Single Kidney GFR Measured using 3D MR Renography and a Multicompartmental Model

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Synopsis
A multicompartmental tracer kinetic model permits analysis of 3D MR renography data in terms of physiologic parameters such as glomerular filtration rate. Validation studies were performed in nine subjects, in whom single kidney GFR measurements were measured using radionuclide clearance methods. Agreement between model-fit values of SKGFR and reference values was high (r=0.77). Other physiologic parameters from the model remain to be validated.

Introduction
The most commonly used clinical tests of kidney function, such as serum creatinine, typically provide global measures and are insensitive to single kidney disease. Gd chelates are good markers of glomerular filtration [1]. Their high relaxivity favors an imaging approach to measure single kidney function in terms of the transit of contrast through the kidneys, referred to as MR renography. Low-dose Gd MR renography has been advocated to avoid T2* effects associated with concentrated Gd in the medulla and collecting system [2]. With low dose Gd and 3D MR imaging methods, whole kidney and intrarenal Gd concentration can be estimated and analyzed using a multicompartmental model of the vascular-nephron system.

Our purpose was to use a multicompartmental model for analysis of MR renography data to determine single kidney glomerular filtration rate (SKGFR) and to compare results with standard radionuclide clearance methods.

Methods
Our compartmental model of the kidney (Fig 1) assumes the tracer, Gd-DTPA, following glomerular filtration is confined in the tubules within the nephron. Qij is the flow of tracer from compartment j to i. In particular, QPA reflects SKGFR. Tracer-free flow, Fi, denotes fluid resorption from each tubular compartment.

Using this model, a set of ordinary differential equations was derived to predict the concentrations of Gd-DTPA in each compartment. Renal cortical and medullary Gd concentrations, as measured from MR renography, were then assumed to represent linear combinations of weighted compartmental concentrations: [Cortex] = fA[A] + fP[P] + fD[D] + fV[V] and [Medulla] = fA[A] + fL[L] + fD[D] + fV[V], where fi represents the fractional volumes of the tissue compartments, and [i] the concentration of tracer in i. The model was implemented using JSIM software (National Simulation Resource, Seattle, Washington). Using the measured function [Ao], the [cortex], [medulla], [ureter] time-concentration curves were fit to MR renography data using an iterative least squares fitting algorithm [3] (Fig 2).

We studied 9 patients using a 1.5T system (Quantum, Siemens, Erlangen, Germany). SKGFR estimates were available for all patients on the basis of 99mTc-DTPA clearance studies for global GFR, and gamma camera imaging for determination of split renal function. Dynamic MR renography was performed using an interpolated 3D spoiled gradient echo sequence (TR/TE/flip angle 2.2/0.8/9°, matrix 134 x 256, FOV 380 mm, 12-16 partitions interpolated to 24-32, 3-4 mm partition thickness, acquisition time 3 sec) in the oblique coronal plane including the abdominal aorta and both kidneys. Unenhanced 3D data sets were acquired, and following a 2 ml (0.01 mmol/kg) bolus of Gd-DTPA injected at 2 ml/sec, 16 3D acquisitions were repeated at variable intervals up to 4 min following injection. 3D volumes were spatially aligned based on parameters derived from the 3D coordinates of the centroid of each kidney. Anatomical regions of interest were manually defined for aorta (input function), renal cortex, medulla, and collecting system using locally developed software. Following correction for coil nonuniformity, measured signal intensities were converted to Gd concentration similar to that reported previously [4].

Results
Among the 9 patients, SKGFRs derived from sclerangiographic studies ranged from 8.6 to 47.6 ml/min. Fig 2 shows Gd concentration-time curves with model fits for renal cortex, medulla, and collecting system in a representative patient. Overall, SKGFR correlated well (Fig 3) with values derived using reference 99mTc-DTPA method (r = 0.77, p < 0.001, n = 18 kidneys). Bland-Altman plot (Fig 3, right) demonstrates lack of systematic bias, with differences between the two methods averaging 5 ml/min ± 9.9.

Discussion
Using low dose Gd contrast and dynamic 3D MR renography, single kidney GFR measurements can be obtained using a multicompartmental model of the renal vascular-nephron system. Other physiologic parameters that can be estimated from the model, including renal perfusion and tubular flow rates, remain to be validated.

References