Variability of renal ADC: limitations of monoexponential model

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Introduction

Intra-renal water transport within the kidneys and its possible change during dysfunction can be potentially characterized by the measurement of apparent diffusion coefficient (ADC). A number of groups have applied diffusion-weighted magnetic resonance imaging (DWI) to assess renal function and disease (1-15). Typically, a mono-exponential model is used to calculate the total diffusion coefficient (ADC_{tot}) from renal DWI data. Published ADC_{tot} values in healthy subjects vary considerably, with cortical values ranging from 2.0×10^{-3} to 4.1×10^{-3} mm^2/s and medullary values from 1.8×10^{-3} to 5.1×10^{-3} mm^2/s (1-15). Protocols vary widely. In these reports, the largest diffusion weighting (b value) ranged from 300 to 1000 s/mm^2, and the number of b values varied from 2 to 10.

Besides diffusion, vascular and tubular flows contribute measurably to the diffusion decay, a phenomenon known as intravoxel incoherent motion (IVIM)(3). We hypothesize that the flow effects make the monoexponential model insufficient for describing renal DWI and lead to large variability in ADC_{tot}.

Methods

Accounting for the perfusion effect in DWI data, the signal decay (S) can be described by

$$S = S_0 \cdot [(1-F_P)\cdot \exp(-b\cdot ADC_D) + F_P \cdot \exp(-b\cdot ADC_P)] \ , \qquad [1]$$

where b is diffusion weighting (s/mm^2), S_0 signal acquired without diffusion weighting, F_P perfusion fraction, ADC_D pure apparent diffusion coefficient, ADC_P pseudo-diffusion coefficient due to perfusion effects.

A healthy volunteer was imaged at 3T MRI (Tim Trio, Siemens) with a combination of the spine coil and body array coil. Coronal single-shot echo planar DWI was acquired using: 5 x 6 mm thick slices; FOV 345×410 mm; matrix: 162×192; TR/TE = 2000/78 ms, 3-Scan Trace mode, iPat = 2. Twenty-seven b values between 0 and 1300 s/mm^2 (intervals of 50 s/mm^2) were performed with 9 repetitions during shallow breathing. The scan duration was 25 minutes. Images were co-registered using cross correlation method to correct for respiratory motion. Registered repetitions were averaged prior to analysis.

Using both large regions of interest for renal cortex, medulla, and an incidental cyst (sizes: 1011, 649, 81 voxels) and individual voxels (Fig.2), diffusion decay curves (Fig. 1) were fitted by Eq [1] over the range $0\le b\le 800$ s/mm^2 to ensure sufficient SNR. Goodness of fit was evaluated by root mean square error (RMS), expressed as a percentage of S_0. ADC_{tot} maps were generated by fitting the standard mono-exponential model to data at three different sets of b values: (A) 0 and 400 s/mm^2; (B) 0 and 800 s/mm^2; (C) 17 b values from 0 to 800, with interval 50 s/mm^2.

In a simulation study, the bi-exponential fitting curves for cortex and medulla obtained in the above ROI analysis were re-sampled at 19 sets of b values used in the literature (1-15) that studied healthy subjects. The re-sampled data points for each set of b values were fitted by a single exponential function, resulting in a single simulated or predicted ADC_{tot}. The predicted ADC_{tot} values were compared with the published values. High correlation (R^2) between predicted and reported ADC_{tot} would indicate that the variability in the reported ADC_{tot} was due in large part to the insufficient monoexponential model.

Results and Discussion

Figure 1 shows the excellent fit for the signals from different tissues using bi-exponential function. Parameter estimates are listed in Table 1. ADC_{tot} estimates for renal parenchyma are significantly different for different b combinations used for monoexponential fitting (Fig. 2). ADC_D map in Fig.2 shows minimal contrast between cortex and medulla. When the 19 different combinations of b values were simulated, predicted ADC_{tot} values varied from 2.1×10^{-3} to 3.1×10^{-3} mm^2/s, and significant correlation was found between the predicted and the reported values for cortex ($R^2 = 0.50$, $p = 0.0007$) and medulla ($R^2 = 0.28$, $p = 0.0204$) (Figure 3).

Conclusions

Substantial variability among reported values of ADC_{tot} in healthy subjects in the literature is due in large part to the application of a monoexponential model to data that are better fitted bi-exponentially. When only limited b-values can be sampled, studies that use ADC measurements fitted monoexpontially should use the same diffusion weightings to ensure comparability across clinical populations and to avoid systematic error. A consensus is needed as to what these weightings should be.

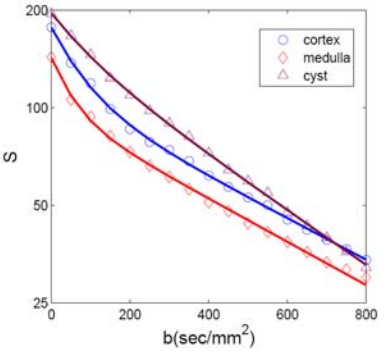

Figure 1: Diffusion profile of renal tissue

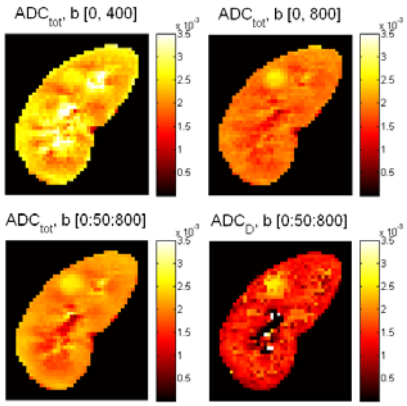

Figure 2: Parameter maps of ADC_{tot} by different b values, and of ADC_D.

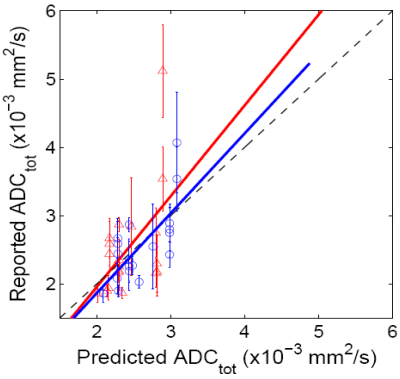

Figure 3: Correlation b/w predicted ADC_{tot} and reported values. Blue circles: Cortex, $R^2 = 0.50$; Red triangle: Medulla, $R^2 = 0.28$.

Table 1: Regional distribution of parameter values in normal kidney

	Mono-exp	Bi-exponential model			
	ADC_{tot} (x10^{-3} mm^2/s)	ADC_D (x10^{-3} mm^2/s)	F_P	ADC_P (x10^{-3} mm^2/s)	RMS
Cortex	2.2±0.1	1.5±0.1	0.38±0.02	11.8±1.0	0.7%
Medulla	2.1±0.1	1.5±0.1	0.32±0.02	17.3±1.7	0.9%
Cyst	2.3±0.1	1.9±0.1	0.21±0.03	9.1±1.5	0.6%

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