Comparison of a Rutland-Patlak plot and a compartmental analysis for the assessment of single-kidney glomerular filtration rate

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Introduction. A number of techniques have been described to estimate glomerular filtration rate (GFR) using MRI. One approach is to perform MR renography and measure Gd-DTPA filtration at the level of the renal parenchyma [1, 2]. A recent study of 28 patients by Hackstein et al [3] demonstrated a good correlation between MRI-derived renal function and GFR. The authors used a Rutland-Patlak plot to estimate function. However, a subsequent study performed in rabbits [4] suggested that better results could be obtained using a bi-directional 2-compartment model. These two studies are noteworthy in that both include a measurement of the renal input function (at the level of the descending aorta), an essential component of such a method. In this study we used a quantitative dynamic contrast-enhanced MRI protocol to compare and contrast the two approaches in a group of patients with atherosclerotic renovascular disease.

Methods. Local Research Ethics Committee approval was obtained to study 35 patients, 4 of whom returned for follow-up studies after revascularization. Data were acquired on a 1.0 T Siemens system employing a spine coil for signal reception. A 3D FLASH sequence was used for pre-contrast T_1 estimation (5° and 20° flip angles) and dynamic contrast-enhanced imaging (20° flip, TR/TE 5.4/2.2 ms). The imaging volume encompassed both kidneys and the descending aorta (80 x 306 x 350 mm FOV). Images were acquired every 4.5 s for 3.5 minutes before and after bolus injection of 0.05 mmol/kg Gd-DTPA.

Data were extracted from representative regions of interest encompassing each kidney (with no attempt to differentiate cortex and medulla) and the descending aorta. Following T_1 correction, the dynamic data were analysed according to three separate methods. The first employs a Rutland-Patlak plot and data acquired between 40 and 110 s after aortic signal rise [3]. The second is derived by a non-linear fit of Eqn. 1 to the entire time course; this follows [3] in principle without the need for data pre-selection. The third uses a non-linear fit of Eqn. 2 to the entire time course [4]. In each case estimates of extraction-flow product (EF_p) were multiplied by parenchymal volume to obtain MR-estimates of split renal function that were compared with radioisotope estimates of single-kidney GFR (SK-GFR).

$$(1)\ C_{paren}(t) = V_p C_p(t) + EF_p \int_0^t C_p(u)du \qquad (2)\ C_{paren}(t) = V_p C_p(t) + EF_p \int_0^t C_p(u)\exp\left(-k_{ep}(t-u)\right)du$$

Operational equations used by Hackstein et al [3], Eqn. 1, and Annet et al [4], Eqn. 2. C_{paren} and C_p are the concentrations of Gd-DTPA measured in the tissue and arterial plasma, respectively. V_p is the blood plasma volume and k_{ep} is the rate constant of parenchymal Gd-DTPA loss.

Results.
Data from a total of 75 kidneys were analysed and estimates of SK-GFR ranged from 0.4 to 85 ml/min (mean, 18 ml/min). The relationship between the MR estimates of split renal function using the Rutland-Patlak plot and definitive SK-GFR is shown in Fig. 1. There was a striking correlation between the values calculated (rho = 0.81, $p < 0.0001$) and a linear regression performed on the data had a slope of 1.3 and an intercept of 2.3 ml/min. MR estimates of split renal function obtained using the compartmental model also correlated strongly with SK-GFR (rho = 0.71, $p < 0.0001$, Fig. 1) and a linear regression performed on the data had a slope of 1.9 and an intercept of 20.9 ml/min.

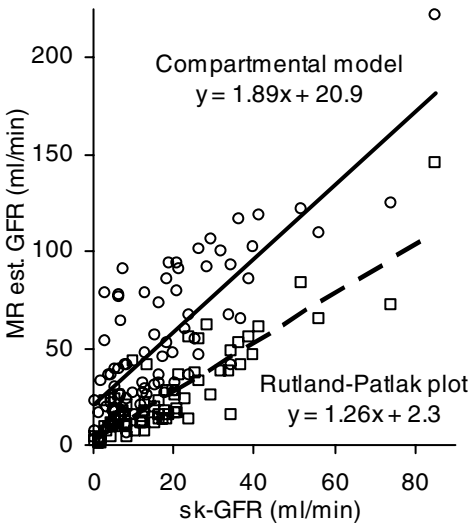

Fig. 1 Estimates of split renal function obtained using a Rutland-Patlak plot (squares) and a compartmental model (circles).

Discussion. Our results are broadly similar to those presented by Hackstein et al [3]. The relationship between MR estimates of renal function made using the Rutland-Patlak plot and definitive SK-GFR are highly correlated with a slope not significantly different from 1. However, this seemingly encouraging result masks an underlying problem with the approach. The selection of a specific subset of the imaging data (i.e. acquired between 40 and 110 s) is a purely empirical choice. By fitting the entire time course to the Rutland-Patlak model (Eqn. 1) we obtain almost identical results (rho = 0.92, $p < 0.0001$; slope = 1.01) but it is apparent that in most cases this model fits the experimental data very poorly. Conversely, the compartmental model described most data sets very well. Indeed, the goodness of fit to the compartmental model (with increased degrees of freedom duly considered) was better than that of the Rutland-Patlak model in 72 of 75 cases. Unfortunately, the correlation between the compartmental model estimates of function and SK-GFR was weaker and the slope closer to 2 (as previously [2]). Thus neither approach provides a wholly satisfactory measure of renal function.

How might we address these problems? Our regions of interest encompass both cortex and medulla thus estimates of EF_p actually represent a combination of both glomerular and tubular function. In further work [5] we plan to separately map the cortical and medullary regions of the kidney [4] following image registration. Kidney motion (predominantly breathing) precludes this mapping in most studies.

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References. **1.** Ros et al *Am J Roentgenol* 165:1447-1451 (1995); **2.** Buckley DL et al *Proc. ISMRM*, 47 (2003); **3.** Hackstein et al *J Magn Reson Imaging* 18:714-725 (2003); **4.** Annet et al *J Magn Reson Imaging* 20:843-849 (2004); **5.** Buckley DL et al *Proc. ISMRM*, 557 (2005).