

## Whole-brain High-resolution ASL at 3T

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**Target audience:** Researchers interested in ASL methods and applications, and MRI physicists.

**Introduction and purpose:** Arterial Spin Labeling (ASL) MRI provides noninvasive quantification of tissue perfusion<sup>1</sup>, an important physiological parameter. The main limitation of ASL is its low intrinsic sensitivity and hence resolution. In brain, ASL images may be noisy and suffer partial volume effects. Methods to optimize the SNR of ASL include pseudo-continuous ASL (pCASL)<sup>2</sup> to maximize labeling and 3D sequences<sup>3,4</sup> combined with background suppression (BS) schemes<sup>5</sup> that suppress the static tissue signal to improve detection of subtle ASL effects. However, resolution is still limited in 3D single-shot acquisitions due to T2 decay. 3D segmented readouts<sup>6</sup> shorten readout times, thus reducing T2 blurring and increasing SNR and resolution, but at the expense of requiring multiple RF excitations or shots to acquire the complete k-space. While this is a limitation for studying dynamic perfusion changes, in many cases ASL MRI is simply used to quantify mean perfusion.

The goal of this study was to implement and evaluate ASL sequences that provide whole-brain high-SNR high-resolution ASL acquisitions. To this end, pCASL was combined with segmented 3D readouts and BS. Two readout schemes with different in-plane trajectories were compared: Cartesian (3D GRASE<sup>6</sup>), and spiral (3D RARE Stack-Of-Spirals<sup>2</sup>). 8-shot in-plane segmented acquisitions were implemented for both schemes. ASL perfusion maps of resolution 2x2x4mm<sup>3</sup> were acquired in 15 volunteers. The quality of the maps was assessed in terms of SNR and GM-WM contrast ratio.

**Methods:** *Subjects:* 15 healthy subjects (8 females; 26±4 years) participated in the study, after signing written informed consents.

*Scanning protocol:* The study was carried out on a 3T Siemens Trio using a 12-channel head array. An anatomical T1-weighted image and a Time-Of-Flight (TOF) angiogram were obtained prior to two whole-brain perfusion images acquired with 3D RARE Stack-Of-Spirals and 3D GRASE in a pseudo-randomized order. During each acquisition, 6 pairs of label-control images were obtained while subjects were resting with eyes closed, in a scan time of 6.67min. Two additional control images without BS were acquired at the end of each scan for CBF quantification.

*pCASL preparation:* The pCASL pulse consisted of 1520 selective RF pulses (Hanning window,  $B_{1\text{avg}}=1.8\mu\text{T}$ , duration=500μs, spacing=500μs,  $G_{\text{avg}}=1\text{mT/m}$ ,  $G_{\text{max}}/G_{\text{avg}}=8$ ) with a labeling duration of 1.5s and post-labeling delay (PLD) of 1.5s. The location of the inversion plane was determined individually for each subject based on their TOF angiograms, and maintained across sequences.

*BS scheme:* 4 presaturation pulses at the beginning of each TR, a slice-selective C-FOCI pulse played right before labeling plus 2 non-selective hyperbolic secant pulses during the PLD, with timings optimized<sup>7</sup> to suppress the static tissue signal to 10% of its equilibrium value.

*Segmented 3D GRASE (Fig. 1a):* TR/TE<sub>eff</sub>=4s/17ms, excitation flip angle (FA)=90°, refocusing FA=180°, resolution=2x2x4mm<sup>3</sup>, 32 nominal partitions with 12.5% oversampling (OS) acquired with a centric encoding scheme and slice PF=6/8, FOV=256x224x128mm<sup>3</sup>, matrix=128x120x27, BW=2298Hz/px, in-plane PE direction=Anterior-Posterior, total readout time=466ms.

*Segmented 3D RARE Stack-Of-Spirals (Fig. 1b):* TR/TE<sub>eff</sub>=4s/8.7ms, excitation FA=90°, refocusing FA=180°, resolution=2x2x4mm<sup>3</sup>, 32 nominal partitions with 12.5% OS acquired with a centric encoding scheme and slice PF=6/8, FOV=256x256x128mm<sup>3</sup>, matrix=128x128x27, 8 interleaved spirals, max slew rate=120mT/(m·ms), max  $G_{\text{amp}}=36\text{mT/m}$ , BW=3125Hz/px, total readout time=350ms.

*Data preprocessing and analysis (SPM8 and Matlab scripts):* Images were realigned and co-registered to the anatomical dataset before subtraction of label and control. Mean perfusion images and CBF maps were computed using the one-compartment model<sup>8</sup>. The perfusion SNR was calculated as the ratio of the whole-brain perfusion signal to the background noise level, after compensating for averaging and magnitude reconstruction. The GM-WM contrast ratio was assessed in the mean CBF maps using segmented GM and WM masks. Statistical differences in SNR and contrast between readout schemes were assessed by means of paired t-tests.

**Results:** Table 1 summarizes the results obtained with both sequences, while Fig. 2 shows four axial slices (the scale of the lower slice has been amplified to visualize background noise) and sagittal view of the mean perfusion maps obtained for one subject. The individual whole-brain mean CBF values present a very high degree of agreement between sequences ( $r=0.95$ ,  $p<10^{-7}$ ). The 3D RARE Stack-Of-Spirals yielded a significant 2-fold SNR increase over 3D GRASE ( $p<10^{-7}$ ). GM-WM contrast ratio was also slightly higher for 3D RARE Stack-Of-Spirals although no statistical significance was reached ( $p=0.17$ ). The high resolution of the perfusion maps can be appreciated in Fig. 3, which illustrates the mean CBF map of a representative subject obtained with the spiral readout compared to its anatomical image, as well as by the increased GM-WM ratios as compared to prior reports<sup>7</sup>.

**Discussion and conclusion:** The combination of pCASL, segmented 3D readouts, and BS provides high-SNR high-resolution ASL acquisitions. 3D RARE Stack-Of-Spirals yielded higher SNR and effective resolution and decreased through-plane blurring due to its inherent central k-space oversampling, reduced effective TE and shorter readout time.

**References:** 1. Detre et al. Curr Opin Neurol 2009; 22:348-55. 2. Dai et al. MRM 2008; 60:1488-97. 3. Guenther et al. MRM 2005; 54:491-98. 4. Fernández-Seara et al. MRM 2008; 59:1467-71. 5. Garcia et al. MRM 2005; 54:366-72. 6. Feinberg et al. Proc ISMRM 2009. 7. Vidorreta et al. NeuroImage 2012; 66C:662-71. 8. Wang et al. Radiology 2005; 235:218-28. Acknowledgements: Grants SAF2011-29344 and RYC-2010-07161, and COST Action BM1103 AID.

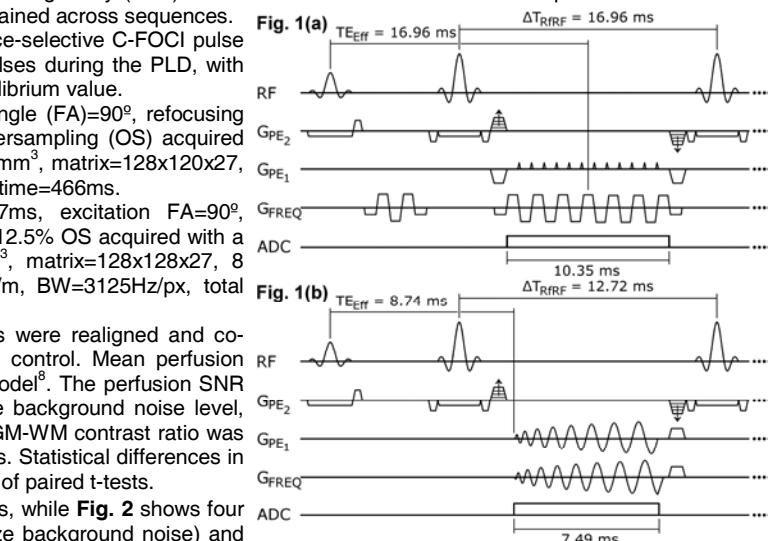


Table 1 [mean ± SD]	Mean CBF [ml/min/100g]			GM-WM CBF Perfusion Contrast	
	Global	GM	WM	SNR	
3D GRASE	57.6±11.7	73.2±14.5	30.1±7.7	2.5±0.3	3.8±1.3
3D RARE Stack-Of-Spirals	57.8±10.9	75.4±13.0	26.5±6.4	2.9±0.3	9.0±2.4

