Diffusion-Sensitive Single-Shot Proton-Echo-Planar-Spectroscopic-Imaging (PEPSI) in Human Brain

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Introduction

Magnetic Resonance Imaging (MRI) of water self-diffusion may provide useful information about tissue structure and function[1-7], but water may not be the most suitable molecule for diffusion measurements due to its ubiquity and due to the permeability of most tissue interfaces, such as membranes, to water molecules. The apparent diffusion coefficient (ADC) of metabolites reflects biophysical parameters such as viscosity, cell swelling, restriction in subcellular structures, cytoplasmic streaming, etc., which are relevant to the study of ischemia and tumors. More than a decade ago we have demonstrated the feasibility of measuring metabolite diffusion in human brain using single voxel spectroscopy[8]. Spatial mapping of metabolite diffusion coefficients in the human brain is challenging due to the motion sensitivity of conventional phase encoded MR spectroscopic imaging (MRSI) methods. Our recently developed single-shot MRSI method using single-shot encoding with parallel imaging[9] strongly reduces intra-scan motion sensitivity. Here we describe the development an MRSI technique that is suitable for mapping metabolite diffusion coefficients in the human brain.

Methods

The single-shot MRSI pulse sequence is based on PEPSI with interleaved blipped phase encoding and SENSE reconstruction[9]. The symmetrical k-space trajectory compensates phase errors due to convolution of spatial and spectral encoding and enables reconstruction of absorption mode spectra. Four-step interleaved phase encoding and 4-fold SENSE acceleration were used to encode a 16x16 spatial matrix with 390 Hz spectral width. Trapezoidal diffusion gradients with 15 ms duration and maximum amplitude of 32 mT/m were simultaneously applied along all axes. Preliminary data in the human brain in a healthy volunteer were acquired on 3T Trio scanner equipped with 32 channel head array. Pulse sequence parameters were: TR: 2 s, TE: 41 or 70 ms, FOV: 210 mm, slice thickness: 15 mm, supra-ventricular axial slice location, spatial matrix: 16x4, 4-fold, maximum b-value; 2354 s/mm2. Non-water suppressed data acquisition with 1 signal average, water suppressed data acquisition with up to 64 signal averages. Data were reconstructed as described previously[9] using individual phase correction of each signal average.

Results

Our data show that single shot localization performance at high b-values does not differ significantly from that at low b-value (Figs.1a and c). Residual eddy currents lead to slight line shape distortion of the water peak at high b-value (Figs. 1b and d). The logarithmic plot of signal attenuation shows nearly exponential signal decrease with b-value, as expected. However, the measured water diffusion coefficient (slice average: 1.2 +/- 0.3 * 10-3 mm2/s) is slightly overestimated as compared to literature values. Spectral quality at in water suppressed data is comparable to our recent study[9] and does not change significantly at high b-value (Figs.2a and b). Uniform spectral quality was obtained across the imaging slice (Fig. 2c).

Discussion

Implementation of navigator data acquisition for motion and frequency drift correction, and development of eddy current compensated gradient switching schemes are in progress. However, the narrow spectral width with this SENSE accelerated single-shot method results in spectral aliasing that impairs quantification of metabolite diffusion coefficients in vivo. We are therefore investigating the feasibility of single-shot PEPSI with superresolution reconstruction method[10] to acquire a smaller central k-space data matrix with larger spectral width. Clinical applications, such as the study of intra-cellular changes in Multiple Sclerosis, ischemia and tumors, may become feasible, thus providing possible novel biomarkers for diagnosis and treatment monitoring.

References

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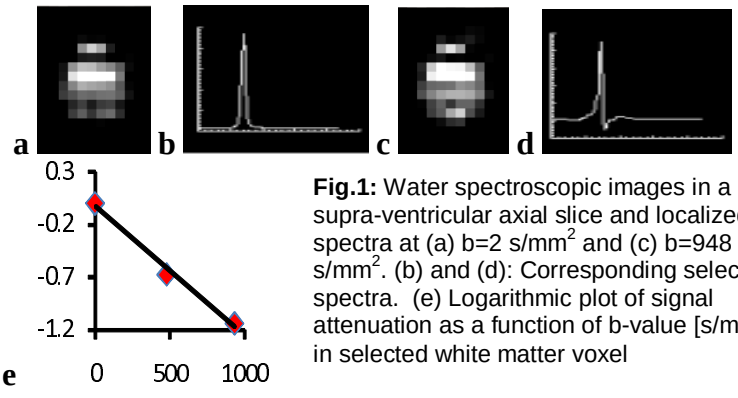

Fig.1: Water spectroscopic images in a supra-ventricular axial slice and localized spectra at (a) b=2 s/mm^2 and (c) b=948 s/mm^2. (b) and (d): Corresponding selected spectra. (e) Logarithmic plot of signal attenuation as a function of b-value [s/mm^2] in selected white matter voxel

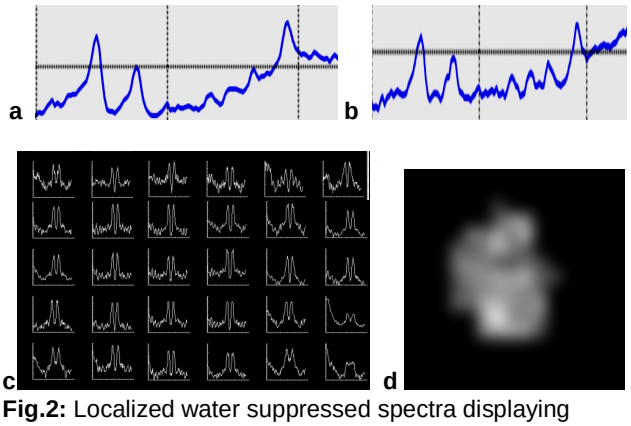

Fig.2: Localized water suppressed spectra displaying Choline, Creatine and NAA in the spectral range from 1.5 to 3.5 ppm measured at (a) b=2 s/mm^2 and (b) b=948 s/mm^2. (c) Spectral array showing Choline and Creatine peaks at b=948 s/mm^2. (d) Spectroscopic image of Creatine measured at b=420 s/mm^2.