

Meeting abstract

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147 ³¹P Cardiac spectroscopy at 3 T: T1 quantification

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Introduction

Phosphorus (³¹P) MRS provides measures of the high energy metabolites, phosphocreatine (PCr) and adenosine triphosphate (ATP), in the heart. It permits the evaluation of ischemic changes during myocardial stress [1], and ATP turnover through the creatine-kinase reaction in the normal and failing human heart[2,3]. Recent cardiac ³¹P MRS studies suggest higher signal-to-noise ratio (SNR) at 3 T compared to 1.5 T in healthy subjects[4]. For accurate metabolite quantification, the longitudinal relaxation times (T1) are needed, and measuring these at 3 T is confounded by the combined effects of: (i) RF field uniformity with surface coil use; (ii) the available RF pulse power and its decrease with depth; and (iii) RF power deposition limits. While prior studies at 1.5 T used low-angle adiabatic (BIR4) pulses [2,3], at 3 T these are limited by low bandwidth and high power requirements. We show, using a Bloch equation analysis that such effects can significantly reduce the accuracy of T1 measurements at long adiabatic pulse lengths (≥ 10 ms) for ³¹P MRS, but that the problems are ameliorated by use of adiabatic half passage 90° (AHP) pulses.

The first aim of this work was to construct a high-SNR surface coil set for 3 T cardiac ³¹P MRS that provides adequate adiabatic pulse power at the depth of the myocardium, while avoiding local power deposition problems. The second aim was to determine the T1 of PCr and γ -ATP in the human heart using a new, efficient dual repetition time (2TR) approach that minimizes T1 estimation errors at 3

T. The method is validated against the conventional saturation-recovery (SR) method.

Methods

A dual ³¹P coil with 17-cm transmitter and 8-cm receiver set was designed and built to optimize the transmit RF field at a 10 cm depth with 4 kW transmit power. Coils were interfaced to a 3 T Achieva (Philips) broadband scanner. RF power deposition was computed and measured calorimetrically in phantoms to ensure safe performance. AHP pulses (10 ms) were tailored to achieve an excitation bandwidth ≥ 200 Hz for depths ≤ 10 cm. Six healthy volunteers (4 M/2 F, 28 ± 6 years) were positioned prone with the heart centered over the surface coils, as verified by scout-MRI. Localized second-order shimming[5] was performed, followed by cine-MRI to determine the period of least cardiac motion. The ³¹P frequency was set between PCr and γ -ATP. Cardiac-gated one-dimensional chemical shift imaging was performed with TR = 2, 4, 12, 32 s with 24, 12, 4, and 2 averages, respectively (16 slices; 10 mm slice thickness; 2.5 kHz bandwidth).

T1 values for the human heart were determined from the signal $S(TR) = M_0(1 - \exp(-TR/T1))$, where M_0 is the fully-relaxed magnetization, in three ways:

1) Conventional SR with a two-parameter least-squares fit;

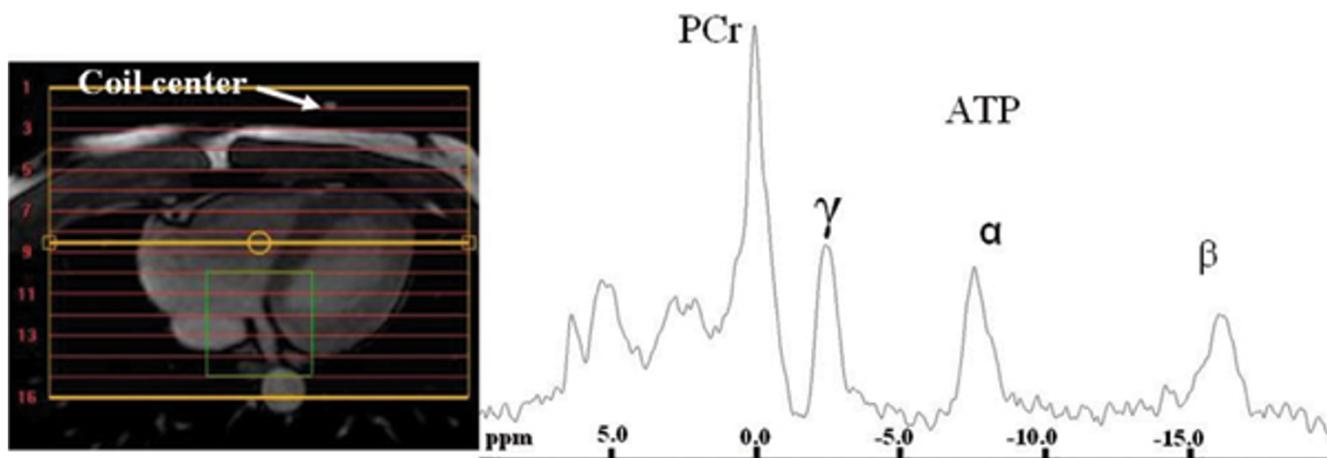


Figure 1
A custom coil and protocol for human cardiac 3 T 31P MRS is used to measure the T1s of PCr and -ATP in the human heart via saturation recovery, and a new, efficient dual-TR approach that reduces bandwidth and power requirements. Left, end-systolic time-frame cardiac image showing coil center and IDC SI slice locations. Right: Cardiac 31P Spectrum (slice 7; TR = 12 s; 10 Hz filter; 13 min).

2) Point estimation (PE) with $M_0 = S(TR = 32\text{ s})$ as prior knowledge;

3) The new 2 TR method (with TRs of 2/12 s and 4/12 s)

In addition M_0 was predicted (M_0^p) from the measured signal at the shorter TR and the estimated T1 from both of the 2 TR methods. Percentage errors were calculated as $(M_0^p - S(TR = 32\text{ s})) / S(TR = 32\text{ s}) * 100\%$.

Results

Cardiac spectra with PCr SNR ≥ 30 were acquired in all 6 volunteers (Figure 1). Conventional SR gave mean T1 values of 5.9 s for PCr and 3.1 s for γ -ATP (Table in Figure 2). Dual TR gave similar T1s in scan-times of 26 minutes, just

46% of the SR scan-time of 56 minutes, albeit with slightly larger errors.

Conclusion

Bandwidth and RF power limitations at 3 T necessitate significant modifications to 31P MRS protocols as compared with 1.5 T. Our new dual-TR method provides fast cardiac 31P spectra acquisition at 3 T, predicting the fully-relaxed magnetization within a 10% error compared with actual fully-relaxed values.

	Method	SR	PE TR=2	PE TR=4	2TR TR 2/12	2TR TR 4/12
PCr	T1 [s]	5.9 ±0.6	6.0±0.7	5.7 ±0.4	5.9 ±0.8	5.3 ±0.9
	M_0 % error	2 ±1			9 ±3	11 ±5
γ -ATP	T1 [s]	3.1 ±0.6	3.2 ±0.5	3.3 ±0.6	2.7±0.5	2.8 ±0.9
	M_0 % error	4 ±2			9 ±4	10 ±3

Figure 2
 Measured T1 values in 6 healthy volunteers (mean ± stdev) for PCr and γ -ATP using the 3 methods as described in the text. Percentage error for the predicted fully relaxed magnetization are reported.

References

1. Weiss : *N Engl J Med* 1990, **23**:1593.
2. Weiss : *PNAS* 2005, **102**:808.
3. Smith : *Circulation* 2006, **114**:1151.
4. Tyler : *ISMRM* 2006:3089.
5. Schär : *MRM* 2004, **51**:799.

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