

# Measurement and Comparison of T1 Relaxation Times in Native and Transplanted Kidney Cortex

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## INTRODUCTION

Due to the link between gadolinium-based contrast agents and nephrogenic systemic fibrosis (NSF) [1], the development of non-contrast MR methods such as arterial spin labeling (ASL) [2] have gained more attention. The technique of ASL generally allows for the measurement of kidney cortical perfusion by assuming a constant and known T1 relaxation time based on typical values for the cortical tissues of native kidneys in the literature. However, the cortex T1 value may vary among different patients, between different kidneys and even between different locations within the same cortex region of interest (ROI). These variations may affect the accuracy of blood flow measures in regional kidney cortex and therefore measurement of T1 on a subject-specific basis may be necessary, particularly as these techniques are translated to clinical studies of disease. This work measures the cortical T1 on a pixel-by-pixel basis in both native and transplanted kidneys. The difference of cortical T1 value between native kidney and transplanted kidney is also investigated.

## MATERIALS AND METHODS

This study complies with HIPPA and was approved by our institutional human subjects review committee. The written informed consents were collected from all subjects. A total of 11 subjects with native kidneys and 11 subjects with transplanted kidneys with a wide range of renal function as determined by the estimated glomerular filtration rate (eGFR) were recruited. The MR examinations were performed by use of inversion recovery single shot fast spin echo (SSFSE) sequence on a 1.5 T MR scanner (Excite HD, GE Healthcare, Milwaukee, WI, USA). A series of abdominal MR images at different inversion times (TI) of 100, 200, 400, 800, 1200, 1600, 3500 msec were acquired with the following readout parameters: TR/TE=4000/25 msec, FOV=34 cm and were represented by 128 x 128 matrices.

The series of abdominal images were first automatically aligned to correct for rigid body motion and then were manually aligned to compensate for more local physiologic motion. By assuming one kidney in different TI images has the same overlapped profile after registration, the kidney was segmented out from the abdomen by manually drawing the outline of the kidney in the image at the first TI point. The T1 map was then calculated on a pixel-by-pixel basis in the whole kidney by fitting the MR data curve using the inversion-recovery equation:

$$S = M_0 \left[ 1 - \alpha \exp\left(-\frac{TI}{T_1}\right) \right]$$

where  $M_0$ ,  $\alpha$  and  $S$  represent the proton density, inversion factor and MR signal, respectively. The measurements of T1 in above procedures were analyzed using custom scripts written in MATLAB (MATLAB version 8.0, The MathWorks Inc., Cambridge, MA, USA). Due to the inherent T1 weighting of the inversion recovery SSFSE images, cortex was brighter than the medulla and could be differentiated with a simple threshold. Therefore, after obtaining a T1 map, we plotted the T1 histogram for the whole kidney and segmented the cortex from the medulla by interactively choosing a T1 threshold. After manually segmenting the vessel region within the central body of the kidney, we were able to delineate cortex from medulla. Finally we calculated the mean value of the T1 over the resulting segmented cortical region.

Given the expected correlation of renal function between two native kidneys in the same patient, we averaged the mean values for the T1 over the two kidneys. This resulted in 11 averaged (or mean of) T1 values from 22 native kidneys and 11 mean T1 values derived from 11 transplanted kidneys. Therefore the mean, standard deviation (SD) and standard error of the mean (SEM) for the T1 within each group were determined, respectively. The statistical difference between native and transplant T1 distribution was analyzed with a paired t test and the p value was obtained.

## RESULTS AND DISCUSSION

The range of eGFRs in the native group was 23-88 (in unit of ml/min/1.73 m<sup>2</sup>). The range of eGFRs in the transplant group was 21-78. Variation in the T1 values within the cortex on an individual basis was observed qualitatively (Fig. 1). The mean, standard deviation (SD) and the standard error of the mean (SEM) of T1 values for the transplanted-kidney group are all higher than those of native kidney group (Table 1). The mean differences were statistically significant (p=0.0022). Figure 2 shows the distribution of mean T1 values for the transplanted vs. native kidney groups.

## CONCLUSIONS

Renal cortical T1 measurements using an inversion recovery SSFSE sequence show native kidneys have a lower cortical T1 relaxation time compared to the cortical T1 in transplanted kidneys. Cortical tissue in transplanted kidneys demonstrates larger T1 variation which indicates the importance of individual calculation of the T1 on a pixel-by-pixel basis.

## ACKNOWLEDGEMENTS

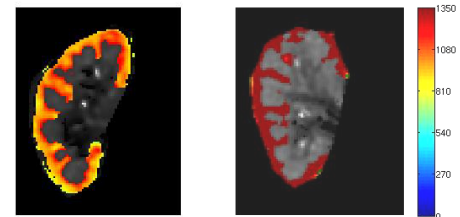
We gratefully acknowledge GE Healthcare, NIH/NIDDK R01 DK073680-01 and NIH R21 DK070243 for support.

## REFERENCES

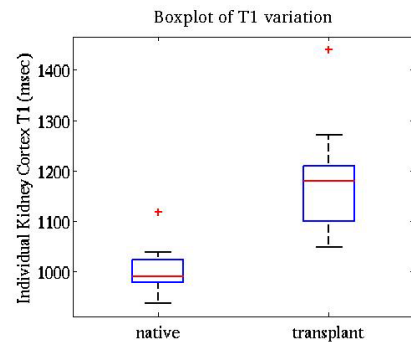
- [1] Marckmann *et al.* J Am Soc Nephrol. 2006; 17(9): 2359-62.
- [2] Martirosian *et al.* Magn Reson Med. 2004; 51(2): 353-61.

Average T1 Relaxation Times of Native and Transplant Kidney Cortex				
Tissue	Mean of T1 (msec)	SD of T1 (msec)	SEM (msec)	
Native	1002	47.4	14.3	
Transplant	1180.2	110.6	33.4	
p-value: 0.0022				

**Table 1.** Comparison of mean, standard deviation (SD) and standard error of mean (SEM) for T1 values in cortical ROI for native kidney group vs. transplanted kidney group.



**Figure 1.** T1 maps of individual native kidney (left) and transplant kidney (right) with color highlight for segmented cortex region. The color bar on right side indicates T1 values in unit of msec.



**Figure 2.** Median and quartile differences in mean T1 values between native and transplanted kidneys.