

## Human Cardiac $^{31}\text{P}$ Metabolite Concentrations at 3T

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**INTRODUCTION.** Phosphocreatine (PCr), is the main energy reservoir in both skeletal and cardiac muscles, supplying ATP energy for contraction via the creatine kinase (CK) reaction. Cardiac  $^{31}\text{P}$  MRS measurements of absolute ATP and PCr concentrations could

benefit from higher magnetic field strengths, but is challenged by  $T_2$ -decay, increased RF power deposition, and field inhomogeneities. While these have been specifically addressed at 3T [1,2], approaches to concentration measurements employing water-referencing and  $^1\text{H}$  signal detection with a single tuned  $^{31}\text{P}$  coil [3] are compromised at 3T due to differences in spatial sensitivity at the higher field strengths.

This work presents a new method and semi-automated tool for measuring PCr and ATP concentrations from 1D chemical shift imaging (CSI)  $^{31}\text{P}$  spectra that compensates for the nonuniform sensitivity. It is validated in phantoms and applied to the human heart.

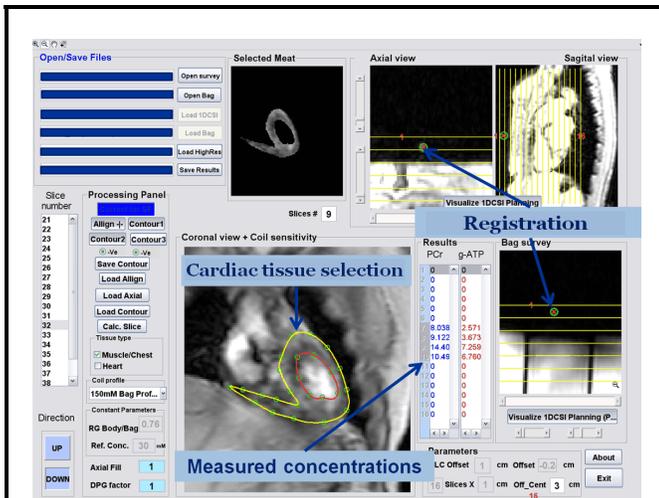
**METHODS.** The method utilizes a single 1D CSI acquisition with a 5ms duration, 7kHz-sweep, frequency-cycled adiabatic half passage pulse [2]. Bloch equation analysis shows that this yields >95% of the magnetization [1]. Using a 17cm/8cm transmit/receive  $^{31}\text{P}$  coil set in a Philips 3T Achieva scanner, this permits cardiac measurements at depths of up to 8-9cm [1,2]. A 2cm diameter sphere filled with  $\text{NaH}_2\text{PO}_4$  and a vitamin pill were both fixed to the coil housing to compensate for loading differences and to register the subject with a concentration reference, respectively. A ~6cm diameter cylindrical phantom containing 30mM  $\text{NaH}_2\text{PO}_4$  was used for the concentration reference. A single 3DCSI scan of a 32x32cm<sup>2</sup> 600mM  $\text{NaH}_2\text{PO}_4$  phantom was used to map the coil's sensitivity profile.

Multi-slice high-resolution  $^1\text{H}$  MRI was used to identify the target tissue. Metabolite concentrations were calculated from:

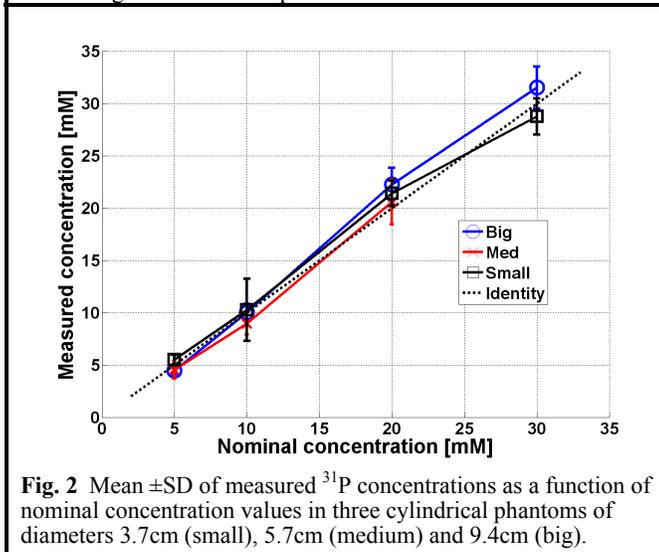
$$[\text{Metabolite}]_{\text{muscle}}^n = \frac{S_{\text{muscle}}^n \cdot (1 - \exp(-TR_{\text{ref}} / T1_{\text{ref}})) \cdot \sum_i \sum_j w_y^{\text{ref}} C_{ij}^n}{S_{\text{ref}}^n \cdot (1 - \exp(-TR_{\text{muscle}} / T1_{\text{muscle}})) \cdot \sum_i \sum_j w_y^{\text{muscle}} C_{ij}^n} \times F_g \times F_m \times [^{31}\text{P}]_{\text{ref}}^n$$

where S is the fitted spectral area, n is the slice number, W is the selected area from images, C is the coil sensitivity,  $F_g$  is the measured loading factor,  $F_m$  is a measured motion correction factor for the heart, determined from free breathing axial cine images, and *ref* denotes the reference phantom. Peak areas were quantified using the CFIT routine [4]. Fig. 1 shows the *Matlab*-based software interface to perform all of the described operations for obtaining concentration values.

**EXPERIMENTS AND RESULTS.** The method was validated in 11 cylindrical phantoms of different diameters (3.7, 5.7 and 9.4 cm) and concentration values (5, 10, 20 and 30 mM). The mean measured  $^{31}\text{P}$



**Fig. 1** Screen shot of the concentration quantification tool illustrating the different steps used.



**Fig. 2** Mean  $\pm$ SD of measured  $^{31}\text{P}$  concentrations as a function of nominal concentration values in three cylindrical phantoms of diameters 3.7cm (small), 5.7cm (medium) and 9.4cm (big).

concentration values agreed with the known phantom concentrations with a root-mean-square error of ~8% on average (Fig. 2).

Institutional Review Board-approved human cardiac studies were performed on 10 consenting healthy volunteers. Cardiac-triggered 16-step 1DCSI  $^{31}\text{P}$  data were acquired with subjects prone on the coil set (field of view=16cm; repetition time  $\approx$ 16s; 2 averages; scan-time <10min). We measured an average cardiac [PCr] of  $9.3 \pm 1.7$  and [ $\gamma$ -ATP] of  $5.2 \pm 1.0$   $\mu\text{mol/g}$  wet wt, in agreement with prior measures at values at 1.5T ([PCr]/[ATP]= $10 \pm 2/5.8 \pm 1.6$   $\mu\text{mol/g}$  [3], and  $9 \pm 1.2/5.3 \pm 1.2$   $\mu\text{mol/g}$  [5]).

**CONCLUSION.** A new semi-automated, image-guided method for measuring  $^{31}\text{P}$  concentrations in the human heart was developed that overcomes a number of challenges at 3T. The approach was validated in phantom studies, and provides PCr and ATP concentrations in healthy human hearts that closely agree with prior measures at 1.5T. The measurements can be performed in ~9min within a patient exam and thus can be part of a practical, quantitative cardiac  $^{31}\text{P}$  clinical research protocol.

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3. Bottomley PA et al. *Magn Reson Med* 1996;35(5):664-670. 4. Gabr RG et al. *J Magn Reson* 2006;179(1):152-163. 5. Meininger M et al. *Magn Reson Med* 1999;41(4):657-663. **Supported by NIH R01 HL56882, R01 HL61912 and a grant from the D.W. Reynolds Foundation.**