Quantitative regional glomerular filtration rate measured from dynamic T1-weighted bolus tracking

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Introduction

Measurements of renal function are most often based on measurements of the glonerular filtration rate (GFR). This parameter can be calculated from nuclear medicine techniques as a single-kidney parameter. Furthermore, recent MRI studies have introduced methods allowing determination of single-kidney GFR indexes. In contrary to these single-kidney techniques, we here demonstrate two mathematical approaches to derive regional GFR maps on a pixel-by-pixel basis.

Methods

All examinations were carried out on female Danish Landrace pigs (n=6). MRI was conducted on a Philips 1.5 T Intera system. Pre-contrast T1 maps were obtained using an IR sequence. Dynamic contrast enhanced imaging was performed using an untriggered IR-TFE sequence, and bolus administration was achieved by accommodating a mixture of Gd-DTPA and ^{99m}Tc-DTPA in a short iv line, and then flushed with 20 ml of saline. Kidney and parenchymal volumes were subsequently assessed by a multislice TFE sequence. Dynamic signal intensity curves were converted into quantitative units (mmol/L of Gd-DTPA) from the analytical pulse sequence expression, the specific Gd-DTPA relaxivity constants in the kidney and measured bulk T1 [1]. Non-invasive estimation of regional GFR was then calculated by two methods: 1) deconvolution analysis based on the indicator dilution theory (slightly modified compared to the original approach presented by Østergaard et al) [2], and 2) the Patlak-Rutland-plot approach [3]. In both cases, a signal intensity curve of the abdominal aorta was used as the arterial input function (AIF). The delay that exists from blood entering the arterial ROI to its arrival in the kidney was accounted for by time-shifting AIF accordingly. All analyses were performed on a pixel-by-pixel level, and average parenchymal GFRs were compared with those obtained by the reference ^{99m}Tc-DTPA method. Before, during and after the dynamic MRI sequence, multiple blood samples of 5 ml were taken (0, 1, 2, 3, 4, 5, 7, 10, 15, 20, 30, 45, 60, 90, 120, 150, 180, 210, 240 min) in heparinized glasses. Plasma samples were assayed for radioactivity. Four hours after administration of the bolus, the pig was transferred to a gamma camera and a renography was performed. Then, reference parenchymal GFR was calculated from measured plasma clearance, functional share and MRI-measured parenchymal volume.

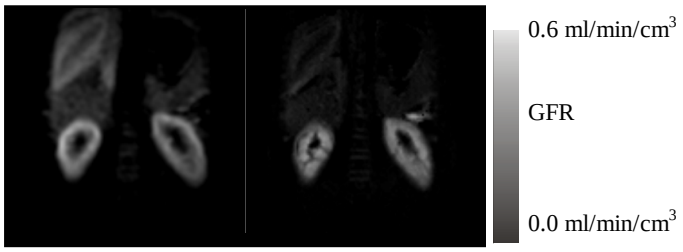
Results

Fig 1 demonstrates parametric GFR maps calculated by deconvolution (a) and by the Patlak-Rutland approach (b), where bright areas represent regions with large glomerular filtration rate. Cortical regions were easily recognized as those having the largest GFR. Measurements based on Gd-DTPA time curves demonstrated a mean cortical GFR of 0.45±0.05 ml/min/cm^3 for deconvolution and 0.49±0.09 ml/min/cm^3 for the Patlak-Rutland approach. The mean reference parenchymal GFR was 0.62±0.09 ml/min/cm^3 (based on parenchymal volume and whole kidney GFR obtained from gamma camera renography and plasma clearance). Calculated GFR values are presented for each kidney in the Table (5 pigs with 10 kidneys).

Discussion

Non-invasive quantification of regional parenchymal GFR was performed using dynamic Gd-DTPA enhanced MRI of the kidney. The regional GFR was calculated from three data sets: T1 measurements, the Gd-DTPA time curve and a volume scan. Although the presented methods (the deconvolution and the Patlak-Rutland approaches) differ conceptually in their mathematical way of handling the tissue curve in relation to AIF, it is striking that measured mean parenchymal GFR did not significantly differ among the two techniques. However, the discrepancy between mean parenchymal GFR values based on MRI and those based on radionuclides may likely be explained by several factors. First, the measurements of regional GFR depend in a proportional manner on the parenchymal volume (since glomeruli are expected to be confined to this segment), and imprecise measurements of this volume will lead to errors in parenchymal GFR. Secondly, the problem of water exchanges is not trivial. Thirdly, the fact that capillary hematocrit is different as compared with large vessel hematocrit should be taken into account. And fourthly, we assumed that all glomeruli were confined to the kidney parenchyma. Future experiments may reveal whether the presented method holds promise for more accurate determination of GFR and, secondly, whether this method holds promise for evaluation of GFR in various renal diseases.

a : deconvolution **b : Patlak-Rutland**



References

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2. Østergaard L, Magn Reson Med 36:726-36, 1996.
3. Pedersen M, Magn Reson Med, *in-press*.

Fig 1: Demonstration of regional GFR maps obtained by deconvolution (a) and the Patlak-Rutland approach (b).

	Regional GFR (ml/min/cm^3)		
Kidney	MRI Patlak-Rutland	MRI deconvolution	Gamma camera renography
Number 1	0,57	0,38	0,62
Number 2	0,53	0,51	0,70
Number 3	0,44	0,46	0,49
Number 4	0,42	0,41	0,69
Number 5	0,36	0,47	0,66
Number 6	0,63	0,47	0,69
Number 7	0,52	0,41	0,56
Number 8	0,48	0,46	0,63
Number 9	0,52	0,39	0,69
Number 10	0,38	0,53	0,47