QUANTITATIVE CARDIAC 31P SPECTROSCOPY AT 3T: PRACTICAL LIMITATIONS AND SOLUTIONS

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Introduction: Phosphorus (^{31}P) MRS measures high energy metabolites, phosphocreatine (PCr) and adenosine triphosphate (ATP) in the heart. It can detect ischemia during myocardial stress [1], and ATP turnover through the creatine-kinase reaction in normal and disease states [2,3]. Cardiac ^{31}P MRS could benefit from higher signal-to-noise ratio (SNR) at 3T compared to 1.5T [4], but uniform flip-angles and metabolite T1 measurements are essential for accurate metabolite quantification given that surface coils are invariably used.

At 1.5T, low-angle adiabatic (BIR4) pulses are used for quantification and dual-angle T1 measurements [2,3], but these are limited at 3T by high RF power requirements and power deposition. When longer BIR4 pulses (≥ 10 ms) are applied instead to reduce the B1 threshold, Bloch equation analysis shows that low bandwidth and T2 decay result in magnetization errors in ^{31}P MRS protocols, and errors in dual-angle T1 measures (Fig. 1). This problem is reduced with 90° adiabatic half passage (AHP) pulses.

We constructed a high-SNR surface coil set for 3T cardiac ^{31}P MRS that provides adequate adiabatic pulse power at the myocardium with a product 4kW broadband power amplifier, while avoiding local power deposition problems. A new efficient AHP dual repetition time (2TR) method is introduced to minimize T1 errors at 3T, and validated against conventional saturation (SR) and inversion recovery (IR) methods. The method is used to determine the T1 of PCr and γ-ATP in human heart.

Methods: A dual 17-cm transmit and 8-cm receive ^{31}P surface coil set was designed and built to optimize the transmit RF field at a 10cm depth with the available power from a broadband 3T Philips Achieva scanner. RF power deposition was computed and measured calorimetrically in phantoms to ensure safety. 10g average SAR was ≤ 10W/kg with 10ms AHP pulses at TR ≥ 1.2s. The AHP pulses were tailored to excite a bandwidth of ≥ 200Hz at depths of ≤ 10cm. The 2TR sequence was validated on 7 NiCl doped H_2PO_4 phantoms with 2s < T1 < 6s using an 11-point IR method. T1s from the 2TR method were estimated from signal ratios at the two TRs, and agreed closely to T1s by IR (Fig. 2).

Human studies: Eight healthy volunteers were positioned prone with the heart centered over the surface coils. Cardiac-gated one-dimensional chemical shift imaging (1DCSI) was performed with TR =2, 4, 12, 32s (Averages=24, 12, 4, and 2l; sixteen 10 mm thick slices). 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 two ways: 1) **SR** with a two-parameter least-squares fit; 2) the new **2TR** method with TRs of 2/12s and 4/12s. In addition, M_0 was predicted from the measured signal at the shorter TR and the estimated T1 from both 2TR methods. The % error vs the measured signal at TR=32s is calculated.

Results: Cardiac spectra with SNR ≥ 30 for PCr were acquired in all volunteers (Fig. 3). Conventional SR gave mean T1 values of 5.8s for PCr and 3.1s for γ-ATP (Table) in 56 min scans, in agreement with 2TR T1s recorded in just 26 min, with some evidence of multiple components.

Conclusion: Bandwidth and RF power limitations at 3T necessitate significant modifications to routine cardiac ^{31}P MRS protocols as compared with 1.5T. Our new 2TR method provides fast cardiac ^{31}P spectra acquisition at 3T, predicting the fully-relaxed magnetization within a 10% error compared to fully relaxed values, which is critical for quantifying absolute concentrations.

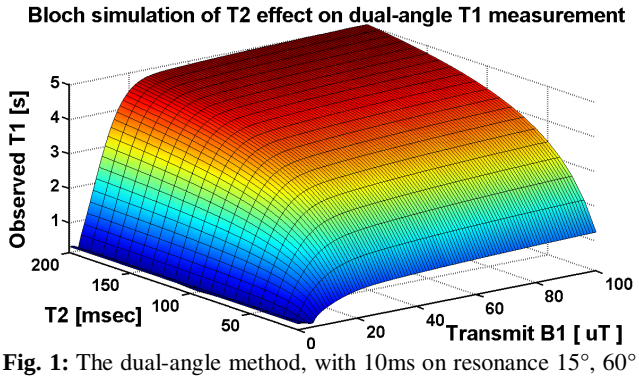

Fig. 1: The dual-angle method, with 10ms on resonance 15°, 60° BIR4 pulses (8kHz sweep and TR=1s), yields an erroneous T1 estimate of ~3.5s for PCr with true T1=6s and T2=70ms. Observed T1=5.9s when using 10ms AHP 2TR method (2/12s).

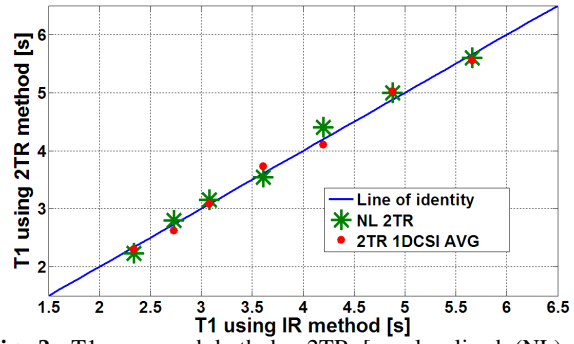

Fig. 2: T1 measured both by 2TR [non-localized (NL) and average 1DCSI (nine 1cm slices)] and 11 point NL IR methods.

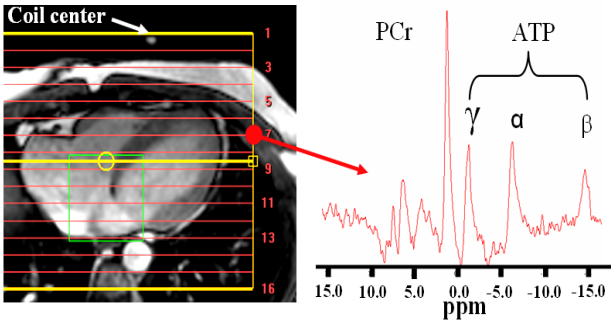

Fig. 3: End-systolic cardiac image showing 1DCSI slice locations, and cardiac ^{31}P MRS (slice 7; TR=12s; 13 min).

	Method	SR	2TR TR 2/12	2TR TR 4/12
PCr	T1 [s]	5.8 ±0.5	5.9 ±0.8	5.3 ±0.8
	M_0 % error	2 ±1	9 ±3	8 ±6
γ-ATP	T1 [s]	3.1 ±0.6	2.8±0.5	2.8 ±0.7
	M_0 % error	4 ±2	9 ±4	9 ±4

Table: Cardiac T1 values for PCr and γ-ATP by SR and 2TR methods and error in predicted fully-relaxed M_0.

References: 1.R. G. Weiss et al, N Engl J Med 1990:323 ;1593; 2. R. G. Weiss et al , PNAS 2005:102 ;808; 3. C. S. Smith et al, Circulation 2006:114 ;1151; 4. D. J. Tyler et al, ISMRM 2006 ;3089;

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