Highly Accelerated Cine-MRI in Mouse Hearts Using Compressed Sensing and Parallel Imaging at 9.4T

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Introduction: Parallel Imaging (PI) and Compressed Sensing (CS) are fundamentally different methods to speed-up Magnetic Resonance Imaging (MRI). More specifically, PI (i.e. TGRAPPA) has recently been demonstrated to provide a three-fold acceleration of cine-MRI in normal mice (1), while CS also allowed for a three-fold reduction in scan time in normal mice and in a murine model of chronic myocardial infarction (2). In both cases, the increase in speed was achieved without impacting on the accuracy and reproducibility of cardiac functional parameters. We now aimed to combine PI and CS to further accelerate cine-MRI in murine models of cardiovascular disease.

Materials & Methods: All experiments were conducted on a horizontal, 9.4T MR system (Agilent) equipped with a 600 mT/m gradient system and 8 receive-channels. Fully sampled cine-data (8-9 short-axis slices and long-axis 2-and 4-chamber views) were obtained in adult C57BL/6 mice (40.4 ± 4.8 g, n = 5), using a double-gated 2D multi-frame GE-sequence (TE/TR=1.79/4.6ms, FOV=30 x 30 mm, matrix size 256 x 256, slice thickness 1 mm, 1 average, 22-26 frames per cardiac cycle) and an 8-channel probehead, respectively. These data were retrospectively undersampled and subjected to a hybrid image reconstruction consisting of two consecutive steps: first, a CS-algorithm exploiting spatio-temporal sparsity as proposed by Lustig et al (3) was utilized to generate an up to 4-fold undersampled k-space. Subsequently, TGRAPPA (4) was applied to obtain fully sampled cine-data. Cardiac functional parameters were then determined by an operator, who was blinded to animal ID and acceleration factor combination, using the Guide Point Modelling approach (5).

Results: Figure 1 shows the end-diastolic frame of a mid-ventricular slice across a mouse heart, comparing the fully sampled image (left) to the corresponding frames with undersampling factors 4, 8, 9 and 16. Reconstruction times were about ~ 5 min per slice on an Intel i5-680 / 16GB RAM computer. Adequate image quality was obtained even for 16-fold undersampled data. The acceleration by CS had a less detrimental effect on image quality compared to PI. Table 1 lists the cardiac functional parameters for fully, and up to 9-fold undersampled data sets. While there seemed to be a trend towards smaller volumes / mass with increasing acceleration factors, functional parameters agreed generally well between unaccelerated and accelerated data.

Figure 1: *Fully sampled, and reconstructions of retrospectively undersampled end-diastolic frames through a mid-ventricular slice across a mouse heart in end-diastole. The scale bar indicates 5mm, and the acceleration factors are given as* R_{CS} *x* R_{PI}*.*

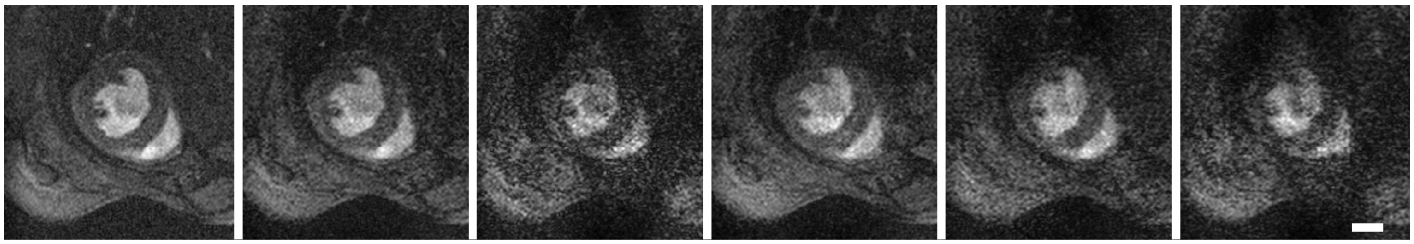

Table 1: *Left-ventricular mass and volumes (mean ± SD, n = 5).*

	LVMass in mg	EDV in µl	ESV in µl	SV in µl	EF in %
1x1	88.8 ± 6.8	56 ± 11	19.0 ± 6.4	37.5 ± 4.9	67.1 ± 4.6
2x2	80 ± 11	55 ± 14	18.5 ± 5.6	36.8 ± 8.8	66.9 ± 2.0
3x3	74 ± 12	50 ± 14	17.2 ± 4.4	32.7 ± 9.7	65.4 ± 2.9

Discussion & Conclusion: Our data suggest that the combination of PI and CS will significantly reduce acquisition time down to the minute-range for cardiac functional MRI in mice at ultra-high magnetic fields. Work is in progress to assess intra-observer variability, to implement this technique directly on the scanner, and to validate it further in a disease model.

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