

Single-shot 3D-EPI PCASL with background suppression

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Target audience MRI physicists and clinicians interested in ASL methods and applications.

Purpose To investigate the feasibility of pseudo continuous ASL (PCASL) using a 3D-EPI¹ imaging module and background suppression. 3D-GRASE has been shown to be a reasonable imaging module for ASL², but it suffers from blurring in slice direction in single-shot use due to T₂ relaxation³. A 3D-EPI readout might be an alternative with similar imaging performance in terms of brain coverage, resolution and readout duration, but reduced slice-blurring since consecutive phase encoding steps in slice-direction (PE2) are excited separately and thus, signal evolution is not bound to fast T₂ decay. Furthermore, the use of low flip angle excitations (< 90°) with reduced SAR may make 3D-EPI pCASL potentially applicable at ultra-high fields⁴ (>3T).

Methods PCASL⁵ labeling with background suppression (BS) was implemented in a custom 3D-EPI sequence (Fig.1) running on a Magnetom Skyra 3T scanner (Siemens Healthcare, Erlangen, Germany). It utilizes variable flip angles (vFA) to improve signal-to-noise ratio (SNR)⁶. The post labeling delay (PLD) was defined to last from the end of the labeling to the excitation of the central PE2 k-space step (k_{PE2}=0). Performance of single-shot 3D-EPI (one complete volume following labeling) in terms of SNR and contrast-to-noise ratio (CNR) was compared to a multi-shot (volume acquisition completed after several labeling-acquisition blocks) 3D-GRASE PCASL⁷ sequence with matched total acquisition time. **Protocol:** 3 healthy male subjects (age 31±3 years) were scanned at 3T with a 32 channel head receiver coil after signing written informed consent. The protocol consisted of one 3D-GRASE PCASL scan, termed G1, with 3mm isometric resolution, 8 segments, and 6 label-control pairs. Further, three different 3D-EPI PCASL scans, E1-E3, were performed, each with 3mm isometric resolution, 1 segment, and 40 label-control pairs. E1: centric PE2 reordering/ constant flip angle (Ernst angle for gray matter); E2: linear PE2 reordering/ variable flip angles (vFA); E3: linear PE2 reordering/ vFA / BS. Additionally, a single-shot comparison was conducted on one subject with a 3D-EPI PCASL scan, E4: 3.5x3.5x4mm³ / 40 label-control pairs/ vFA/ BS, and a 3D-GRASE PCASL scan, G2: 3.5x3.5x4mm³ / 1 segment / 40 label-control pairs. For each subject an additional MPRAGE sequence and for all ASL sequences static tissue magnetization M₀ scans were acquired. **Further 3D-EPI parameters:** TR=4050ms, TE=11.4ms, total readout duration T_{EPI}=398ms, scan duration TA~6min, nominal excitation flip angle (E1-3) FA₀=12°, (E4) FA₀=70° (for vFA: FA(t) = FA₀(1 - δ cos(2π(t/TR)^κ)), where (E1-3) δ =0.8 or (E4) δ =0.3 and κ =-log(2)/log(T_{max}/T_{EPI}) such that vFA is maximal at (E1-3) T_{max}=0.4T_{EPI} or (E4) T_{max}=0.95T_{EPI}, respectively), echo spacing 0.5ms, nominal PE2 steps (E1-3) 32, (E4) 24 with 37.5% oversampling, FOV=192mmx192mmx96mm, readout bandwidth 2298 Hz/pixel, PF (PE2) 6/8, GRAPPA 2(PE1)x2(PE2). **3D-GRASE parameters:** TR=4000ms, TE=22.76ms, total readout duration per segment T_{SEG}=288ms, scan duration TA~6min, excitation flip angle 90°, refocusing flip angle 120°, nominal partitions (G1) 40 or (G2) 24 with 20% oversampling, readout bandwidth 2298Hz/pixel, FOV 192mmx192mmx120mm. **PCASL:** The PCASL labeling with duration T_{Label}=1800ms and post labeling delay T_{PLD}=1800ms consisted of selective Hanning shaped pulses (balanced scheme⁵, duration 500μs, spacing 460μs, G_{max}= 6mT/m, G_{avg}=1mT/m, FA=25°). A constant labeling offset of 85mm inferior to the imaging volume center was used for all subjects. **Background suppression (BS):** The BS consisted of a presaturation (4 sinc pulses with following spoilers, flip angle 90°, duration 10240 μs) of the imaging slab and 2 non-selective inversions (HS-6⁸ pulses, duration 10240 μs, B₁=7.1 μT, BW=3.4 kHz) after the labeling. The timing of the BS pulses (T_{BS1}=1800ms, T_{BS2}=2950ms) was chosen to preserve ~20% of static tissue magnetization⁹. **Data analysis:** All data analysis was performed with FSL tools (FSL 5.06, FMRIB, Oxford) and custom scripts. The acquired images were quantified according to the single compartment model recommended by the perfusion study group¹⁰. Motion correction and coregistration to MPRAGE were performed using mcflirt (6dof) and flirt (12dof), respectively. Gray

matter (GM), white matter (WM) and global CBF were calculated using partial volume maps obtained from tissue segmentation (fast) of the MPRAGE acquisition. Noise standard deviation, SD, was estimated from background ROI and used to calculate SNR = CBF / SD and CNR = ((CBF_{gm} - CBF_{wm}) / SD).

Results At 3mm isometric resolution the segmented 3D-GRASE (G1) still has a ~30% SNR and CNR advantage over single shot single-shot vFA (E2-3) and even ~150% SNR and CNR advantage over constant FA 3D-EPI (E1) acquisitions. The 3.5x3.5x4mm³ resolution results show comparable SNR for both single-shot sequences (E4, G2). However, the 3D-EPI CNR is increased by 100% compared to 3D-GRASE, which is due to significantly decreased blurring, as depicted in Figure 2.

Discussion & Conclusion The reduced blurring (PE2) and similar SNR in single-shot 3D-EPI compared to 3D-GRASE opens up the possibility of improved functional ASL. For high-resolution CBF quantification a segmented 3D-EPI approach should be investigated as segmented 3D-GRASE shows superior results in this domain. The use of vFA has been shown to be beneficial (doubled SNR) and should be further investigated to increase SNR. Additionally, the low excitation flip angles will help overcoming SAR restrictions at ultra high field strength (7T). In summary, a PCASL labeling with background suppression and 3D-EPI imaging module has successfully been implemented and shown to reduce blurring in comparison to single-shot 3D-GRASE.

References [1] Poser et al., NeuroImage 2010,[2] Vidorreta et al., NeuroImage 2012,[3] De Vita et al., ISMRM 2014,[4] Hall et al., ISMRM 2006,[5] Dai et al., MRM 2008,[6] Stirnberg et al., ISMRM 2014,[7] Wang et al., Stroke 2012,[8] Tannus, et al. NMR Biomed 1997,[9] Mani et al., MRM 1997,[10] Alsop et al., MRM 2014

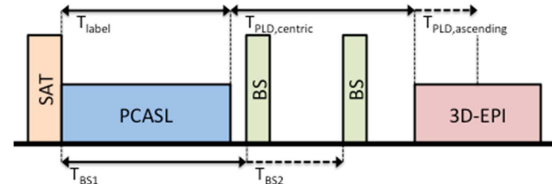


Figure 1 3D-EPI PCASL sequence with background suppression

Sequence	Reordering	BS	CBF [ml/100g/min]			SNR	CNR
			Global	GM	WM		
E1 (cFA)	centric	OFF	54.9±3.4	66.0±5.8	43.5±4.4	5.0±0.3	2.7±0.6
E2 (vFA)	ascending	OFF	60.4±5.0	70.7±8.6	49.1±1.3	10.1±0.4	4.5±0.6
E3 (vFA)	ascending	ON	57.0±12.0	72.7±17.6	42.7±3.5	9.0±0.5	4.7±0.5
G1	centric	ON	61.5±13.3	74.7±15.4	52.4±9.7	12.7±0.2	5.9±0.5
E4 (vFA)	centric	ON	40.2	45.6	38.4	15.1	3.4
G2	centric	ON	49.8	51.1	47.9	14.5	1.7

Table 1 The first 4 rows show mean values for 3 subjects, the last 2 values for 1 subject.

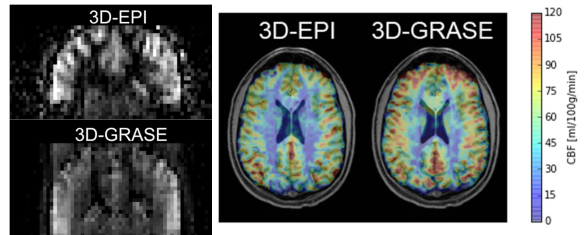


Figure 2 Mean perfusion weighted images (left) and mean CBF maps (both E4/G2) on top of MPRAGE scans (right)