: MRS of the brain was performed on a 3T whole body system (Magnetom Trio, Siemens Medical AG, Erlangen, Germany) with a double tuned ^{1}H/ ^{31}P volume head coil (Rapid Biomedical, Würzburg, Germany). For ^{1}H MRS, a 1.5 cm axial slice including the basal ganglia was recorded with 2D chemical shift imaging (CSI, circular phase encoding on a 16x16 matrix extrapolated to 32x32, 240 mm^2 FOV, TR 1500 ms, TE 144 ms, see Fig.1a). A 3D CSI sequence with WALZ4 proton decoupling was used for ^{31}P MRS. Circular phase encoding was employed with a weighted acquisition scheme on a 10x10x8 matrix extrapolated to 16x16x8 resulting in a series of axial slice with nominal 2.5 cm thickness and 17.5x17.5 mm^2 in plane resolution (flip angle 60°, TR 2000 ms, TE 2.3 ms, see Fig.1b). The additional 3D ^{1}H sequence used geometry parameters from the ^{31}P examination and sequence parameters from the 2D ^{1}H examination. For all modalities, slice (slab) angulation were identical, the offset of the 2D 1H CSI slice was in the center of a 3D slice. For tissue segmentation a sagital oriented MP-RAGE (Mugler, 1990, MRM) with the following parameters was performed: 1.3 mm isotropic resolution, Baseresolution 192, FoV: Read (F/H): 250 mm, Phase(A/P): 230 mm, Partition (R/L) = 208 mm. The aquisition parameters were TR/TE/TI/ALPHA/BW = 1600ms/2.63ms/900ms/9°/200(Hz/Px), duration of 4:08 min. The segmentation was done by SPM5 (http://www.fil.ion.ucl.ac.uk/spm/). To registrate this data onto the CSI, a second MP-RAGE was measured aligned with the 31P MRS. The sequence duration was 1:39 min which was achieved by reduced resolution (2 mm isotropic). To avoid aliasing a oversampling of 38% in F/H was applied.

Data Processing: Registration of CSI to the anatomy was done with FSL(http://www.fmrib.ox.ac.uk/fsl/). The inverse registration matrix was used to rotate the segmented data onto the CSI. Downsampling and filtering the anatomical informations to CSI resolution was done with Matlab following the procedure described by Gasparovic (Gasparovic, 2006, MRM). MRSI spectra were analysed using jMRUI (http://www.mrui.uab.es/mrui/) and quantified with the phantom replacement method (Michaelis, 1993, MRM).

Results and Discussion

B1-mapping revealed a homogeneous field for ^{31}P. Increasing B1-field in the center of the phantom was observed for ^{1}H. While this caused augmented signal from the center in a simple FID-CSI sequence, the effect was barely visible when a PRESS sequence was applied.. Fig.2 summarizes the results for the tCho signal. Linear regression analysis was performed for both ^{1}H data sets. The 2D data show a sufficient spreading over the entire range of gray matter fractions, which allows the estimation of pure white or gray matter tCho concentration. Due to large voxel size and PSF, the respective analysis is not accurate for 3D data, but within the 95% significance level, is in accordance to the 2D data. Fig. 3 shows concentrations for all components of the tCho signals. Glycerphosphocholine (GPC) and phosphocholine (PCho) were taken from the ^{31}P data while choline (Cho) was calculated as difference from the regression analysis of 2D data (Fig.2, red line) and the sum of PCho and GPC. The significant decrease in GPC indicates that reduced tCho in gray matter can be primarily attributed to a decrease in GPC. This study demonstrates that application of tissue segmentation in combination with quantitative ^{31}P and ^{1}H MRSI can resolve the distribution of the components of the tCho signal in gray- and white matter.