Whole Brain Proton MRSI Using a Multiple 2D Sequence

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Introduction

A multi-planar MRSI sequence [1] has been used by many groups for nearly 15 years [2] because, compared to PRESS [3] and STEAM [4] sequences, it has the advantages of providing greater coverage of regions of interest, dynamic shimming, and time efficiency during data acquisition [5]. However, current implementations of the sequence have several shortcomings, including the limited number of slices and the spacing between slices. These shortcomings provide incomplete acquisition of information and pose substantial difficulties for the co-registration of MRSI with anatomical MR images. Increasing the number of slices will proportionally increase total scan time, and reducing the spacing between slices can cause "cross talk" or "cross excitation" across slices and thereby produce signal loss [6, 7]. We show that by adjusting sequence parameters, we can increase the number of slices without significantly increasing total scan time and we can eliminate spacing between slices without significant reducing the signal-to-noise ratio. Whole brain MRSI can be realized using this approach.

Methods

MR Measurements We acquired MR data on a phantom and on human volunteers using a whole body 3T scanner (Signa 3T HDx, GE Healthcare, Waukesha, WI). First, we acquired scout images using a 3 planar MRI sequence. We then prescribed the MRSI slices and acquired the localizer MRI images. MRSI data were acquired using a multiplanar MRSI pulse sequence [1] with the following parameters for both the phantom and human subjects: Number of slices = 7; Slice thickness = 10 mm; Spacing between slices = 4, 2, 1, 0 mm for phantom and 3, 2, 0 for human, respectively; Nominal number of phase encodings = 16 x 16; TR/TE = 3000/144 ms; Spectral width = 2400 Hz; Number of data points in the echo = 256. The time for an MRSI scan was about 9 minutes. Total scan time including MRSI slice prescription, Outer Volume Suppression band placement and field shimming was about 22 minutes. When repeating the MRSI scans with different spacing, the position of the central slice (the 4th slice) did not change. For each MRSI scan with different spacing, we performed an Auto-Prescan for field shimming and optimization of transmitter gain. Then receiver/transmitter gains were manually adjusted if needed to keep the same values for all MRSI scans. For human scans, MRSI slices were placed in the oblique axial plane parallel to the AC-PC line. All the protocols were approved by the local IRB.

Data Processing We applied spatial filtering to the k-space MRSI data using a Hamming window function and then transformed imaging data to the spatial domain using a 2D Fourier transform. Voxels from the same region of interest in the 4th slice for all datasets with differing spacings were selected, and the peak areas for three major metabolites -- N-acetyl-aspartate (NAA), Creatine (Cr) and Choline (Ch) -- were measured using a program for spectral fitting in the frequency domain. The ratios of the areas of the same metabolites from the same voxels in datasets with differing slice spacings were calculated. A paired t-test was applied for statistical analysis of the differences of peak areas.

Results

The prescription of slices and an example of localizer images for a human scan are show in Fig. 1. The average ratios of the peak areas of the three major metabolites between datasets with different slice spacings are summarized in Table 1 and Table 2 for phantom and human scans, respectively. Paired t-tests show no significant differences between signals from datasets with differing slice spacing for phantom data. The human data showed a reduction of < 10% of the peak areas of metabolites for data with 0 spacing compared with 3 mm spacing. The SNRs of NAA are 44, 49, and 42 for spacing = 3, 2, and 0 mm, respectively. NAA images were calculated for all slices (Fig.1).

Tab. 1. Average Ratios of Peak Areas between Datasets with Different Spacings Using a Phantom

4 mm to 2 mm			4 mm to 1 mm			4 mm to 0 mm		
NAA	Cr	Ch	NAA	Cr	Ch	NAA	Cr	Ch
0.986	0.997	1.004	1.015	1.053	0.981	1.003	1.023	1.014
±0.026	±0.024	±0.052	±0.049	±0.128	±0.054	±0.036	±0.042	±0.040

Tab. 2. Average Ratios of Peak Areas between Spacings in Human Brain

3 mm to 2 mm			3 mm to 0 mm		
NAA	Cr	Ch	NAA	Cr	Ch
0.994	0.993	1.000	1.098	1.079	1.090
±0.215	±0.229	±0.308	±0.218	±0.208	±0.315

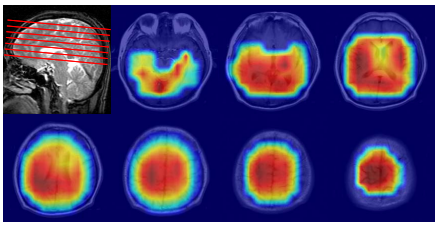

Fig. 1. Slice prescription and NAA images overlaid on MR images.

Discussion

"Cross talk" is caused by the imperfect slice profile that induces excitations in slices adjacent to the slice that is being acquired. These unwanted excitations induce partial saturation that reduces signal. The effect of cross talk can be reduced by interleaving slice excitation and by increasing the TR. Conventionally, the pulse sequence [1] is used for only four slices and TR = 2300 ms. Even though the slices are excited in 1-3-2-4 fashion, all the slices are not fully interleaved. In the present work, any adjacent slices are interleaved by at least two excitations, with a time delay of or 857 ms, or 29% of the TR. Therefore, cross excitations will largely relax before excitation of the adjacent slice begins. The reduction of signal in humans when spacing is zero indicates that the slice profile may also relate to field shimming. In conclusion, we have shown that whole brain MRSI with contiguous slices can be realized with a multiple 2D sequence. A 75% increase in the number of slices is achieved at the price of a 25% increase in TR, and spacing between slices is removed without incurring a substantial reduction in SNR.

References

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