Rapid T_2 Mapping of Mouse Heart Using CPMG Sequence and Model-based Compressed Sensing Reconstruction

Y. Chen[1,2], W. Li[1,2], and X. Yu[1,2]
[1]Department of Biomedical Engineering, Case Western Reserve Univ, Cleveland, OH, United States, [2]Case Center for Imaging Research, Case Western Reserve Univ, Cleveland, OH, United States

Quantification of proton transverse relaxation time T_2 provides important information in a variety of pathological conditions. To date, mouse models have been widely used for the study of genetic factors in cardiovascular diseases. However, due to the small size of a mouse heart and its fast heart rate, an accurate T_2 measurement of mouse heart has been challenging. The purpose of this study was to develop a novel method for rapid T_2 mapping of mouse heart in vivo. Our results demonstrate that a high temporal resolution of ~15 seconds can be achieved by combining a fast multi-echo spin-echo sequence with a model-based compressed sensing (CS) reconstruction.

Methods MRI experiments were conducted on a 7T Bruker (Billerica, MA) horizontal bore scanner. Standard Carr-Purcell-Meiboom-Gill (CPMG) sequence was modified for rapid acquisition of T_2 mapping. The slice thickness of refocusing pulse was adjusted to three times of the excitation pulse to minimize the stimulated echo effect [1]. A minimum TE of 4.5 msec was achieved by reducing gradient encoding time and RF pulse duration. With the reduced minimum TE, more echo images can be acquired under the same data acquisition window to achieve more robust T_2 fitting.

The accuracy of T_2 values obtained with the CPMG sequence was validated using a multi-compartment phantom of $MnCl_2$ solution at various concentrations. T_2 values measured with a long-TR single-echo spin-echo sequence were used as the gold standard reference. For the single-echo sequence, the imaging parameters were: TR = 5s, TE = 4.5-300 msec (13 TEs). For the CPMG measurement, TR = 200 msec, TE = 4.5 ~ 45 msec, echo number = 10.

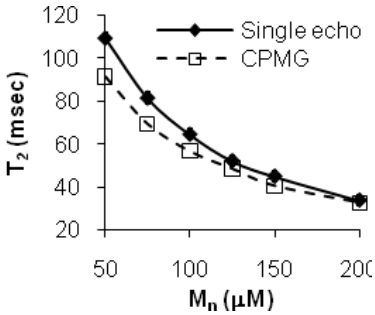

Fig. 1. Measured T_2 values at various $MnCl_2$ concentrations using single-echo and CPMG sequence.

In vivo cardiac T_2 mapping from four C57BL/6 mice (3~6 months) were obtained with an ECG-triggered CPMG sequence at mid-ventricle. A TR of 200 ~ 400 msec was used, corresponding to triggering at every two or three cardiac cycles. Total data acquisition time for one T_2 map was about 25~50 seconds. Depending on the heart rate, 8 to 10 echo images were acquired during mid- to end-diastole to minimize the motion artifact. Other imaging parameters were: matrix size, 128×64; number of averages, 2. A separate long-TR (~1000 msec) CPMG measurement was also performed to compare with the results obtained from the short-TR measurement.

Further reduction of acquisition time can be achieved through random under-sampling of the k-space lines and reconstruction of the images using compressed sensing. The accuracy of such an approach was evaluated by retrospectively under-sampling the fully-sampled images with a data reduction factor of 2. A mono-exponential model was used to describe the MR signals acquired under multiple TE values for each voxel. The undersampled images were then reconstructed using orthogonal matching pursuit (OMP). Using an over-complete dictionary that included T_2 values from 2 msec to 1000 msec, eight atoms with the highest correlation to the measured signal were selected [2]. The T_2 map was then calculated from the reconstructed images and the results were compared to those obtained from fully sampled dataset.

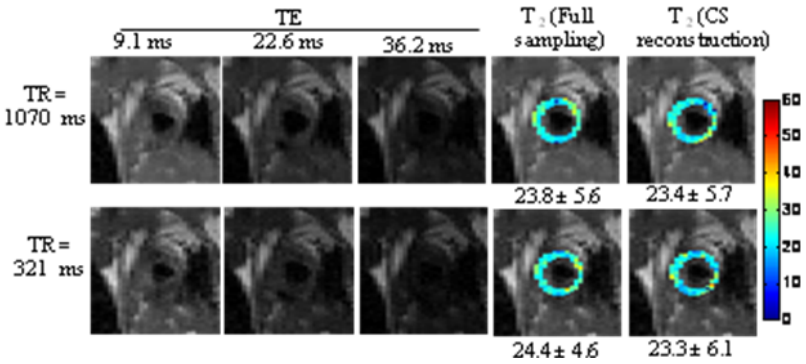

Fig. 2: Representative T_2-weighted images and T_2 mapping of mouse heart acquired using CPMG sequence at two different TRs. T_2 mapping was calculated with both full sampling and CS reconstruction (R = 2).

Results Results from phantom study suggest that T_2 values acquired with the short-TR CPMG sequence agreed well with the results from long-TR single-echo sequence when T_2 was <50 msec (Fig. 1). The discrepancy at longer T_2 values was mainly caused by the choice of a relatively short maximum TE value of 45 msec for the short-TR CPMG method. For in vivo study, both short-TR and long-TR CPMG methods yielded similar T_2-weighted images and T_2 maps of mouse hearts (Fig. 2). The average T_2 values for the four mice were 23.2 ± 4.1 and 21.9 ± 4.4 msec, respectively (Fig. 3).

Accurate T_2 mapping was also achieved from CS reconstruction with a data reduction factor of 2 (Fig. 2). The average T_2 values for short-TR and long-TR methods with CS reconstruction were 21.7 ± 3.7 and 20.6 ± 4.5msec, respectively, which agrees well with the results obtained from fully sampled data (Fig. 3). These results suggest that the imaging acquisition time can be further reduced by half.

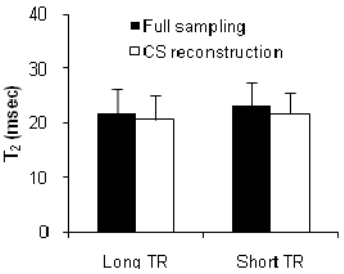

Fig. 3: Mean T_2 of mouse heart with full sampling and CS reconstruction.

Conclusions In this study, a modified CPMG sequence was developed for rapid T_2 mapping of mouse heart. Using a model-based CS approach, accurate T_2 mapping was achieved with highly reduced data sampling. These methods combined together can be used to provide accurate and efficient T_2 measurement of mouse heart at 15 s temporal resolution.

References

[1]Pell GS, et al., JMRI, 2010. [2] Tropp Jand Gilbert A, IEEE Trans Inf Theory, 2007.