Measurement of the Longitudinal Relaxation Time (T_1) of Cardiac Phosphorous Metabolites at 3T

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INTRODUCTION

^{31}P spectroscopy is a valuable technique for the in vivo measurement of high energy metabolites, which allows the assessment of tissue energy metabolism. However, the technique is limited by an inherently low SNR due to low metabolite concentrations (~10mM) and low gyromagnetic ratio. The emergence of clinical 3T systems may provide the increased SNR required to drive ^{31}P spectroscopy forward as a clinical tool.

^{31}P spectra are normally acquired with a short repetition time and multiple averages, which means that for quantitation purposes, they must be corrected for the effects of saturation. The ratio of PCr to ATP provides a measure of the energetic state of the heart and is an indicator of cardiac failure[1]. However the T_1's of PCr and ATP are known to be very different and to obtain reliable PCr/ATP ratios we require knowledge of the different metabolite T_1 values, as well as the TR and local flip angle. In this work we have for the first time attempted to measure the longitudinal relaxation times of PCr and γ-ATP using the 'dual angle' method[2] at 3T

METHODS

^{31}P cardiac spectra were acquired in six normal healthy subjects. Spectra were obtained on a 3T clinical system (Siemens Trio) using an ECG-gated, chemical shift imaging (CSI) protocol. The RF coil consisted of a standard Siemens 1.5T ^{31}P coil that was modified for use at the higher field strength, this coil is composed of a large transmit element, and quadrature loop and butterfly receive elements. Four sets of cardiac gated spectra were acquired (TR=2 heart-beats, to remain within SAR limits, TE=8.2 ms, Bandwidth=1000Hz, Resolution=20x40x40 mm, 2 Averages), oriented along the short-axis of the heart, with alternating flip angles of 25° and 90°. Accurate local flip angles were obtained with the surface transmit RF coil through the use of BIR-4 excitation pulses implemented as BIRP[3].

A voxel was chosen at the centre of the anterior-posterior axis of the cardiac septum and the resulting spectra were processed in jMRUI, using the AMARES algorithm[4] to fit for PCr and γ-ATP. The fitted amplitudes were used to calculate the T_1 values of PCr and γ-ATP, after correction for the effects of T_2 decay during the pulses (pulse length=16 ms).

To demonstrate the advantages offered by 3T acquisition, further scans were run on two volunteers with a resolution of 15 mm x 15 mm x 12.5 mm (2.8 ml voxel), TR=1 heart-beat (~1s), 16 x 16 x 16 matrix, 16 averages, local flip angle at heart ~ 45°, bandwidth=4000Hz.

RESULTS

The T_1 value of PCr at 3T was measured to be 3.8±0.3 s (Mean±SEM) and of γ-ATP was 2.4±0.5 s. Individual values are shown in figure 1. These values are similar to those previously reported (PCr 4.1s for humans at 1.5T, and γ-ATP 2.4s across a range of field strengths and species)[5]. Figure 2 shows example cardiac and skeletal muscle spectra acquired with the high resolution scan, which we believe to be the highest resolution ^{31}P human cardiac spectra yet presented. The cardiac muscle spectra shows limited blood contamination, as indicated by the low levels of 2,3-DPG.

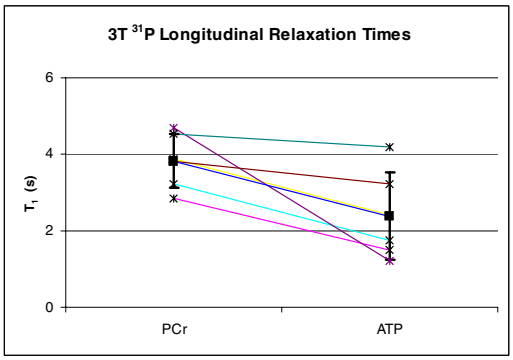

Figure 1: Cardiac ^{31}P T_1 Values at 3T

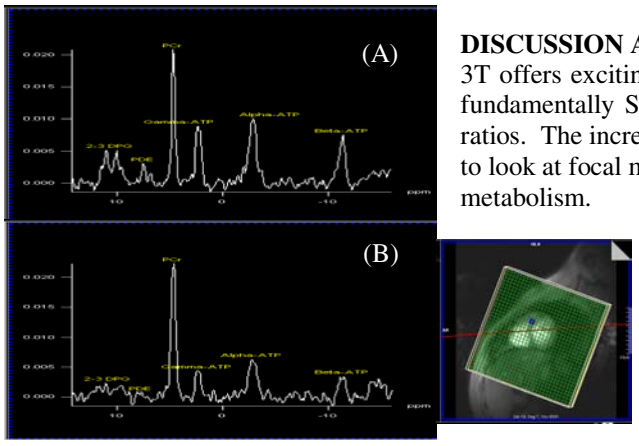

Figure 2: Examples of High-Resolution Cardiac (A) and Skeletal (B) Muscle ^{31}P Spectra at 3T

DISCUSSION AND CONCLUSION

3T offers exciting opportunities for the development of cardiac ^{31}P spectroscopy, which is fundamentally SNR limited. These T_1 values will allow us to quantify accurate PCr/ATP ratios. The increased SNR at 3T will enable us to perform high spatial-resolution ^{31}P exams to look at focal metabolic changes, and the use of ^{31}P to monitor dynamic changes in cardiac metabolism.

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