Sensitivity Encoded Three Dimensional Echo Planar Spectroscopic Imaging (3D-EPSI) of Human Brain at 4T

X. Zhu[1], A. Ebel[2], J. X. Ji[3], M. W. Weiner[1], N. Schuff[1]

[1]Radiology, VAMCSF/UCSF, San Francisco, California, United States, [2]Northern Institute for Research & Education, San Francisco, California, United States, [3]Electrical Engineering, Texas A&M University, College Station, Texas, United States

Introduction

MR spectroscopic images covering the whole brain can be obtained using a 3D echo planar spectroscopic imaging sequence (3D-EPSI) (1). However, routine applications of EPSI are still limited by a long scan time, although acquisition speed is one order of magnitude faster than conventional spectroscopic imaging. Parallel imaging, which uses multiple receiver coils to reconstruct un-aliased images from under-sampled image data, can further reduce scan time. Previously, sensitivity encoding (SENSE) was incorporated for 2D spectroscopic imaging data (2, 3). Here, we present an extension of SENSE to 3D-EPSI, in which one phase-encoding (PE) direction is under-sampled and un-aliasing accomplished by standard SENSE reconstruction (4, 5).

Methods

3D EPSI data was acquired from a healthy volunteer. The acquisition matrix dimensions were s = 800, x = 50, y = 50, and z = 18, where s is the spectral dimension, x and y are the read-out and PE dimension respectively, z is the number of partitions of the 3D volume. Water reference 3D-EPSI data set of the same spatial dimensions was acquired interleaved with the metabolite data. An eight-channel (phased-array) receiver coil was used on a 4 Tesla Bruker MedSpec whole-body scanner. EPSI re-sampling was carried out as described previously (6). For each point in k_z, standard SENSE reconstruction was carried out for $\mathbf{d} = I(k_x, k_y, t)$ after removal of every other PE step to obtain a factor 2 acceleration (A = 2), according to:

$$I(\mathbf{r}, t) = (\mathbf{E}^H\mathbf{E})^{-1}\mathbf{E}^H\mathbf{d}$$

where $\mathbf{E}$ is the sensitivity map, $\mathbf{E}^H$ is Hermitian transpose of $\mathbf{E}$, and $I(\mathbf{r}, t)$ are reconstructed metabolite image frame at time t. This procedure was carried out in parallel for metabolite and water reference EPSI data. Subsequently, the metabolite and water EPSI data were Fourier transformed along the time direction, yielding metabolite $I_m(\mathbf{r},\omega)$ and water reference $I_w(\mathbf{r},\omega)$ images. Frequency shifts of metabolite resonances due to local B_0 inhomogeneities in the brain were corrected based on the water resonance line in $I_w(\mathbf{r},\omega)$ (7). k-space extrapolation was carried out to reduce lipid contamination (8) in $I_m(\mathbf{r},\omega)$. Finally, $I_m(\mathbf{r},\omega)$ images were convolved by Gaussian apodization functions in the k-space domain for a better signal-to-noise ratio. For comparison, a full k-space sampled 3D-EPSI data was processed following a similar procedure.

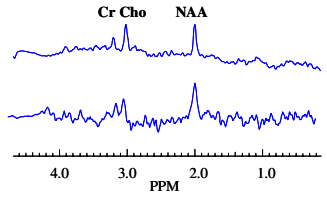

Figure 1. ^{1}H spectrum from SENSE (A=2) (top) and full k-space sampled EPSI (Bottom).

Results

Figure 1 shows a typical ^{1}H MR spectrum from a gray matter area after SENSE reconstruction of a factor 2 under-sampled EPSI set. The same spectrum from the fully k-space sampled EPSI set is also shown, depicting the degradation of signal-to-noise ratio (SNR) and spectral resolution after SENSE reconstruction. Figure 2 shows images of brain N-Acetyl Aspartate (NAA) from the full 3D-EPSI data. Figure 3 shows the aliased metabolite images from a factor 2 under-sampling. Figure 4 shows transaxial images of NAA, creatine (Cr) and choline (Cho) after SENSE (top) compared with full k-space (bottom) reconstruction.

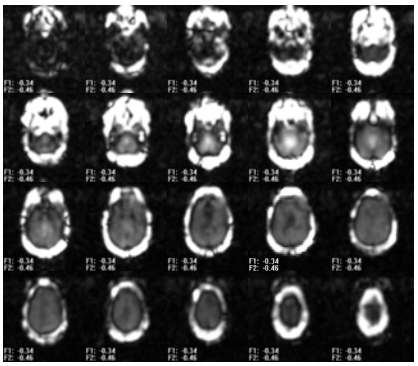

Figure 2. 3D NAA images from full k-space sampled EPSI.

Discussion and Conclusion

Factor 2 under-sampled 3D-EPSI data with SENSE reconstruction are presented, demonstrating feasibility of sensitivity encoded 3D-EPSI acquisition. Although a decrease of SNR by $\sqrt{2}$ is expected due to a factor 2 under-sampling of EPSI, additional SNR degradation occurred. An additional reduction of SNR induced by SENSE is not surprising, since the underlying encoding system is inherently ill-posed and SENSE reconstruction using least squares inversion is liable to suffer from noise amplification, especially in metabolite images with inherently poor SNR. The degradation of spectral resolution also results from incomplete unfolding. This fundamental aliasing-to-noise limit cannot be overcome, unless more information about the image data is exploited, for example, by Bayesian estimation methods (9).

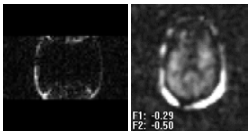

Figure 3. An NAA image with aliasing correspond to A = 2 (left) and after SENSE (right).

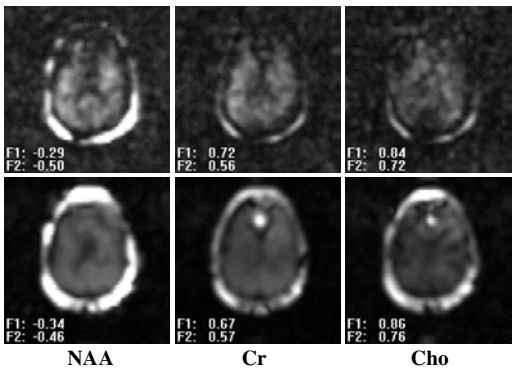

Figure 4. Metabolite images from SENSE (A = 2) (top) and full k-space sampled EPSI (bottom).

References

1) Ebel A et al, MRM 46:1072 (2001). 2) Dydak U et al, MRM 46: 713 (2001). 3) Lin F-H et al, Proc ISMRM 2005, p. 489. 4) Pruessmann KP et al. MRM 42: 952 (1999). 5) Rane SD and Ji JX, Proc ISMRM 2005, p. 2457. 6) Ebel A et al, MRM 54: 697 (2005). 7) Ebel A et al, Magn Reson Imaging 21:113 (2003). 8) Haupt CI et al, MRM 35: 678 (1996). 9) Raj A and Zabih R. Proc ISMRM 2004, p2411.