A 16-element receive array for human cardiac ^{31}P MR spectroscopy at 7T

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Purpose: Phosphorus MR spectroscopy (^{31}P-MRS) is an important tool for studying cardiac metabolism, but clinical applications of ^{31}P-MRS have been hindered by low intrinsic signal-to-noise ratios (SNR). Human cardiac ^{31}P-MRS has recently been demonstrated at 7T[(1)]. In that work, an SNR gain of 2.8x was reported comparing 10cm loop coils at 7T and 3T. However, these 10cm loop coils had a limited field-of-view, which made coil positioning critical. Theory predicts that a 7T receive array coil could increase this SNR still further, while also increasing the field-of-view, making coil placement less critical, making it straightforward to scan women as well as men, and perhaps allowing spectra to be acquired from all regions of the heart. We therefore introduce the first receive array for human cardiac ^{31}P-MRS at 7T and compare its performance against a 10cm loop coil.

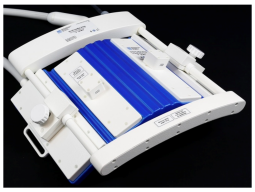

Figure 1: Novel 7T ^{31}P 16-element receive array.

Methods: All scans used a Siemens Magnetom 7T MRI scanner. The array coil shown in Figure 1, designed in collaboration with Rapid Biomedical GmbH, comprises an anterior 4x4 matrix of 8x5.5 cm^2 diameter flexible receive loops (adapted from a 3T ^{1}H cardiac array coil) and a 28x27 cm^2 single loop ^{31}P transmit element. The coil has no ^{1}H elements, but does have ^{1}H traps so a separate ^{1}H coil can be placed behind the array for localization. Five 18mm od plastic spheres filled with phenylphosphonic acid solution[(1)] were mounted on the flexible receive array housing.

Coil performance was tested using a phantom comprising 18L of 73mM $NaCl_{(aq)}$ inside which sits a height-adjustable 2cm $KH_2PO_{4(aq)}$ cube. Fully-relaxed non-localised FIDs were acquired for a range of excitation voltages. Using a custom Matlab tool, the KH_2PO_4 peak amplitude in each spectrum was determined using AMARES. These amplitudes were then fitted to a sinusoid to determine the voltage for a 1ms 180° hard pulse at that depth. Finally, a fully relaxed spectrum with 90° excitation was acquired to characterise receive performance at the same depth.

Twelve normal volunteers (7 men, 5 women) were recruited in compliance with local regulations. Subjects were positioned head-first-supine, CINE FLASH localizers were acquired using a 10cm ^{1}H loop (Rapid Biomedical GmbH). This coil was then swapped for *either* the 16-element ^{31}P array *or* a 10cm ^{31}P loop[(1)] as a control. ^{31}P FLASH projection images and non-localized inversion recovery FIDs (IR FIDs) were acquired. From these, a custom Matlab tool finds the coil geometry and computes a B_1^+ map. UTE-CSI ^{31}P spectra were then acquired from a 16x16x8 matrix with 240x240x200 mm^3 FOV adjusting the number of acquisition weighting averages to give a 28min duration for each scan. With the 10cm loop, we set TR=1000ms; with the 16-element array, initial tests with TR=1000ms showed poor SNR because the flip angle in the septum at maximum voltage was ~20°. The Ernst angle for PCr at TR=1000ms is 44°, while for ~20° flip angles, TR=192ms (PCr) or TR=63–113ms (α,β,γ-ATP) will maximise SNR efficiency. The PCr/ATP ratio is perturbed less by a TR a little longer than the Ernst optimum. Therefore, we chose to test TR=330ms and TR=130ms in vivo. In some scans, we revised the BISTRO saturation scheme to split the HS8 pulse-train across 5 readouts (allowing higher V_{max} for equal SAR) instead of 5x HS8 pulses per readout. Bloch simulations predict this saturates better. Later, the spectrum in the mid-septal voxel was fitted with AMARES in Matlab[(2)], metabolite SNRs and ratios were computed, and then finally corrected for partial saturation and blood contamination[(1)].

Results/Discussion: Figure 2a compares B_1^+ for the 7T 16-element array, the 7T 10cm loop and two other 3T ^{31}P coils available in our lab. At the depth of the heart (10cm), the 10cm loops require ~2x the voltage for a 1ms 180° at 7T, the same applies to the other coils which have very similar transmit element geometries. To excite the full range of metabolites in the heart by 90°, a hard pulse would need to run with 2650V, i.e. 140kW!

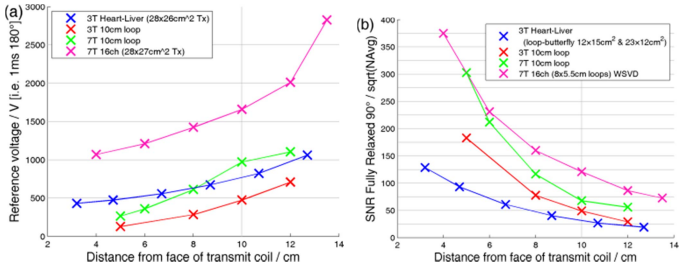

Figure 2: Phantom calibration of (a) transmit and (b) receive performance comparing four ^{31}P coils operating at 7T or 3T. Lines are only to guide the eye.

In terms of SNR, Figure 2b shows SNR for a 90° pulse in the phantom. At 10cm depth, the 16-element array outperforms all our other 31P coils – the array has 1.8x greater SNR than the 7T 10cm loop and 3.6x greater SNR than the "Heart-Liver" coil (Siemens) which was our benchmark coil at 3T[(3)]. In vivo, a paired comparison in 5 men (see Table 1) shows a modest increase in SNR for both PCr and ATP. To disentangle the effect of limited peak B_1^+, we extrapolate to a hypothetical fully-relaxed 90° excitation which would have α-ATP SNR = 44 ± 13 for the 7T 10cm loop and 77 ± 14 for the 16-element 300ms TR data, i.e. a 75% increase. The other metabolites show comparable increases. Comparing men and women, the 330ms SNR in women is reduced by an average of 13% for ATP and 5% for PCr, which means that the 16-element array can be used without complication to scan women as well as men. Finally, we also ran with TR=130ms for the 5 women. This showed a modest 6% decrease in ATP SNR and a 22% decrease in PCr SNR, but the saturation corrected PCr/ATP changed by only 0.1. This suggests that saturation correction is operating correctly and that TR=330ms is close to optimal given our limited B_1^+.

Table 1: Summary of human cardiac ^{31}P-MRS results.	10cm male (N=5)	16ch male 330ms (N=5)	16ch female 330ms (N=5)	16ch female 130ms (N=5)
PCr SNR	26 ± 6	38 ± 16	36 ± 12	28 ± 12
γ-ATP SNR	16 ± 5	19 ± 4	15 ± 2	14 ± 3
PCr linewidth / Hz	35 ± 8	31 ± 10	36 ± 15	40 ± 10
Flip angle / °	28 ± 8	18 ± 1	19 ± 2	19 ± 2
Sat. corr. PCr/ATP	1.7 ± 0.3	2.0 ± 0.5	2.2 ± 0.6	2.1 ± 0.7
+ blood correction	2.0 ± 0.5	**2.4 ± 0.5**	**3.0 ± 0.7**	**2.7 ± 0.8**

However, critically, we observe that the blood- and saturation-corrected PCr/ATP ratios are considerably higher than the normal ~1.8-2.2 range[(4)], particularly for the women. We have probed 5 possible explanations: (1) Failing blood fitting (Fitted 2,3-DPG/PCr ratios were 78% in women vs 59% in men. We constrained the 2,3-DPG linewidth to match that in the average spectrum from surrounding voxels. These 2,3-DPG fits were clearly excellent, but left PCr/ATP = 2.9 ± 0.7); (2) Failing blood correction (TR < 1xR-R now, so blood may show partial saturation. Correction needs blood 2,3-DPG and ATP T_1s and % in-flow.); (3) Skeletal muscle contamination due to poor saturation (But the theoretically improved "split-saturation" scheme actually increased PCr/ATP to 3.0 vs 2.8 before.); (4) Contamination due to the very high surface receive sensitivity of the array (see Fig. 2b); or (5) Changes in T_1^{eff} at short TR due to CK flux.

Conclusion: The receive SNR at the heart is 1.8x better for this array than a 10cm loop. But, B_1^+ is inadequate to achieve reliable saturation of skeletal muscle or for Ernst angle excitation with 1s TR at the heart, so our standard CSI protocol yields physiologically implausible PCr/ATP ratios.

1. Rodgers, MRM, 2013. 2. Purvis, ISMRM, 2014. 3. Tyler, NMR Biomed, 2008. 4. Bottomley, Encycl. MR, 2009. Funded by the Wellcome Trust and the Royal Society (098436/Z/12/Z) & MRC.