Estimating single kidney glomerular filtration rate from MR renography: Is cortical and medullary segmentation necessary?

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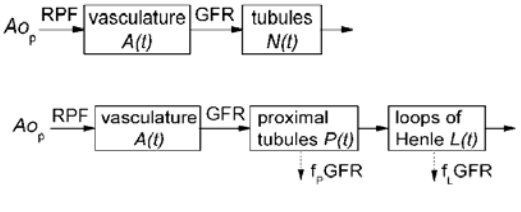
Introduction

MR renography (MRR), a dynamic contrast-enhanced imaging technique for assessment of the renal function, is gaining acceptance as a method for determination of single kidney glomerular filtration rate (GFR). Various compartmental models have been used to calculate GFR using the whole kidney [1], cortical [2], and both cortical and medullary MRR data [3,4]. Clinical suitability of MRR as a quantitative tool requires evaluation of the accuracy of such GFR estimates. We compared the performance of two variants of a 2-compartment (2C) model applied to the whole kidney [1] and to cortex only [2] and a 3-compartment (3C) model for parallel analysis of the cortical and medullary data [3] and correlated the model-derived GFR values with the reference nuclear medicine measurements.

Methods

Ten patients referred for suspected renovascular disease underwent Gd-DTPA-enhanced MRR. Imaging was performed at 1.5 T (Avanto, Siemens) using 3D FLASH sequence in oblique coronal direction (TR/TE/flip angle=2.84/1.05/12°, 1.7x1.7x2.5 mm^3 voxel, 3 s acquisition time). After a 4 ml bolus of Gd-DTPA and 20 ml saline flush, both injected at 2 ml/s, dynamic images were acquired at separate breath holds for at least 10 min after the injection. Kidney images were co-registered and segmented into cortex and medulla and tissue volumes were measured using semiautomatic segmentation algorithm [5]. One kidney was rejected due to presence of multiple cysts. Blood signal was sampled in an ROI placed in the aorta at the level of the kidneys. Aortic, cortical, and medullary signal intensity (SI) values were extracted. Whole kidney SI was calculated as an average SI of cortex and medulla, weighted by their volume fractions. SI data were converted into Gd concentration using a reference phantom curve method [6]. Pre-contrast whole kidney, cortical, and medullary T1 values required for the conversion were measured by low-flip angle TrueFISP [7]. Reference GFR values were determined using ^{99m}Tc-DTPA plasma clearance and scintigraphy performed on the same morning as MRR.



$$\frac{dA}{dt} = \frac{RPF}{V_a}\left(Ao_p - A\right) \quad (1a)$$

$$\frac{dN}{dt} = \frac{GFR}{V_N}A - kN \quad (1b)$$

$$\frac{dA}{dt} = \frac{RPF}{(V_{aC}+V_{aM})}\left(Ao_p - A\right) \quad (2a)$$

$$\frac{dP}{dt} = \frac{GFR}{V_P}\left(A-(1-f_P)P\right) \quad (2b)$$

$$\frac{dL}{dt} = \frac{GFR}{V_L}\left((1-f_P)P-(1-f_P-f_L)L\right) \quad (2c)$$

$$K(t) = \frac{V_a}{V_K}A(t) + \frac{V_N}{V_K}N(t) \quad (1c)$$

Fig. 1: 2C model schematic and equations (Eqs. 1(a-c).)

$$C(t) = \frac{V_{aC}}{V_C}A(t) + \frac{V_P}{V_C}P(t) \quad (2d)$$

$$M(t) = \frac{V_{aM}}{V_M}A(t) + \frac{V_L}{V_M}L(t) \quad (2e)$$

Fig. 2: 3C model schematic and equations (Eqs. 2(a-e)). Solid lines indicate flow of tracer; dashed lines denote water reabsorbed in the tubules.

The 2C model (Fig. 1) represents the kidney (K) as a system of vascular (A) and nephron (N) compartments and yields four parameters: renal plasma flow RPF, vascular volume V_a, GFR, and outflow rate *k*. The 2C model [1,2] was applied to 1) whole kidney concentration (2C-kidney) and 2) cortical concentration alone (2C-cortex). The 3C model [4] (Fig. 2), in addition to A (shared by cortex and medulla) includes the structural components of the nephron: proximal tubules (P), contained in the cortex (C), and the loops of Henle (L) contained in the medulla (M). The 3C model enables fitting with six free parameters: RPF, cortical and medullary vascular volumes V_{aC} and V_{aM}, GFR, and the rates of water reabsorption from P and L compartments, $GFR \cdot f_P$, $GFR \cdot f_L$. 3C model was applied to cortical and medullary concentrations. In both models, measured aortic plasma concentration (Ao_p) was used as an arterial input function (AIF).

Results

Model fits converged in all cases (Fig. 3). Because of the necessity of fitting two measured datasets, the average residual for 3C model (0.023mM) was approximately twice as high as that for 2C-kidney (0.013 mM) or 2C-cortex (0.014 mM). 3C GFR (Fig. 4) correlated with the nuclear medicine GFR (y=0.81x, r=0.934) slightly better than 2C-kidney GFR (y=0.73x, r=0.908) or for the 2C-cortex GFR (y=0.42x, r=0.865). Better agreement of the 3C results was mostly achieved due to better fitting of the high GFR cases. When correlation was restricted to kidneys with reference GFR<60 ml/min, 2C GFR agreed with the reference data better than the 3C results (3C: y=0.69x, r=0.858; 2C-kidney: y=0.6x, r=0.920; 2C-cortex: y=0.36x, r=0.941). Although reference values for RPF and vascular volumes were not available, these parameters showed good correlation across models (Fig. 5).

Discussion

All models yielded adequate fits and GFRs that correlated well with the reference data. All three methods underestimated GFR, especially 2C-cortex. This is likely due to the systematic underestimation of the upslope of the tubular concentration. In the kidneys with high GFR (>60 ml/min), 3C model outperformed 2C model, but did not offer the same advantage in the kidneys with lower GFRs. This can be attributed to the difficulty of correct segmentation of diseased kidneys, which often show decreased corticomedullary differentiation that leads to poor definition of the medullary curve. Hence, the choice of an appropriate model may be influenced by the patient's kidney condition, the quality of the image segmentation, and the need for measuring additional parameters, such as perfusion and tubular function.

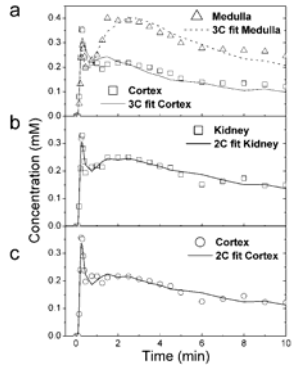


Fig. 3: Data and fits for kidney with GFR=63.3 ml/min: a) 3C, b) 2C-kidney, c) 2C-cortex.

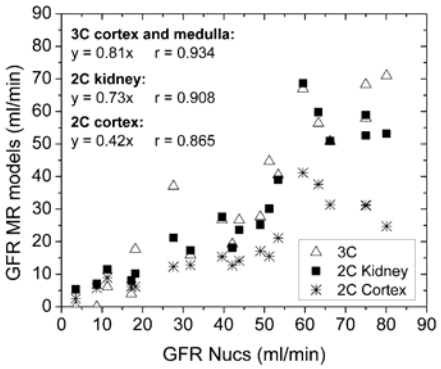


Fig. 4: Model-derived GFR vs nuclear medicine GFR. Linear regression results are given with fixed zero offset.

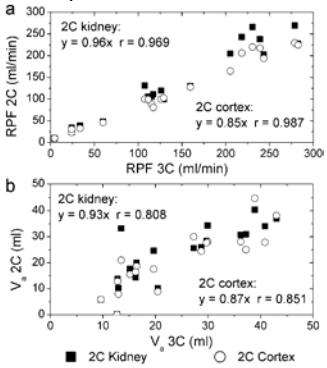


Fig. 5: 2C-kidney and 2C-cortex vs 3C: a) RPF; b) V_a vs $V_{aC}+V_{aM}$ from 3C model.

References

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