501-04-002 ISMRM ABSTRACT

Reproducibility of renal PCASL sequences at 3.0 T: preliminary results from a multicenter and multivendor study

Primary: Contrast Mechanisms - Perfusion 〉 **Secondary:** Body - Kidney 〉 **Oral** · 11 min | Applications of Quantitative MRI in the Body · 4:11 PM–4:22 PM · Session: 4:00–5:50 PM · Hall 1A 〉 **Keywords:** REPRODUCIBILITY HARMONIZATION PCASL KIDNEY MRI ARTERIAL SPIN LABELLING (ASL)

Rebeca Echeverria-Chasco [1,2], **Leyre Garcia-Ruiz** [1], **Malene Aastrup** [3], **Verónica Aramendía-Vidaurreta** [1], **Michela Bozzetto** [4], **Paolo Brambilla** [5], **Esben S Hansen** [6], **Jose Maria Mora-Gutierrez** [7], **Siria Pasini** [8], **Anish Raj** [9], **Steffen Ringgaard** [6], **Anika Strittmatter** [9], **Manuel Taso** [10], **Ioana Urdea** [11], **Tau Vendelboe** [6], **Marta Vidorreta** [12], **GIULIA VILLA** [4], **Niels H Buus** [13], **Nuria Garcia-Fernandez** [7], **Matias Trillini** [4], **David C Alsop** [14], **Susan Francis** [15], **Christoffer Laustsen** [6], **Frank G Zoellner** [16], **Anna Caroli** [4], **Maria Fernandez-Seara** [1,2]

[1]Radiology, Clinica Universidad de Navarra, Pamplona, Spain
[2]Navarra Institute for Health Research (IdiSNa), Pamplona, Spain
[3]Aarhus University, Aarhus, Denmark
[4]Istituto di Ricerche Farmacologiche Mario Negri IRCCS, Ranica (BG), Italy
[5]ASST Papa Giovanni XXIII, Bergamo, Italy
[6]MR Research Centre, Aarhus University, Aarhus, Denmark
[7]Nephrology, Clinica Universidad de Navarra, Pamplona, Spain
[8]Bioengineering, Istituto di Ricerche Farmacologiche Mario Negri IRCCS, Ranica (BG), Italy
[9]Heidelberg University, Heidelberg, Germany
[10]Siemens Medical Solutions USA, Inc., Malvern, United States of America
[11]Siemens, Brasov, Romania
[12]Siemens Healthcare, Madrid, Spain
[13]Aarhus University Hospital, Aarhus N, Denmark
[14]Beth Israel Deaconess Medical Center, Boston, United States of America
[15]Sir Peter Mansfield Imaging Centre, University of Nottingham, Nottingham, United Kingdom
[16]Computer Assisted Clinical Medicine, Medical Faculty Mannheim, Heidelberg University, Mannheim, Germany

Presenting Author: *Rebeca Echeverria-Chasco (recheverriac@unav.es)*

Impact

Harmonized PCASL sequences across centers and vendors show promising multicenter and multivendor results for measuring cortical perfusion in the kidneys.

Synopsis

Motivation: enabling reproducible renal perfusion MRI across multicenter and multivendor settings

Goals: assessing reproducibility of harmonized pseudo-continuous arterial spin labeling (PCASL) sequences at 3.0T in 4 clinical centers with scanners of two different vendors

Approach: Fifty-seven healthy volunteers were scanned in two separate days (7-14days). Harmonized PCASL sequences were employed. Renal blood flow (RBF) maps were computed. Reproducibility was assessed visually (Bland-Altman) and quantitatively(CVws, ICC).

Results: RBF values in the 4 centers were in the same range. Reproducibility was good for all the centers (CVws<11%). These findings provide evidence in favor of ASL harmonization across vendors to allow reliable multicenter perfusion studies.

Introduction

Quantitative renal MRI has seen substantial progress in recent years, particularly with the adoption of non-contrast Arterial Spin Labeling (ASL) for perfusion assessment. Clinical translation of perfusion biomarkers requires robust validation of ASL sequences across multiple centers and MRI vendors. To date, renal ASL has typically been tested on individual systems using vendor-specific sequences.

To our knowledge, no previous study has evaluated renal ASL sequences with harmonized labeling configurations across scanners from different manufacturers—a challenging task due to the need for cross-vendor sequence standardization.

This international study aimed to assess the reproducibility of renal blood flow (RBF) measurements using harmonized PCASL sequences at 3T across multiple sites and vendors, within the European RESPECT Project.

Methods

The study was approved by the local Ethics Research Committees. Written informed consent was obtained from all subjects.

Study Design:

Four centers (Centers 1–4) participated in this study. MRI acquisitions were performed on 3T scanners from two vendors (Vendor 1, 2). A total of 57 healthy participants were enrolled.

Each subject underwent three scans: two on the same day (exams 1,2) and a third 7–14 days later (exam 3) (Figure 1).

MRI Protocol:

The imaging protocol included anatomical and ASL sequences using the scanner integrated spine coil and a flexible body array coil. ASL was performed with PCASL sequences optimized for renal perfusion[1], incorporating background suppression and 2D readouts.[2,3]

Sequences were harmonized in terms of labeling parameters, post-labeling delay, and labeling duration (Figure 1). ASL included slice-selective presaturation pulses at the start of the TR to suppress in-plane signal and background suppression pulses optimized for T1 values between 1000–2500ms. BS was implemented using a selective FOCI inversion pulse before labeling, followed by nonselective inversion pulses post-labeling.

Detailed parameters are provided in Figure 2. Labeling duration was 1500ms, with post-labeling delays of 1525ms (Vendor 1) and 1500ms (Vendor 2), $B1_{average}$ of 1.4 µT and 1.6 µT, average gradient 0.5 and 0.4mT/m, respectively, and ratio = 7 for both sequences. In Vendor 1, one M0 image and 14 ASL pairs were acquired; and in Vendor 2 one M0 image and 25 ASL pairs. Readout parameters: Vendor 1: 2D SS-FSE, TE/TR/FA= 40 ms/6000 ms/90°, bandwidth = 1953 Hz/px, matrix= 128x128, FOV=340x340mm², 1 slice; Vendor 2: 2D SE-EPI, TE/TR/FA= 22 ms/5000 ms/90°, bandwidth = 2056 Hz/px, matrix= 128×128, FOV= 384×384 mm², parallel imaging factor= 2, 5 slices.

ASL Postprocessing:

Data from exams 1 and 3 were analyzed. ASL images were motion-corrected using non-rigid transformation algorithms. Renal blood flow (RBF) was quantified using the single-compartment model[1]. The renal cortex was manually segmented in the central slice of the M0 image or T1 maps, avoiding cysts and artifacts.

Statistical Analysis:

Reproducibility was assessed per vendor and center using Bland-Altman plots and quantified with intraclass correlation coefficients (ICC)[4] and within-subject coefficient of variation (CVws). Differences in cortical masks volumes between visits were assessed using paired t-test.

All analyses were conducted using custom scripts in MATLAB and R.

Results and discussion

Participants with incomplete data or unsuccessful motion correction were excluded, along with those in whom ASL planning errors occurred, resulting in a final sample of 47 subjects, n(vendor 1)=23, n(vendor 2)=24.

Figure 3 summarizes demographic characteristics, showing comparable age and sex distributions, particularly for Centers 1 and 2. Figure 4 presents RBF values, which are in the same range for all the centers. RBF maps for the two centers and exams are shown in Figure 5.

Bland–Altman plots (Figure 5) indicate strong agreement between repeated scans for both vendors in the cortex. Quantitative reproducibility metrics are detailed in Figure 4. demonstrating good reproducibility of RBF measurements in the cortex, with consistent results across centers and vendors. Segmentation volumes showed no significant differences between exams. Notably, reproducibility was higher than previously reported[5,6], likely reflecting the optimized ASL configurations used in this study.

This study demonstrates that harmonized PCASL sequences can provide consistent renal perfusion measurements across different MRI vendors. Both implementations yielded reproducible RBF values, which were within the expected range for the participants age.

Several limitations should be acknowledged. Motion correction, essential for accurate RBF estimation, was not always successful in free-breathing acquisitions. Manual segmentation may have introduced variability, although efforts were made to maintain consistent slice location and ROI volumes across exams. The sample size was relatively small; however, data collection is ongoing. Future work will include additional participants and patients with chronic kidney disease.

Conclusion

These findings highlight the importance of ASL sequence harmonization across vendors to enable reliable multicenter renal perfusion MRI studies. PCASL yielded high reproducibility of cortical RBF, across both vendors.

Acknowledgements

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Figures and Tables

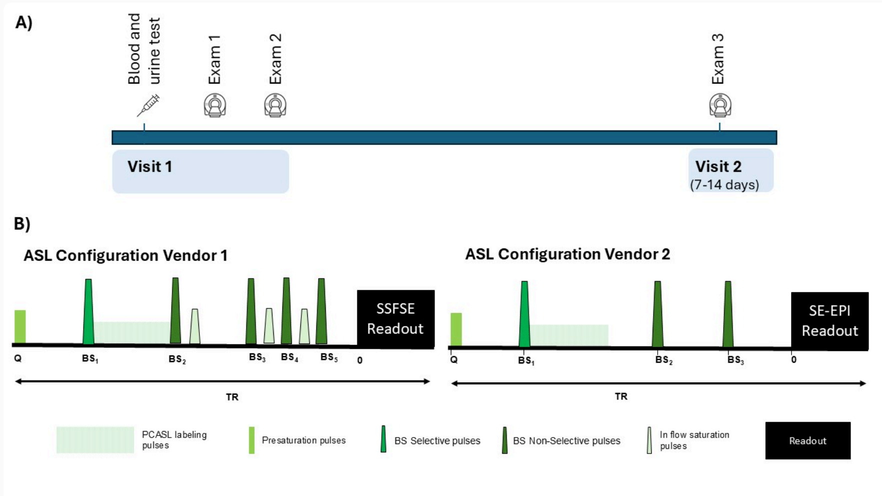

Figure 1: A) Study protocol timeline. B) PCASL sequence diagram

Vendor 1

READOUT PARAMETERS

SE-EPI

TR/TE (ms)	5000/22	**Number of slices**	5
Flip angle	90	**Slice gap (mm)**	2.5
Partial Fourier	0.75	**Phase oversampling**	25%
GRAPPA	2	**Bandwith (Hz/pixel)**	2056
FOV (mm2)	384x384	**Fat suppression**	FAT SAT
Acquisition matrix	128x128	**Slice orientation**	Coronal-oblique
Slice thickness (mm)	5	**Slice Acq. Order**	Central Slice First
Voxel Size (mm)	3x3x5	**Breathing strategy**	respiratory trigger

PCASL LABELING PARAMETERS

Labeling duration	1500	**B1 (uT)**	1.6
Post-labeling delay	1500	**BS Slice Selective**	FOCI
Average Gradient	0.4 mT/m	**BS No-Selective**	Tanh
Ratio	7	**Number of images**	25 label, 25 control, 1 M0

Vendor 2

READOUT PARAMETERS

SSFSE

TR/TE (ms)	6000/40	**Number of slices**	1
Flip angle	90	**Slice gap (mm)**	--
Partial Fourier	0.54	**Phase oversampling**	--
GRAPPA	None	**Bandwith (Hz/pixel)**	1627
FOV (mm2)	340x340	**Fat suppression**	NONE
Acquisition matrix	128x128	**Slice orientation**	Coronal
Slice thickness (mm)	5	**Slice Acq. Order**	
Voxel Size (mm)	2.7x2.7x5	**Breathing strategy**	free breathing

PCASL LABELING PARAMETERS

Labeling duration	1500	**B1 (uT)**	1.4
Post-labeling delay	1525	**BS Slice Selective**	FOCI
Average Gradient	0.5 mT/m	**BS No-Selective**	HS
Ratio	7	**Number of images**	14 label, 14 control, 1 M0

Figure 2: Sequence parameters

	Center 1	Center 2	Center 3	Center 4
N	20	20	10	7
Age (years)	58 ± 11	60 ± 13	47 ± 14	30 ± 8
Female, %	10 , 50%	9 , 45%	5 , 50%	1 , 14%

Figure 3: Demographic characteristics for all the subjects.

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Scan for high-resolution version

Scan for high-resolution version

	Vendor	n	RBF (ml/min/100g) Exam 1	RBF (ml/min/100g) Exam 3	Inter-session reproducibility CVws (%)	Inter-session reproducibility ICC [95% CI]	Time between Scans (days)
Center 1	**1**	17	210.65 ± 37.53	216.10 ± 36.48	9.3%	0.45 (-0.05 to 0.76)	12 ± 4
Center 3	**1**	5	192.07 ± 29.37	214.73 ± 36.52	11.3%	0.66 (-0.11 to 0.96)	8 ± 2
Center 2	**2**	19	245.84 ± 54.26	237.75 ± 61.94	9.9%	0.84 (0.64 to 0.93)	13 ± 4
Center 4	**2**	5	208.98 ± 30.42	219.42 ± 41.45	10.5%	0.68 (-0.28 to 0.96)	8 ± 3

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Figure 4: Cortical Renal Blood Flow (RBF) measurements for each center, and reproducibility metrics.

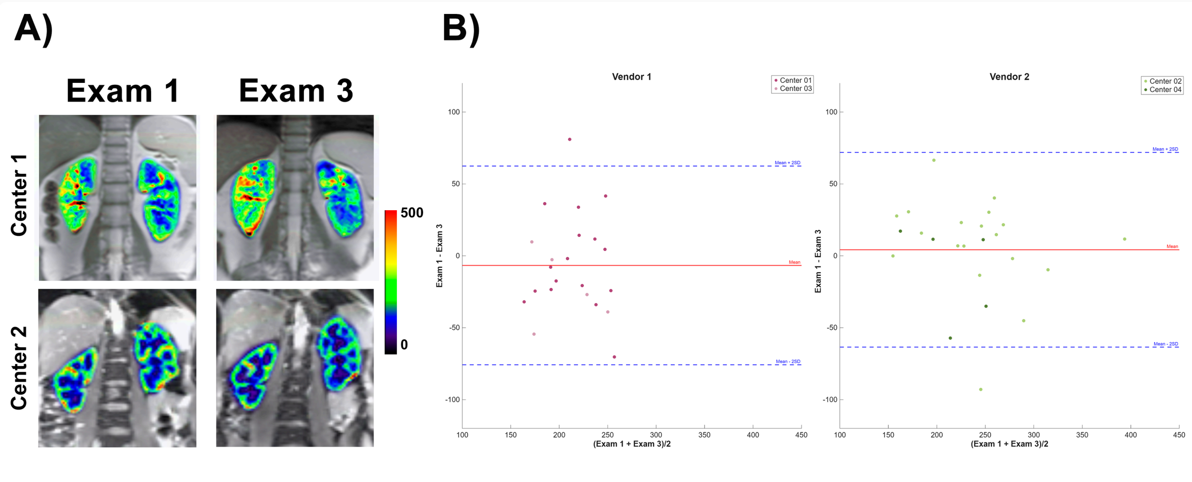

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Figure 5: A) Example of RBF maps in exams 1 and 3 of a representative subject of each center. B) Bland Altman plots for Vendor 1 and Vendor 2 and the two exams (Exam 1 and Exam 3) separated 7-14 days, for the cortical region.