Improved PCr/ATP Ratio Mapping of the Human Head by Simultaneously Imaging of Multiple Spectral Peaks with InterLeaved Excitations and Flexible Twisted Projection Imaging Readout Trajectories (SIMPLE-flexTPI) at 9.4 Tesla

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INTRODUCTION

Phosphocreatine (PCr) and ATP concentrations provide information about the metabolic flux through the central high-energy metabolic pathways (1,2). Obtaining such information in the human brain with MR imaging is challenging due to the low detection sensitivity of ^{31}P and the low concentrations and unfavorable imaging characteristics (long T1 relaxation times) of these metabolites. The feasibility of using a novel acquisition strategy, now termed SIMPLE-flexTPI for Simultaneously Imaging of Multiple Spectral Peaks with InterLeaved Excitations and Flexible Twisted Projection Imaging Readout Trajectories, to simultaneously sample PCr and γ -ATP signals has been demonstrated previously (3). By optimizing the acquisition software and hardware, we now report improved ^{31}P imaging results on entire human head at 1.5 cm isotropic resolution in 33 minutes at 9.4 Tesla. The spatial distributions of the PCr, γ -ATP signals and their ratio are demonstrated in the corresponding partially transparent 31P images superimposed over sodium images that are used as an anatomical reference. The obtained ratios are in agreement with literature values.

MATERIALS AND METHODS

The SIMPLE-flexTPI sequence is illustrated in **Fig. 1**. During each repetition time, the PCr resonance was sampled once while the γ -ATP resonance was sampled twice to take advantage of the shorter T1 of γ -ATP spins. Immediately following each excitation, the free induction decay (1st echo) signal was sampled with a flexTPI readout trajectory to minimize T2 relaxation. A 2nd echo was also sampled to extract T2* information without any time penalty. Gradient timing errors and eddy currents are measured and corrected to minimize the sensitivity of the flexTPI readout to gradient system imperfections (4).

Imaging on three human volunteers was performed on a 9.4T scanner with an 80cm bore under an IDE from the FDA, with approval from the IRB and informed consent from volunteers. Optimized custom-built, single-tuned head RF coils were used. ²³Na imaging was performed with the conventional flexTPI sequence for anatomical reference and for B0 mapping with a 3.3mm isotropic resolution. ³¹P imaging used a 7.2 ms minimal phase RF

pulse for spectrally selective excitation with a pass-band of 380 Hz. Data collection with a flexTPI readout used a radial fraction of 0.15 and a gradient strength of 0.4G/cm with a ultra-short TE (UTE) of 10 μs for the 1^{st} echo. TE for the 2^{nd} echo was 8.6 ms. The readout duration for each echo was 7.7ms. Two averages were used to improve SNR. B0 inhomogeneity was further mitigated using B0 field maps obtained from co-registered ^{23}Na imaging during image reconstruction (5).

RESULTS AND DISCUSSION

The average SAR was minimal with the acquisition parameters used (< 0.25W). Fig. 2 shows the PCr and γ-ATP images reconstructed from the 1st echo and PCr/y-ATP ratio map interpolated and superimposed over the high-resolution sodium images. The isotropic resolution provided by the sequence allows the images to be visualized in three planes. The skull base and lateral aspects over the head containing muscle show higher PCr signal than brain parenchyma. The ATP signal is more homogenous across the head than the PCr signal. The SNR values for PCr and γ-ATP in the brain tissue are comparable at ~ 13 . The PCr/ γ -ATP ratios are approximately 1 to 2 in brain tissue and higher at 3 to 5 in muscle outside the brain. The white-matter dominated voxels in the central brain region show lower ratio values of ~1 as compared to other brain regions. The cerebellum tissues show higher ratio values (~2) than gray and white matter tissues. The reduced PCr or ATP signal due to partial volume effects with CSF can be clearly appreciated (e.g, the lighter red color indicated by the arrows). The average PCr/\gamma-ATP ratios over the entire brain region in the three

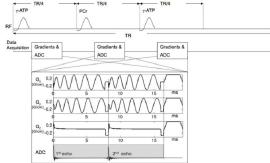


Fig. 1 Illustration of the SIMPLE-flexTPI sequence for collecting PCr and γ-ATP signals simultaneously.

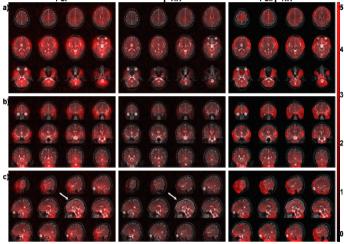


Fig.2 Partially transparent PCr (left,red), γ -ATP (middle,red) and the PCr/ γ -ATP ratio images (right, red) superimposed over sodium images (gray) in (a) axial, (b) coronal and (c) sagittal planes collected with the SIMPLE-flexTPI sequence in 33 minutes. The nominal spatial resolution is 1.5 cm isotropic and the TR is 8 s. The vertical color bar shows the color scale of the ratio maps.

volunteers were 1.46 \pm 0.27, 1.43 \pm 0.26, and 1.46 \pm 0.31, respectively. These ratios are in agreement with previously reported values (6). At a TE of 8.6 ms, appreciable signal is present in the 2nd echo images for PCr (images not shown). However, little signal is present in the 2nd echo images for γ -ATP, indicating the relatively short T2* of γ -ATP and the need for short TE imaging.

CONCLUSIONS

Combining the increased sensitivity at 9.4T and the efficient SIMPLE-flexTPI acquisition has allowed simultaneous acquisition of PCr and γ -ATP signals of the entire human head with reasonable resolution and SNR. The PCr/ γ -ATP bioscale can thus be calculated without registration errors or B1 modulation. This method may provide a useful tool for studying disease states of altered oxidative phosphorylation.

REFERENCE 1. Sappey-Marinier et al. J Cereb Blood Flow Metab 1992;12:584. 2. Rango et al. J Cereb Blood Flow Metab 2001; 21:85. 3. Lu et al., Proc. 18th ISMRM 2010. p980. 4. Lu et al., MRM 2010; 63:1583-93. 5. Noll et al., MRM 1992; 25:319-333. 6. Hetherington et al., MRM 2001; 45:46-52.