

Measurement of Single-Kidney Glomerular Filtration Rate (GFR) by Arterial Spin Labeling

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Introduction: Single kidney glomerular filtration rate (GFR) is an important clinical measurement of renal function. It is traditionally measured with quantitative radiosciintigraphy or CT imaging technique (1), and more recently, MR dynamic contrast-enhanced (Gd-DTPA) imaging techniques (2). All require injection of exogenous agents and may not be appropriate for all patients. When labeled water in the blood reaches renal cortex, a fraction of the water is ultra-filtered via glomeruli into renal tubules. The remaining unfiltered labeled water flows to the peritubular capillary bed and equilibrates with parenchyma water due to high permeability of renal capillaries (3). The labeled water within renal corpuscle or renal tubule is devoid of protein and other macro-molecules and would undergo much slower T1 ρ decay rate. In this study, we used the arterial spin labeling (ASL) technique to label blood as an endogenous tracer to determine the feasibility of estimating single kidney GFR on the basis of the distribution of the labeled water in the renal parenchyma and renal corpuscle compartments.

Methods: All experiments were performed on 3T Siemens Trio scanner using spine/body matrix receive coils. Three healthy volunteer subjects were scanned. Previously reported T1 ρ preparation technique (4) was further modified to minimize sensitivity to B0 and B1 field inhomogeneities. The B1 field for spin-lock was set at 8 μ T (350 Hz). FAIR preparation pulses (5) with QUIPSS II technique (6) was used to generate arterial spin labeling. The labeling duration (TI) was 1800 ms and the post saturation delay (TD, time from QUIPSS II saturation RF pulse to the beginning of data acquisition) was 800 ms. MR parameters for True-FISP single shot imaging were: FOV of 320 x320 mm²; slice thickness of 8 mm; in-plane resolution of 1.7x1.7 mm²; TR of 4.5 s; TE of 1.43 ms; centric reordering; and the total acquisition time was 3 min with 40 repetitions. During the scan, the subject was instructed to conduct short breath-holding times (about 1 sec) during each image acquisition stage.

Results: Fig. 1 shows a T1 ρ weighted tissue image and a set of renal perfusion images with varying TSL's from a healthy subject. Perfusion signal contrast between the renal cortex and medulla is well demarcated. To enhance SNR, ASL perfusion signal in the cortex was averaged within a single kidney. Fig. 2 shows the corresponding decay profile (in logarithm scale) of the ASL signal and the parenchyma signal (reduced by 40-fold) at different spin-lock times. The dropping of ASL at TSL of 40 ms may result from the contribution from the labeled water in renal venules (T1 ρ of venous blood is around 100 ms). The estimated T1 ρ value of the ASL signal (143 ms) was significantly longer than that of the cortex parenchyma (123 ms), indicating the presence of slow-decaying labeled water within renal corpuscle or tubule. Assuming this water has the same T1 ρ as the CSF (500 ms), water filtration fraction (F) by glomerulus was estimated at 18%. The cortex renal blood flow (RBF) was estimated 179 ml/100g/min (assuming T1 = 1670 ms in the blood and 1200 ms in the cortex). This is at the lower end in comparison to other RBF measurements (7) and may be due to the fact that the labeling bolus was shorter than expected from QUIPSS. Assuming the renal cortex weighs 120 g, the single kidney GFR corresponding to the product of water extraction fraction and renal blood flow, was 39 ml/min. This is within the range of measurements by other invasive techniques (8).

Discussion: In this preliminary study, single kidney GFR was estimated from the glomerulus water filtration fraction on the basis of the apparent T1 ρ difference between the renal corpuscle and cortex parenchyma. With appropriate validation, we believe this technique is highly promising as a convenient, non-invasive MR based assessment of renal function. In addition, it allows us to measure both RBF and GFR simultaneously.

Several assumptions made in this study need further justification. First, the labeled water filtered from glomerulus capillary tuft was assumed to be confined mainly within the renal corpuscle or at the initial portion of proximal renal tubule to minimize a possible exchange into cortex interstitial/parenchyma space. This can be indirectly supported by the fact that the mean transit time of water in proximal tubular is quite long (18 seconds, compared with vascular transit time less than 4 seconds) (9). Secondly, the labeled water arriving in the peritubular capillary bed was assumed to be at equilibrium with the remaining parenchyma water at the time of data acquisition. This is plausible since renal capillary is highly permeable to water (its apparent diffusive water permeability is about 10 to 100 times higher than that of the brain capillaries forming the blood-brain barrier) (3).

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