Fast 31P Chemical Shift Imaging Using Multi-Spiral Acquisition at 9.4T

Yuchi Liu[1], Yun Jiang[1], Charlie Yi Wang[1], Mark Alan Griswold[1,2], and Xin Yu[1,2]

[1]*Biomedical Engineering, Case Western Reserve University, Cleveland, Ohio, United States,* [2]*Radiology, Case Western Reserve University, Cleveland, Ohio, United States*

Target Audience

Researchers interested in hetero-nuclei chemical shift imaging and non-Cartesian acquisition scheme.

Introduction

Chemical shift imaging (CSI) allows the measurement of metabolite distribution in vivo. However, it has found limited applications due to the prohibitively long acquisition time, especially for imaging low concentration metabolites such as phosphate metabolites. To accelerate acquisition, non-Cartesian k-space trajectory has been proposed to encode spatial information[1]. In addition, off-resonance artifact from the non-Cartesian trajectory could be problematic at ultra-high field, such as 9.4 T, especially for the ^{31}P imaging that has a wide off-resonance range. In this study, a multi-spiral sequence was developed for accelerated ^{31}P CSI acquisition. A reconstruction method was proposed to deblur the metabolite maps of off-resonance species. An acceleration factor of 23 was achieved compared to traditional Cartesian CSI method with the same spatial resolution.

Methods

A spiral trajectory using the minimum-time gradient design[2] was used to acquire data in a field-of-view of 4×4 cm^2 with the matrix size 16×16. The spiral trajectory is zero moment compensated. For each repetition, the spiral trajectory was repeated 4 times, spanning 8.8 ms during the entire readout period (Fig. 1a). To compensate the gradient performance, the 4-repeated spiral trajectory was measured[3] (Fig. 1b). Chemical shift encoding was achieved by delaying the start of the readout gradients in the subsequent repetitions by 200 μs, leading to a spectral bandwidth of 5000 Hz (30.8 ppm). A total of 11 repetitions were acquired, covering 10.8 ms along the chemical shift dimension.

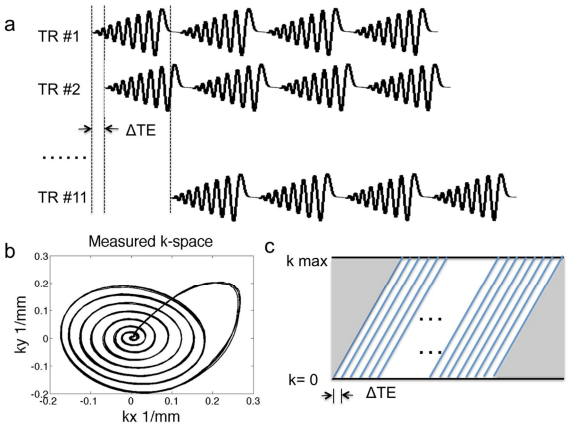

Figure 1. a. Multi-spiral CSI acquisition scheme. b. Measured k-space trajectory. c. Reconstruction method to deblur off-resonance metabolite map.

To correct the off-resonance artifact, the proposed reconstruction method is shown in Fig. 1c. Blue lines indicate acquired k-space data. The two corners of the k-space without acquired data (shaded gray areas) were zero padded, leading to a nominal spectral resolution of 92.6 Hz. The 3D k-space (k_x, k_y, t) was segmented into 51 bins along the time dimension, with a duration of 200 μs for each bin. The spiral data within the same bin were gridded by NUFFT[4]. The gridded data were zero-padded in the spatial dimensions to a matrix size of 32×32 and 3D Fourier transform was performed to get the spatial distribution and the spectra. The same spatial zero padding was performed on Cartesian CSI data.

Phantom studies were performed on a Bruker 9.4T horizontal scanner using a home-made ^{31}P transmit/receive saddle coil. Two phantoms with 800 mM inorganic phosphate (P_i) and 1 M phosphocreatine (PCr) respectively were scanned. Acquisition parameters were: TR, 2 s; TE, 0.51 ms for first repetition; FOV 4×4 cm^2; matrix size 16×16; slice thickness, 2 mm. Traditional Cartesian CSI was performed using the same spatial resolution, TR, and excitation pulse as the spiral acquisition, with a spectral resolution of 2.44 Hz.

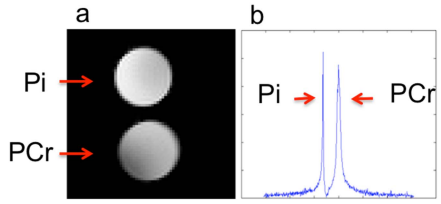

Figure 2. ^{1}H reference image (a) and non-localized ^{31}P spectrum (b).

Results

Fig. 2 shows the ^{1}H image of both phantoms and a non-localized ^{31}P spectrum. Fig. 3 shows results from Cartesian CSI (Fig. 3a) and spiral CSI (Fig. 3b). Acquisition time of 1 single average was 8.5 min for Cartesian CSI and 22 s for spiral CSI. The carrier frequency for both Cartesian and spiral acquisition was set at the resonance of PCr; hence, the Pi peak was 518 Hz off-resonance. ^{31}P spectra from imaging pixels with the highest signal intensity (labeled with red dots in Fig. 3) are also shown. Off-resonance metabolite map was successfully deblurred using the proposed reconstruction method. Root mean square error of PCr map and Pi map for spiral CSI against Cartesian CSI were 8.29% and 8.62%, respectively.

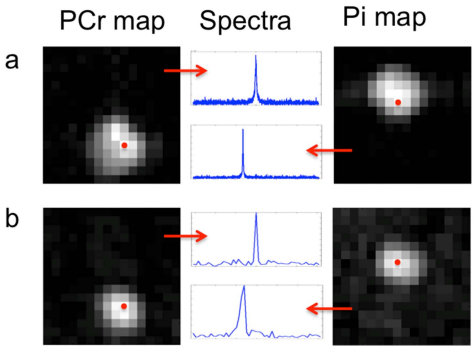

Figure 3. Maps of PCr and Pi and representative spectra from Cartesian (a) and spiral (b) CSI.

Discussion & Conclusion

This study proposed a fast ^{31}P spiral CSI sequence and a data reconstruction method. The spiral CSI sequence was designed to achieve an appropriate spectral width/resolution to encompass/differential all ^{31}P metabolites that exist in living organisms. Spiral CSI acquisition achieved an acceleration factor of 23 and showed good agreement with Cartesian CSI. This preliminary work demonstrates the potential of ^{31}P CSI in imaging the spatial distribution of phosphate metabolites in vivo.

References

1. Adalsteinsson et al. *MRM* 1998.
2. Lee et al. *MRM* 2003.
3. Duyn et al., *JMRI*, 1998.
4. Fessler and Sutton. *IEEE Trans. Signal Process.* 2003.