Multi-slice Look-Locker T_1 mapping for the mouse heart

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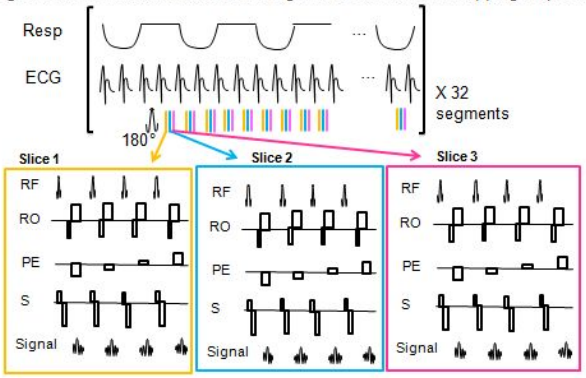
Introduction: Perfusion refers to blood flow at a capillary level, which is a vital parameter in cardiac physiology and for cardiac research studies. Perfusion can be measured non-invasively using arterial spin labelling (ASL) MRI. Accurate T_1 mapping is particularly important for the application of cardiac ASL. However, T_1 mapping tends to be quite challenging in the mouse heart due to very fast heart rates and respiratory corruption of images. To date, ASL has been performed in the mouse heart by small number of groups [1,2,3], using single-slice ECG-gated Look-Locker T_1 mapping. This T_1 mapping approach traditionally requires long scan times (20-30 minutes for one T_1 map). Other studies have investigated 3-dimentional T_1 mapping of the myocardium in the mouse [4,5].

In this study, we present the first multi-slice ECG-gated Look-Locker T_1 mapping sequence, with segmented k-space, for multi-slice T_1 mapping of the mouse heart. Using this sequence, T_1 mapping of multiple slices can be completed in less than 10 minutes. This sequence will be highly applicable to generate multi-slice ASL data sets in a time-efficient manner.

Methods: The ECG-gated Look-Locker from Kober et al [1] was modified so that four lines of k-space are acquired with gradient echo readout, for *s* slices, during each cardiac cycle throughout T_1 recovery. Inversion recovery was repeated 32 times to generate a full 128x128 k-space matrix. The sequence, for 3 slices, is shown in Figure 1. Approximately 10ms was required for the acquisition of each slice segment. The small angle approximation of the Look-Locker T_1 correction factor was used to correct for the saturation effects of un-evenly spaced RF pulsing during T_1 recovery [6].

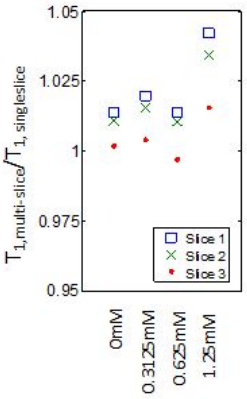
The multi-slice Look-Locker T_1 mapping sequence was implemented on a Varian 9.4T system (Varian Inc. Palo Alto, CA, USA) and all image analysis and curve fitting was performed in MATLAB. The accuracy of the multi-slice T_1 quantification was verified using Ni^{2+}-agar phantoms of varying concentration, using 3 slices. As a preliminary *in vivo* investigation, the sequence was applied to one male CD-1 mouse with 3 slices. Single slice T_1 map and multi-slice T_1 maps with global inversion pulse were compared (TE/TR(inv)/TR(RF)=1.18ms/13.5s/1.2ms, flip angle=5°, in-plane resolution=200µm, slice thickness=1.5mm, number of slices = 3, slice gap = 1mm, number of points in IR = 50). Timings of each R-wave, respiration event and RF pulse were recorded on a data logger. A 3-parameter T_1 recovery curve was fitted pixel-wise, using the mean inversion times computed from the data logger information. In addition, the data logger recording was used to reject respiration-corrupted images.

Figure 1: Time-efficient multislice ECG-gated Look-Locker T1 mapping sequence



Results: Figure 2 presents a comparison of single slice and multi-slice T_1 values in Ni^{2+} phantoms. T_1 values agreed within 4% for all Ni^{2+} concentrations. Figure 3 presents the *in vivo* T_1 maps using single-slice and multi-slice T_1 mapping. The mean T_1 values were calculated for an ROI of the entire myocardium and it was found that T_1 values agreed within 10%.

Figure 2: Verification of T1 mapping in a phantom. $T_{1,multi\text{-}slice}/T_{1,single\text{-}slice}$ is plotted. The error is <4% for all concentrations. Slice 2 = single slice acquired



Discussion: A multi-slice ECG-gated Look-Locker T_1 mapping sequence was successfully implemented and tested in a phantom and in-vivo. It was found that T_1 values from single and multi-slice T1 mapping agreed very well within a phantom and *in vivo*. There was a suggestion of a slight slice bias in the T_1 quantification in the phantom. *In vivo*, the slight decrease in T_1 when using multi-slice acquisition could be due to magnetisation transfer effects [7]. This hypothesis is supported by the fact that the T_1 decrease correlates to the slice acquisition order. However, magnetisation transfer effects are fairly subtle in this multi-slice T_1 mapping sequence compared to others, due to the very small RF pulses used. Since the acquisition time for each slice segment is approximately 10ms, there may be small differences in the cardiac phase between slices, which will depend on physiological factors and gating.

When applying this technique to ASL, it is important that the inversion pulse is centred around the slice pack for the slice-selective inversion. This sequence could also be applied to observe changes in perfusion in the same slice throughout the cardiac cycle. Applying this multi-slice T_1 mapping to ASL will provide cardiac researchers with a comprehensive methodology to assess cardiac perfusion, which could generate new insight into cardiac disease.

In conclusion, a multi-slice Look-Locker sequence has been designed for implementation in the mouse heart. Time-efficiency and multi-slice capabilities of this sequence give it great potential utility in studying perfusion in cardiac disease models. There is opportunity for further sequence development and investigation into magnetisation transfer, slice order and application to ASL. However this preliminary study indicates that even in its present form, multi-slice T1 mapping of the mouse heart has great potential for the study of cardiac disease.

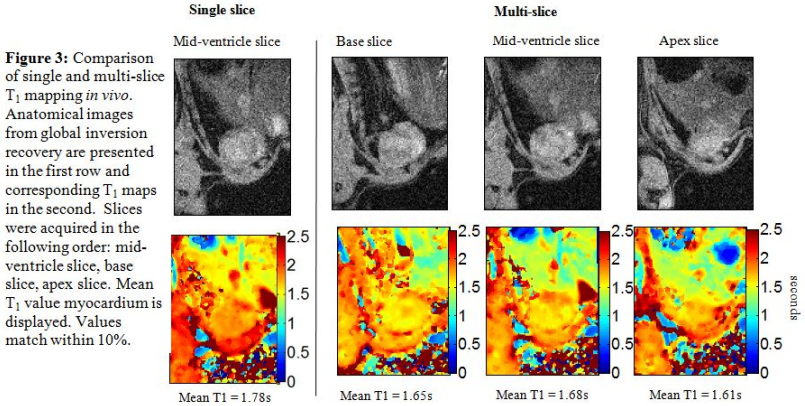


Figure 3: Comparison of single and multi-slice T_1 mapping *in vivo*. Anatomical images from global inversion recovery are presented in the first row and corresponding T_1 maps in the second. Slices were acquired in the following order: mid-ventricle slice, base slice, apex slice. Mean T_1 value myocardium is displayed. Values match within 10%.

References: [1] Kober et al, MRM **51**: 62-67 (2004). [2] Streif et al, MRM **53**: 584-592 (2005). [3] Vandsburger et al, MRM **63**: 648-657 (2010) [4] Coolen BF et al, *NMR Biomed* (2010), Published Online. [5] Bohl S et al, *Am J Physiol Heart Circ Physiol* **296**: H1200-1208 (2009). [6] Deichmeann R and Haase A, *JMR* **96**:608-612 (1992). [7] Shin W et al, *MRM* **62**: 520–526 (2009).