31P Magnetic Resonance Spectroscopy and Imaging at 7T and signal dependence on Brain Tissue Types

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Introduction: High energy phosphorous (HEP) compounds like ATP, ADP and PCr are essential elements of the cellular energetic and metabolism (1, 2). It has been demonstrated in several brain disorders that there are significant changes from their normal concentration levels. High magnetic field, with its approximately linear dependence of signal to noise ratio on magnetic field strength, affords an improved sensitivity and detection (frequency dispersion) (2, 3). The purpose of this study was to develop a methodology to estimate HEP in gray matter (GM) and white mater (WM) brain regions while properly accounting for signal contributions from skeletal muscle (SM) to the phosphate metabolite signal/concentration at high magnetic field.

Methods: MR data acquisitions were performed on a whole-body 7T system (Siemens MAGNETOM 7T) using singly-tuned RF coils. An eight-channel phased-array RF coil (Rapid Biomedical) was used for acquiring ^1H_2O MRI. Subjects (n=4, age: 20-32 yrs, 2 male, 2 female) were positioned in the RF coil and referenced in the magnetic field direction (z) using laser fiducials. After $\mathbf{B_0}$ shimming and RF pulse calibration, four sets of whole brain T_1-weighted images (FOV: 192mmx256mmx192mm, Data matrix: 192x256x96, TR=2.5s, TE=2.3ms) were acquired at TI (ms) = 300, 900, 1200, 2100 and without inversion pulse for tissue segmentation. These images were used to generate T_1 maps by solving for Bloch equation. Routines developed in FSL program were used to remove non-brain tissue and segment T_1 maps into CSF, GM, WM and SM.

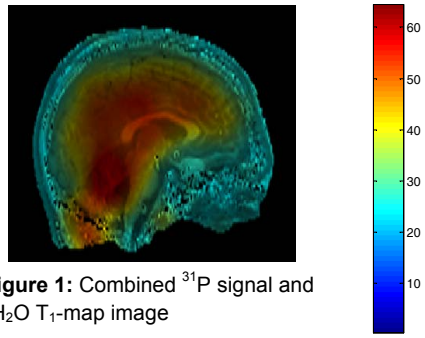

Figure 1: Combined ^{31}P signal and ^1H_2O T_1-map image

After completion of the ^1H_2O MRI acquisition, the subject was removed from the magnet and the RF coil was switched to the ^{31}P coil – a modified circularly polarized High Pass proton Birdcage coil from a 3T Siemens system. Subject was carefully re-positioned in the ^{31}P RF coil and referenced with laser markers to be in the same z-location. A ^{31}P MRSI gradient-echo FID acquisition was performed with an echo time of 2.3 ms (FOV: 250 mmx250 mmx200mm, data matrix: 20x20x16, TR =300 ms, $\alpha=24^0$). An optimized sinc RF pulse of 600 μs duration centered at PCr resonance frequency with a bandwidth-time product of 6.57 was used to uniformly excite the phosphorous metabolites and avoid signal contribution from outside the region of interest. This large bandwidth also minimized spatial mis-registration during the slab selection in z-direction (e.g. 1.4 mm dispersion between PCr and γ-ATP peak). A cosine-weighted 3D- spatial phase encodings (2379, ns=12, total 7476) were performed to minimize the acquisition time while maintaining a high signal to noise ratio. Overall, were performed with a total acquisition time of 37.5 min. Two low resolution MRSI acquisitions (FOV: 240mmx240mmx200mm, data matrix: 16x16x16, TR=220 ms, TE=2.3 ms) were acquired with different flip angles (10 and 20 degrees) to map the B_1- field at 120.3 MHz...

A 3D map of total ^{31}P signal data was co-registered to anatomic images using FSL tools programs (rotations and translations in x and y-planes – 4 degrees of freedom) (**Figure 1**). This transformation matrix was used to calculate inverse transform to generate segmented tissue images co-registered to ^{31}P spectroscopic data. Spectral data showed a significant baseline roll due to finite delay between RF pulse and fid acquisition (2.3 ms). Therefore, a time-domain fitting -AMARES routine-in jMRUI 3.0 software was used for processing (**Figure 2**). Software routines developed in Matlab were used to preprocess MRSI raw data (exponential line broadening of 20 Hz) and analyze jMRUI results. Linewidths of ATP peaks were constrained to be equal, J-coupling of 16.6Hz and peak positions were soft-constrained to be within +-30 Hz except PCr and Pi peaks. Any voxels with a PCr linewidth greater than 100 Hz and/or SNR less than 6 were excluded from the fitting routine. Fitted resonance peak amplitudes were corrected for B_1 and T_1-saturation effects based on the steady-state signal calculation.

Segmented images were convoluted with the spatial response function (SRF) of the spectroscopic acquisition to generate tissue contribution maps (**Figure 3**). An ANOVA analysis was performed for PCr/γATP peak areas ratio of central slices in the brain region (4-5 slices) for dependence on GM or WM tissue fractions (**Figure 4**).

Discussion and Results: PCr/ATP values in GM and WM were 1.68±0.2 and 0.92±0.1 respectively. These results are in excellent agreement with 4T literature values of 1.64 and 0.98 respectively (2). The small difference may indicate a tissue dependent variation in T_1 values of PCr or ATP resonances due to chemical shift anisotropy contribution at high magnetic field. This methodology in combination with absolute concentration determination can be useful in assessing variation in cellular metabolism in healthy humans and subjects with neurological disorders or neural degeneration.

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References: 1. Chen, Zhu, *Conc. Magn. Res. A.*, **27**: 84-121, (2005). 2. Hetherington, Spencer, Vaughan, Pan, *Magn. Res. Med.* **45**:46-52 (2001). 3. Lei, Zhu, Zhang, Ugurbil, Chen, Magn. Res. Med. 49:199-205 (2003).

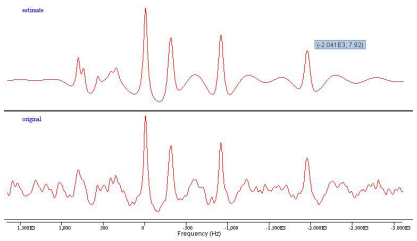

Figure 2: Signal and fitted spectrum

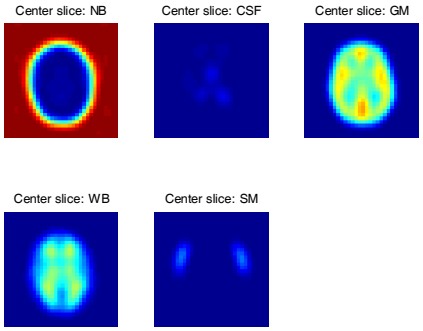

Figure 3: Tissue contribution images

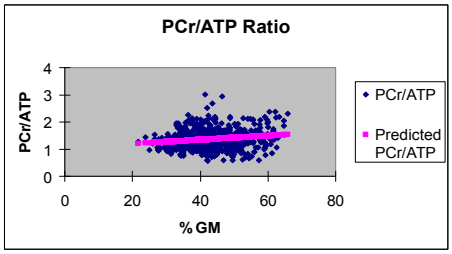

Figure 4: Individual subject data