Renal Perfusion Imaging with Pseudo-continuous Arterial-Spin Labelling (pCASL) at 3.0T: Repeatability in Healthy volunteers.

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PURPOSE:
Renal diseases are associated with abnormalities in renal perfusion. Furthermore, characterisation of focal renal lesions such as carcinomas is dependent on the assessment of renal vascularity. Traditionally renal perfusion imaging has relied on contrast agents, which are nephrotoxic. Arterial Spin Labelling (ASL) allows for the assessment renal perfusion without contrast agent injection. Furthermore ASL offers quantification of renal blood flow (RBF) which may be a useful imaging biomarker. This work aims to assess repeatability of pseudo-continuous ASL[1] (pCASL) in healthy volunteers.

METHODS:
Institutional and Research Ethics Committee approval was obtained for this study.
MRI Protocol: 7 healthy adult volunteers were recruited to this study (3 females, age 25-35). All subjects underwent renal ASL perfusion measurements in a 3.0T Phillips Ingenia wide-bore MR scanner. Volunteers were positioned with their arms extended on dedicated armrest above their heads. Respiration and cardiac cycles were monitored with respiratory bellows and pulse oximetry. The main protocol consisted of localiser scans, pseudo-continuous Arterial Spin Labelling (pCASL) and phase contrast MRA. A coronal-oblique ASL imaging volume was positioned along the long axis of both kidneys to reduce in and out of plane motion. The labelling plane was carefully positioned above the kidneys, perpendicular to the descending aorta. Labelling duration (τ) was 1.65s, post labelling delay 0.9s. pCASL labelling train consisted of 0.5ms Hanning RF pulses with FA=18°, maximum gradient 0.6 G/cm and Gmax/Gmean equal to 10. Gradient-echo EPI was used for the readout module with 108x99 acquisition matrix, 320x320 FOV,10 slices (2mm gap), SENSE factor of 3 and TE/TR = 7/4000ms. 20 control-label pairs were acquired. To reduce motion between acquisitions, two pairs were acquired within a 16s breath-hold. To estimate labeling efficiency, quantitative, a cardiac-gated phase contrast scan was also acquired at the exact position of labeling plane (2x2x5mm^3 FOV, VENC = 90-100, TR/TE 5.6 / 3.3, 12 phases). 5 volunteers underwent a repeat pCASL MRI during the same scanning session. Perfusion data was acquired from both kidneys in each of 12 separate pCASL acquisitions with a total of 24 data sets.
Motion Correction. To further reduce misalignment between consecutive pairs, post-processing motion correction was employed. First, the images were cropped to restrict FOV to the region of left and right kidney separately. Next, a mask was drawn manually on each kidney and used to constrain the rigid registration to the region of interest. Control and labelled images were registered to a template created by refined registration of control images using DTITK[2] software.
Pairwise subtraction was then performed, and these were averaged to create a perfusion-weighted image (PWI). These processing steps improved the quality of PWIs, especially in volunteers that performed breath holds in an inconsistent manner.
Labelling Efficiency estimation. Maximum velocity measured in each cardiac cycle phase was used to estimate labelling efficiency by numerical simulation of the Bloch Equations, assuming laminar flow. Then, all efficiencies were integrated over one full cardiac cycle. The resulting estimated efficiency fraction was used for RBF quantification.
Quantification. The general kinetic model was used to quantify RBF using FSL[3,4], with blood T1 set to 1.65s and partition coefficient $\lambda = 0.9$. Mean value of M0 within whole kidney mask was used for calibration. Cortical RBF was calculated by averaging signal within a manually segmented cortex mask created for each kidney.

RESULTS:
Imaging Findings: Maximum and mean velocity in the descending aorta are shown in Figure 1. Mean labelling efficiency, calculated from phase-contrast imaging was 0.72 (range 0.71-0.74) and was used in the quantitative model of RBF. A typical renal perfusion map is shown in Figure 2. Tissue contrast and spatial resolution of the imaging allowed for differentiation between cortex, medulla and renal columns. Mean perfusion values for the whole kidney were 209±39 mL/100g/min (range 104-271 mL/min/100g) and for the renal cortex 243±55 mL/100g/min. Mean perfusion difference between the left kidney (241mL/100g/min) and right kidney (245mL/100g/min) was not significantly different from zero.
Repeatability: Mean perfusion difference was not significantly different from zero for both whole kidney and cortex. Bland-Altman plot showing inter-scan variability is shown in Figure 3. Mean difference between repeat perfusion measurements was 2.2mL/min/100g (95%CI -49.2 to 53.7mL/min/100g)

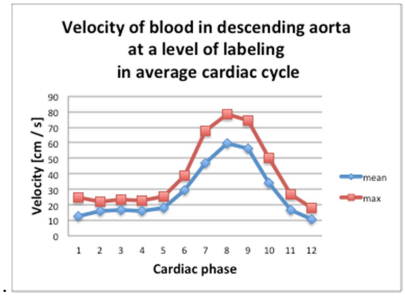

Figure 1. Velocity of blood in desending aorta for averaged cardiac cycle

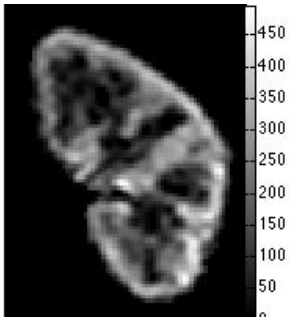

Figure 2. Calculated RBF image of right kidney (masked)

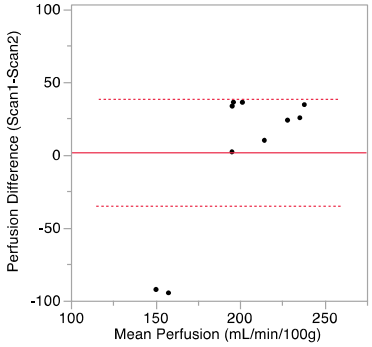

Figure 3: Bland-Altman plot showing perfusion variability between repeat scans

CONCLUSION:
In this preliminary study we have demonstrated the feasibility of using pCASL-GEPI to measure renal perfusion in healthy volunteers. The technique is quick to acquire and both tissue contrast and spatial resolution suggest likely utility in the clinical setting. The inconsistency between test-retest for one volunteer can be most likely caused by a reduction of labelling efficiency due to variable B0 homogeneity in the labelling plane. Repeatability within same scanning session appears acceptable, but long-term repeatability needs further investigation.

REFERENCES:
1. Dai et al. MRM 60:1488–1497 (2008) 2. http://dti-tk.sourceforge.net 3. http://fsl/fmrib.ox.ac.uk/fsl 4.Chappell et all IEEE Transactions on Signal Processing 57(1):223-236, 2009