

Renal perfusion in Acute Kidney Injury: Comparison of Quantification Approaches

Frank G Zöllner¹, Fabian Zimmer¹, Sarah Klotz², Simone Hoeger², and Lothar R Schad¹

¹Computer Assisted Clinical Medicine, Medical Faculty Mannheim, Heidelberg University, Mannheim, Baden-Württemberg, Germany, ²Department of Medicine V, University Medical Centre Mannheim, Heidelberg University, Mannheim, Baden-Württemberg, Germany

Introduction

The assessment of kidney function by measuring renal microvascular perfusion is crucial to diagnose and treat renal diseases like acute kidney injury (AKI). MRI provides two techniques to assess renal perfusion: Dynamic contrast-enhanced (DCE)-MRI and arterial spin labeling (ASL). DCE-MRI involves the injection of a contrast agent to measure the renal blood flow (RBF). Recently, feasibility of DCE-MRI and ASL in a model of acute kidney injury was shown [1]. In this work, we compared a deconvolution analysis as in [1] and a dedicated two-compartment filtration model [2] for DCE-MRI quantification. Further, we also compared both methods with ASL perfusion quantification.

Material and Methods

A total of six male Lewis rats (260g – 290g) were examined, five of which had an ischemic AKI of the left kidney. All procedures conducted with the animals were approved by our institutional animal committee. All measurements were performed on a 3T scanner using an 8 channel receive-only volumetric rat array (RAPID Biomedical GmbH, Rimpf, Germany) for signal detection.

ASL measurements were performed imaging a single axial slice of 4mm thickness using a FAIR-TrueFISP sequence [3] including both kidneys. Images without magnetic preparation M_0 , with global inversion (ns-IR) and with slice-selective inversion (ss-IR) were recorded in an interleaved manner and an inter image time of 6s. Overall, 90 images were acquired. The ss-IR slab had a thickness of 8mm and covered the imaging volume completely and symmetrically. True-FISP parameters were: TE/TR/TI/FA = 2.7ms/5.4ms/1.2s/70°, BW = 651Hz/pixel, matrix = 256 x 256, FOV = 140 x 140 mm² and GRAPPA 3. The total measurement time was 9 min. Immediately after the ASL measurement DCE-MRI was performed using a time-resolved angiography with stochastic trajectories (TWIST) sequence [4] with the following parameters: TR/TE/FA=3.4ms/1.4ms/20°, matrix = 192 x 84, FOV = 114 x 50 mm², GRAPPA 2 and 28 slices. The nominal temporal resolution was 0.9s per volume. Images were continuously acquired for 6 minutes. After the 15th volume, 0.05ml of contrast agent (Dotarem, Guerbet, France) was manually administered in the femoral vein, followed by a saline flush.

ASL perfusion maps were calculated with an in-house MATLAB script (The MathWorks, Natick, MA, USA), averaging the images and calculating the ΔM image by subtracting the average ss-IR from the average ns-IR image. Perfusion maps were calculated on a pixel-by-pixel basis according to: $f = \lambda/2T_1 \Delta M/M_0 \exp(TI/T_1)$. The blood-tissue water partition coefficient λ was set to 0.8 ml/g [5] and $T_1 = 1.14s$ [6]. Quantification of DCE-MRI was performed using a pixel-by-pixel deconvolution [1] approach (DCE-DECON) and a two-compartment filtration model [2] (DCE-2CFM). The arterial input function was determined by placing a region of interest (ROI) in the abdominal aorta. All data were normalized by subtracting the mean intensity of 15 baseline volumes, and a linear relationship of the contrast agent concentration to the measured signal intensities was assumed. The cortical RBF was assessed by drawing a ROI into the DCE and ASL perfusion maps depicting the kidney cortex. Both left and right kidney of each rat has been evaluated. A paired t-test was applied to compare the quantification methods to each other and healthy and diseased kidneys, respectively.

Results

Table 1 shows the estimated RBF for ASL, DCE-DECON and DCE-2CFM. Values for the latter two methods are in good agreement whereas ASL perfusion is lower than the DCE based values (cf. Fig.1). The Bland-Altman plots show that all values lie in the range of 1.96 times the standard deviation except one value and that their mean values scatter over the whole range. Differences between healthy and diseased kidney were significant for all three methods (P<0.05). No significant difference was found between DCE-2CFM and DCE-DECON (P>0.05). RBF estimated by DCE-MRI were systematically higher than RBF calculated from ASL measurements.

Discussion

This study showed that ASL and DCE-MRI provide significantly different values for the perfusion of healthy kidneys and kidneys with ischemic AKI. This shows that all methods are capable of distinguishing the hypoperfusion of a kidney with AKI from the perfusion of a healthy kidney. The 2CFM produces slightly higher values than the deconvolution analysis, however these are not significant. In conclusion, when just aiming at RBF as marker, a deconvolution analysis can provide similar values to the 2CFM. If contrast agent is not applicable, ASL provides an alternative. If parameters like glomerular filtration rate are needed, the 2CFM is suitable.

References:

- [1] Zimmer F et al., ISMRM, 20:889, 2012
- [2] Sourbron S et al., Invest Radiol, 43:40-48, 2008
- [3] Martirosian P et al., Magn Reson Med, 51(2):353-361,2004
- [4] Song T et al., Magn Reson Med, 61(5):1242-1248, 2009
- [5] Roberts DA et al., Radiology, 196:281– 286, 1995
- [6] de Bazelaire CM et al., Radiology, 230:652-659, 2004

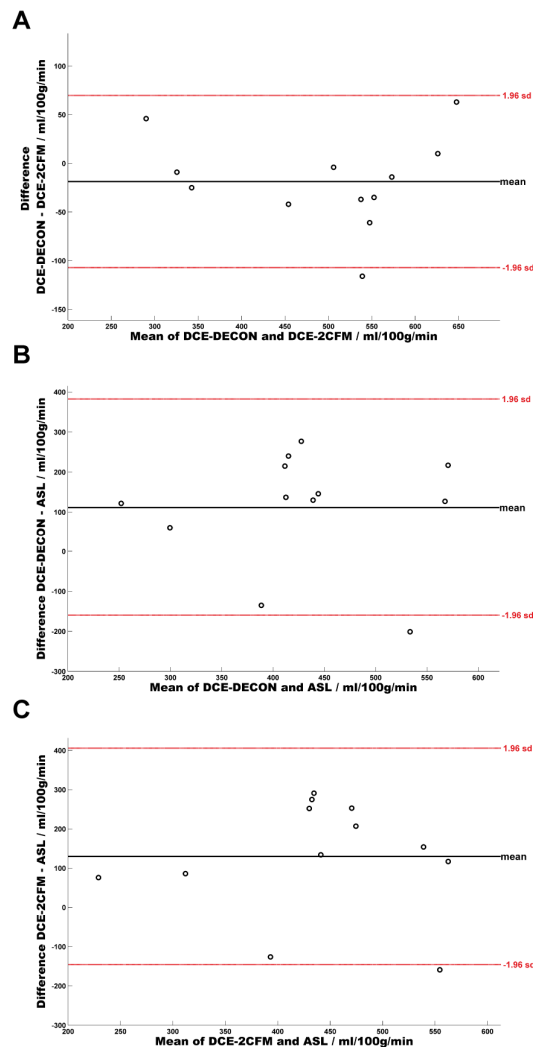


Fig.1: Pair wise Bland-Altman plots for the three quantification methods. (A) deconvolution vs. 2CFM, (B) deconvolution vs. ASL, (C) 2CFM vs. ASL. Each data point depicts one kidney.

animal	ASL		DCE-DECON		DCE-2CFM	
	left	right	left	right	left	right
1*	295	304	535	519	570	556
2	456	634	321	433	330	475
3	191	344	313	481	267	597
4	289	504	566	631	580	621
5	374	462	504	679	508	616
6	269	371	355	578	330	517
mean	316	416	407	542	408	573
± std	±102	±124	±119	±85	±131	±49

Table 1: Results of the three quantification approaches of RBF for left and right kidney. The left kidney was subject to AKI, 1* denotes rat with two healthy kidneys. All values in units of ml/100g/min.