Two-compartment T2 Decay for Prostate Cancer Diagnosis

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Target audience: Researchers who focus on advanced T2W MRI, k-space under sampling, bi-exponential modeling of T2W MRI techniques and radiologists using T2W MRI for prostate cancer (PCa) diagnosis.

Purpose: Evaluate single and two-compartment T2 decay modeling for prostate cancer diagnosis.

Introduction: T2W MRI forms the backbone of prostate MRI to identify PCa with high sensitivity in high resolution tri-planar T2W MR Images. Prostate tissue has glandular structure with luminal volume and epithelial cells forming the walls of gland. The underlying physical phenomenon in prostate cancer can be accurately captured using two-compartment T2 decay modeling. However, it is not possible to acquire MR images to perform accurate multi-compartment T2 decay model in clinically feasible scan times since multiple T2W MRI images over a wide range of echo times are required. Recently a fast multi-echo TSE (ME-TSE) T2 mapping technique, k-t-T2 MRI was developed to obtain high resolution T2 maps in clinically feasible scan time [1-2]. In this study, a repeated k-t-T2 and an un-accelerated ME-TSE were acquired to access the reproducibility of k-t-T2 and performance of mono and bi-exponential T2 modeling for prostate cancer detection.

Methods: This IRB-approved study included nine patients with biopsy proven prostate cancer. The average age of the patients was 65.5 years; range 54-79 years. Index lesions were identified and nine cancer and nine normal regions of interest (ROIs) were outlined on ADC/T2WI images by an experienced radiologist and MRI physicist based on systematic biopsy reports. k-t-T2 and ME-TSE were acquired in axial view on a Philips 3T Achieva scanner. with thirty-two echoes; ΔTE=12ms (TE= 24ms to 396ms); scanning resolution=1.0x1.0 mm^2 in-plane resolution, FOV=160×160mm^2; slice thickness=3mm; TR=3060 ms; scan time=4:30min. k-t-T2 uses k-t space under sampling method for image acquisition, with 3-D kernel reconstruction (kx-ky-TE) to accelerate the scan. ME-TSE was acquired using the same parameter as k-t-T2, with the slice number reduced to half and number of averages reduces from 3 to 2, to keep the scan time same as that of k-t-T2. Three ME-TSE datasets were analyzed using non-linear least square fitting to mono-exponential and bi-exponential decay model [3]:

$$S = S0(a * e^{-\frac{TE}{T2fast}} + (1-a) * e^{-\frac{TE}{T2slow}}).$$

Where, a1 and a2 are the compartmental fraction of the fast and slow T2 components, respectively. $T2_{fast}$ and $T2_{slow}$ represent the calculated fast and slow decay components from bi-exponential decay model. a, $T2_{fast}$, $T2_{slow}$ and $T2_{mono}$ were compared for prostate cancer and normal ROIs using two sample t-test for paired comparison. Results from two k-t-T2 data sets were compared (using Kruskall–Wallis test) to evaluated the sequence reproducibility.

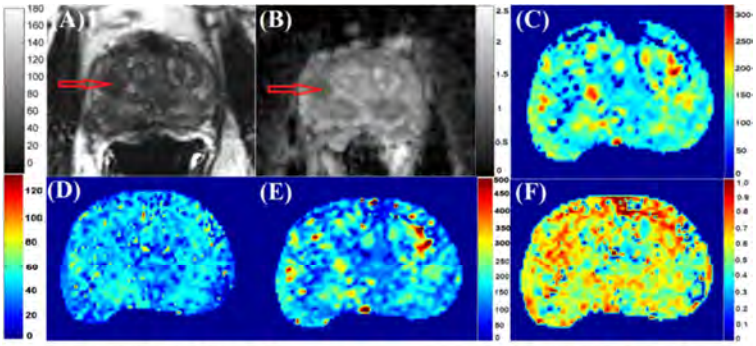

Figure 1. (A) T2WI, (B) ADC, (C) T2map mono-exponential decay model, (D)-(F) fast, slow T2map and compartmental fraction of fast T2 map.

Table 1. Comparison of T2 values and compartmental fractions

	Cancer ROI			Normal ROI		
	k-t-T2 (1)	k-t-T2(2)	ME-TSE	k-t-T2(1)	k-t-T2(2)	ME-TSE
Mono-exp T2(ms)	143.8±50.5	142.3±60.8	143.6±35.6	200.4±62.44	249.4±105.3	192.2±31.3
p-value	0.018	0.044	0.0009			
Fast-T2(ms)	42.3±9.6	44.68±8.61	44.90±6.05	49.45±9.05	52.73±10.13	50.14±4.06
p-value	0.035	0.003	0.009			
Fast comp-fraction	0.38±0.03	0.39±0.03	0.39±0.02	0.37±0.02	0.36±0.02	0.37±0.01
p-value	0.10	0.16	0.01			
Slow-T2(ms)	182.1±85.9	182.8±108.7	172.7±60.3	286.8±84.9	317.8±81.2	285.1±73.9
p-value	0.015	0.016	0.008			
Slow comp-fraction	0.62±0.03	0.61±0.03	0.61±0.02	0.63±0.02	0.63±0.02	0.63±0.01

Results: ROI based analysis shows that there are significant differences ($p<0.05$) between cancer and normal ROIs using T2 values of single-compartment as well as both fast and slow compartment ($p<0.05$) using k-t-T2 and ME-TSE data. For fast compartmental fraction, k-t-T2 data showed no significant difference ($p>0.1$) and ME-TSE showed significant difference ($p<0.05$) between cancer vs. normal ROI. Figure (1A), is a T2WI (cancer on right lateral region), (1B) is an ADC map (mm^2/sec), (1C) is T2 map calculated using mono-exponential model, (1D)-(1E) are fast and slow T2 maps using bi-exponential fitting, (1F) is the fast compartmental fraction map. Both cancer and normal T2 values from k-t-T2 and conventional FSE are comparable in mono-exponential and bi-exponential model fittings (Table 1). Conventional FSE T2WI showed less in group variation using both mono- and bi-exponential model fitting. Fast k-t-T2 sequence back to back study results show the results are reproducible ($p<0.01$), two compartmental fractions in group variation is less than 5%, large variations -10%/+15% were observed in fast and slow T2s in cancer ROIs between patients.

Conclusion and Discussion: Significant changes between cancer and normal ROI of fast and slow T2 components were observed in both k-t-T2 data and ME-TSE using the bi-exponential model fitting, the values of cancer and normal ROIs are comparable with mono-exponential fitting (Table 1). There is significant difference in the slow compoment coefficient between cancer and normal ROIs in bi-exponential model fitting. This may be caused by the slow decay of T2-weighted signals decay of cancer cells compared with normal cells, therefore, they are more resistive to the long TEs. The ROI based reproducibility analysis of two fast k-t-T2 data results are comparable (variations<5%) which maybe due to patient motion and signal noise.

References: [1] Liu, W. et al. MRM 65.5:1400-1406, (2011). [2] Agarwal, H.K., et.al., ISMRM 2401, (2012). [3] Toivonen, J. et al. MRM (2014).