

# Quantification of Renal $T_1$ using a Modified Respiratory Triggered Inversion Recovery TrueFISP Scheme

E. F. Cox<sup>1</sup>, C. L. Hoad<sup>1</sup>, and S. T. Francis<sup>1</sup>

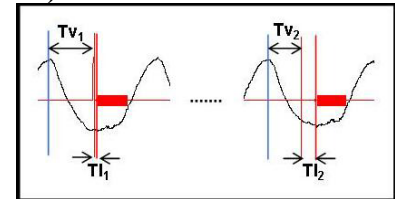
<sup>1</sup>SPMMRC, School of Physics & Astronomy, University of Nottingham, Nottingham, Nottinghamshire, United Kingdom

**Background:** Quantification of the longitudinal relaxation time ( $T_1$ ) across the entire kidneys is important as: it is likely to be altered with age and in disease, itself reflecting altered pathology;  $T_1$  measures are required for accurate perfusion quantification using ASL [1]; and  $T_1$  changes can be used to assess kidney oxygenation using oxygen enhanced MRI (OE-MRI) [2,3]. However accurate measurement of  $T_1$  is not trivial due to breathing induced organ movement, and there are few reports of kidney  $T_1$  values in the literature [4,5]. A conventional inversion recovery (IR) sequence collects images at various inversion times ( $TIs$ ), but the inherent variation in contrast across these images means it is difficult to correct for patient movement without model-based registration methods to account for the underlying contrast change. Breath holding is commonly used, but mis-registration of images can still occur due to variability in patient position during breath holding. It is advantageous to allow patients to breathe freely to reduce patient discomfort and avoid inducing hypercapnic responses, and free breathing is required for studies which assess dynamic changes in  $T_1$  such as studies which modulate  $O_2$  or  $CO_2$ . Here we use a modified IR-TrueFISP sequence to measure  $T_1$  across the entire kidney volume in a short scan time. To avoid the need for breath hold, we introduce a modified triggering procedure which uses an additional delay ( $T_V$ ) after the respiratory trigger to ensure that for each  $TI$  slices are acquired at the same point during the 'stationary' near-end expiration period, here slices are collected at a constant time  $T_V+TI=1100$  ms after the respiratory trigger (Fig. 1). Using this technique prevents the need for model-based registration methods.

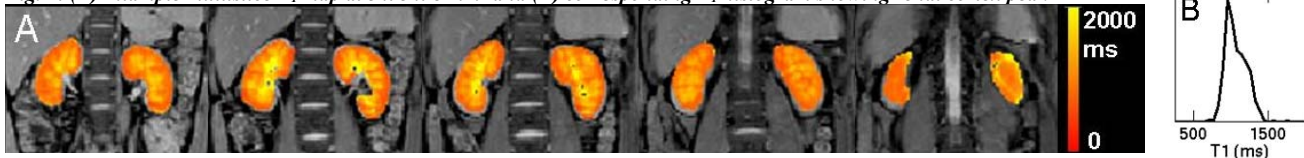
**Methods:** The study was approved by the NHS Ethics Committee and all volunteers gave informed written consent. 12 healthy male volunteers were scanned ( $21 \pm 1$  yrs) using a 1.5 T Philips Achieva whole body scanner and 4-channel receive torso coil. A modified IR-TrueFISP sequence (288 mm x 384 mm FOV,  $3 \times 3 \times 8$  mm<sup>3</sup> voxel, 8 slices coronal-oblique through long axis of kidney) was used with SENSE acceleration factor of 2. IR-data were acquired using a non-selective hsc pulse at 9  $TI$  values (100 - 900 ms in 100 ms steps), with each  $TI$  being collected at the same point in the respiratory cycle (1100 ms) by introducing the additional delay  $T_V$  (first slice acquired at  $TI$ , subsequent slices spaced 138 ms apart). The procedure was performed twice, for ascend and descend slice order acquisition, to increase the dynamic range of  $TI$ 's acquired for each slice (total imaging time ~3 mins). All volunteers were scanned on two separate occasions to assess reproducibility of the  $T_1$  measures. In addition to this, the method was applied to assess the applicability of this triggered technique to high resolution  $T_1$  mapping to monitor spatial heterogeneity ( $1.5 \times 1.5 \times 3$  mm<sup>3</sup> voxels, slice spacing 455 ms, 16-channel torso coil).

**Data Analysis:** Data were fitted on a voxel-by-voxel basis to a 2 parameter model to generate a  $T_1$  and  $M_0$  map using Powell minimization. A binary kidney  $T_1$  mask, threshold at 2000 ms to exclude major vessels, was used to obtain a histogram of  $T_1$  values across the kidneys, from which the renal cortex and medulla were segmented and the median (and IQR)  $T_1$ 's for each volunteer calculated. These values were averaged across subjects to obtain an estimate of mean  $T_1$  in the cortex and medulla. Intra-class correlations (ICC) and coefficients of variation (CV) were calculated as measures of reproducibility between scan days and the Pearson coefficient calculated.

**Fig.1: Modified respiratory triggering shown for short ( $TI_1$ ) and long  $TI$  ( $TI_2$ ). The readout (red block) is acquired at a constant time after the trigger delay (blue line) at  $T_V+TI = \text{constant} = 1100$ ms here**



**Fig. 2: (A) Example multislice  $T_1$  map at  $3 \times 3 \times 8$  mm<sup>3</sup> and (B) corresponding  $T_1$  histogram showing renal cortex peak**

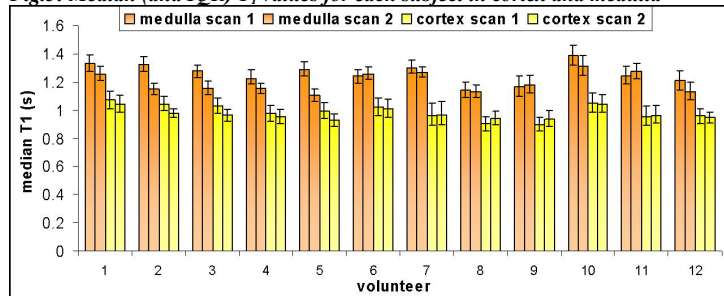


**Results and Discussion:** Fig. 2A shows multislice  $T_1$  maps at 3 mm in-plane resolution which show distinct spatial variability between the cortex, outer and inner medulla and the corresponding histogram (Fig. 2B) showing a peak at the cortex  $T_1$ . Fig. 3 shows  $T_1$  values (median and IQR) for all subjects in cortex and medulla. The mean ( $\pm$  stdev)  $T_1$  for this subject group was  $950 \pm 40$  ms in the renal cortex and  $1210 \pm 60$  ms in the medulla; the cortex is in good agreement with the literature [4,5] but the medulla was lower than expected, suggesting partial volume effects of the inner and outer medulla. Inter-day comparisons demonstrated ICC's and CV's of: 0.84 and 3.7% for the cortex; 0.73 and 5.2% for the medulla. The Pearson coefficient was 0.777 ( $*p=0.01$ ) for the cortex and 0.616 ( $*p=0.05$ ) for the medulla indicating reproducibility between the scan days. The reduced reproducibility in the medulla is likely to reflect different contributions of inner and outer medulla between scan days. Fig. 4 shows a single slice of the high resolution  $T_1$  map. Heterogeneity is seen (Fig 4B) with mean  $T_1$  ( $\pm$  stdev across ROI)  $1060 \pm 69$  ms for cortex and  $1442 \pm 123$  ms for medulla, the stdev reflecting this variation between outer (green) and inner medulla (red).

**Conclusions:** It is possible to measure  $T_1$  in the kidneys using respiratory triggered data acquisition, even at high in-plane resolution. The high resolution  $T_1$  maps showed variations across the cortex and medulla is difficult to resolve at lower resolution.

**References:** [1] P Martirosian *et al.* MRM 2004; **51**: 353-361, [2] RA Jones *et al.* MRM 2002; **47**: 728-735, [3] JPB O'Connor *et al.* MRM 2007; **58**: 490-496, [4] CM de Bazelaire *et al.* Radiology 2004; **230**: 652-659, [5] L Bokacheva *et al.* MRM 2006; **55**: 1186-1190.

**Fig.3: Median (and IQR)  $T_1$  values for each subject in cortex and medulla**



**Fig. 4: High resolution maps: (A) graded colour bar, (B) segmented  $T_1$  values**

