Reproducibility of 31P Cardiac Magnetic Resonance Spectroscopy at 3T

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Objectives

The purpose of this work was to take advantage of the emerging clinical field strength of 3Tesla to develop an optimized chemical shift imaging (CSI) acquisition protocol to produce high quality spectra with high specificity to the myocardium within a clinically feasible scan time. Further, we wished to develop an analysis method dependent purely on anatomical location of spectra, and, as such free from any potential bias caused by inference from spectral information or quality.

Materials and Methods

All scans were performed on a Siemens 3T Tim Trio system (Erlangen, Germany) using a dedicated cardiac ^{31}P MRS coil. Data were acquired with a 3D acquisition-weighted chemical shift imaging sequence (AW-CSI) [Pohmann; MRM, 2001], 16x16x8 matrix, 240x240x200 mm FOV, 10 averages at k-space centre. The CSI grid and saturation bands were positioned as illustrated in Figure 1, on a slice designated as the first short axis slice in which the papillary muscle becomes visible. The CSI acquisition utilized the UTE-CSI [Robson; MRM, 2005] technique to reduce the interval between excitation pulse and signal acquisition (TE = 0.3 ms), thereby maximizing acquired signal whilst minimising first order phase effects. Nuclear Overhauser Enhancement (NOE) was used to increase SNR. Correction factors for NOE, RF saturation (identified in previous experiments) and blood correction factors [Neubauer; Circ., 1992] were used in analysis. An optimized RF pulse, centred between the γ- and α-ATP resonance frequencies was used to ensure uniform excitation of all spectral peaks (Figure 2). This allowed PCr/ATP ratios to be calculated using both an average of all three ATP peaks and the γ-ATP peak alone to assess which method proved the most reliable. Non-localized inversion recovery spectra were also acquired to measure the flip angle at a reference vial containing phenylphosphonic acid (PPA) located inside the RF coil housing. This information was used in conjunction with a calculated RF field profile to determine the flip angle of the spectral voxels.

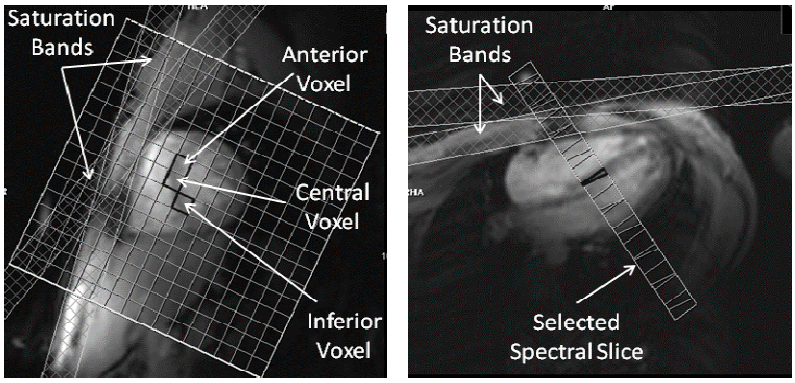

Figure 1: Orientation of the CSI matrix shown in 2 chamber cardiac short axis and 4 chamber cardiac horizontal long axis views. Grid rotation maximizes specificity of voxels to septal myocardium. The position of the two saturation bands was adjusted to cover the chest wall, minimizing skeletal muscle contamination.

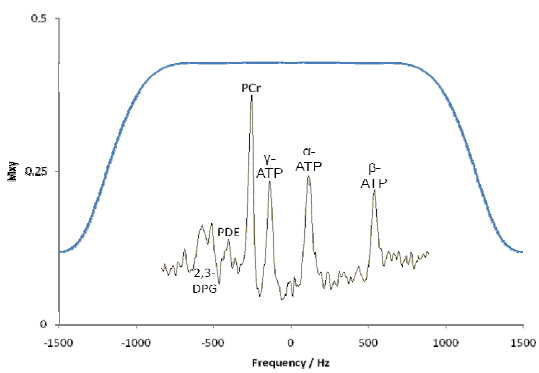

Figure 2: Profile of the optimized RF pulse providing uniform excitation of the measured peaks. An example 31P spectrum is overlaid on the plot to demonstrate the location of the spectral peaks within the excitation profile.

20 fasting, healthy, male subjects were scanned on two separate occasions using the optimized chemical shift imaging protocol at 3 Tesla. Data were analyzed for intra and inter subject variability, as well as intra and inter observer variability. No data were excluded.

Results

The average PCr/ATP value across subjects for scan 1 was 2.07 ± 0.38 and scan 2 was 2.14 ± 0.46, showing no significant difference between scans. Intra subject variability was 0.43 ± 0.35 (percentage difference 20%) and the inter subject coefficient of variation was 18%. The intra observer variability, assessed as the absolute difference between analyses of the data by a single observer, was 0.14 ± 0.24 and showed no significant difference between analyses. The inter observer variability showed no significant differences between the PCr/ATP value measured by four different observers demonstrated by an intra class correlation coefficient of 0.763.

Conclusions

The increased signal available at 3T, in conjunction with acquisition optimization has improved spatial resolution and increased myocardial specificity in cardiac ^{31}P measurements. We present a technique that routinely provides high quality spectra, coupled with a robust analysis method based on anatomical location and blind to spectral information or quality. The presented technique is suitable for widespread application both across research groups and across disease models.