SCALE PWI: A Pulse Sequence for Quantitative Cerebral Perfusion Imaging

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INTRODUCTION

Quantitative cerebral perfusion is a fundamental physiologic parameter that reflects the severity and progression of a broad range of pathologies including: cancer, stroke, Alzheimer's Disease, and cerebrovascular occlusive disease. The "Bookend" technique [1,2] allows quantification of cerebral blood flow (CBF) and cerebral blood volume (CBV) with dynamic susceptibility contrast (DSC) MRI and fast T_1 measurements before and after DSC. This technique has been proven to be reproducible, reliable and accurate [3]. The current implementation consists of 3 sets of MRI scans performed sequentially requiring a cumulative scan time of 5 minutes. A simplified scan protocol and automatic image processing would enable not only a broader dissemination of this technology but also its utilization in emergency settings such as acute stroke to obtain immediate and accurate diagnosis. Our goal was to come up with a **"**single**"** (push-button) MRI pulse sequence that: (1) produces quantitative images of cerebral perfusion without the need for additional "Bookend" scans, (2) eliminates the need of special technologist training, (3) is less prone to motion artifacts, and (4) produces quantitative images of cerebral perfusion without the need for offline post-processing.

MATERIALS AND METHODS

Sequence Development

Our pulse sequence produces an absolute scale for the quantification of cerebral perfusion. Self CALibrated Epi Perfusion Weighted Imaging (SCALE-PWI) consists of a 3-step gradient-echo (GRE) single-shot echo planar imaging (EPI) sequence (Figure 1), based on the Bookend technique [1,2]. The first and third steps involve a Look-Locker (LL) inversion recovery (IR) for a single calibration slice. The middle step corresponds to a conventional dynamic susceptibility contrast (DSC) scan during the injection of a bolus of gadolinium-based contrast agent. The last phase of the sequence acquires a post-gadolinium image for calibration.

Validation in Healthy Volunteers

A study of 19 healthy volunteers scanned on a 1.5 T MR scanner (MAGNETOM Espree, Siemens AG Healthcare Sector, Erlangen, Germany) using SCALE PWI was performed to compare SCALE-PWI to the Bookend technique, which served as a reference. Images were acquired with a single-dose injection of Gd-DTPA (0.1 mmol/kg b.w.) at a rate of 4 ml/s: TE/TR = 34/1090 ms, flip angle = 20°, FOV = 220 mm x 220 mm, resolution = 128 x 128, GRAPPA with acceleration factor = 2, for 13 slices in the brain (slice thickness = 5 mm) and a total of 50 measurements. In this setting, 35 time series of LL measurement for T_1 mapping were acquired after each IR pulse for a single "calibration" slice, with a time gap between acquisitions = 84 ms. The total scan time of SCALE PWI is under 2 minutes. The SCALE PWI scan was preceded and followed by a segmented LL-EPI scan of the same calibration slice, according to the current Bookend protocol, in order to obtain a reference calibration for the relative DSC perfusion measurements.

Image Processing and Experimental Calibration

The SCALE PWI scan was processed using a fully automatic reconstruction program developed in MATLAB V7.2 (Mathworks, Natick, MA, USA). Quantitative (absolute) CBV in white matter (qCBV-WM) was calculated from the post-gadolinium T_1 change in the blood pool and white matter of the "calibration" slice, and a water exchange correction (WEC) factor was determined based on the T_1 change in blood, according to Shin et al [2]. No empirical scaling of white matter to "normal" flow was needed. qCBV-WM and WEC were used to calibrate the relative CBF and CBV values in both the reference (segmented LL-EPI) and SCALE PWI (single-shot LL-EPI) cases. Finally, to improve the T_1 measurement acquired with the single shot acquisition, CBV values were adjusted based on the following expression: $C = 2.4507R^2 - 6.6349R + 6.1801$,where R and C are the products of qCBV-WM and WEC before and after calibration, respectively.

RESULTS

We found excellent agreement between the perfusion values obtained with the SCALE PWI sequence and the reference protocol. Table 1 shows the comparison between mean qCBF and qCBV values for white matter (WM) and gray matter (GM); the p and r values are also given.

Table 1
Comparison of qCBF and qCBV values obtained with SCALE PWI and Reference protocol

Tissue		qCBF (ml/100g-min)	qCBV (ml/100g)
Mean ± SD			
WM	*SCALE PWI*	20.7 ± 4.9	1.48 ± 0.23
	REFERENCE	20.5 ± 5.2	1.49 ± 0.29
GM	*SCALE PWI*	75.5 ± 16.1	3.33 ± 0.40
	REFERENCE	75.0 ± 16.0	3.27 ± 0.48
p(r)			
WM		0.72 (0.87)	0.90 (0.76)
GM		0.78 (0.83)	0.57 (0.43)

Figure 2 (A,B) shows the comparison between representative qCBF images, and Figure 2 (C,D) shows the results of the qCBF and qCBV correlation analysis for WM and GM. For qCBF, slope = 0.98, offset = 1.35, r = 0.97 and $p < 10^{-3}$. For qCBV, slope = 0.94, offset = 0.17, r = 0.93 and $p < 10^{-3}$.

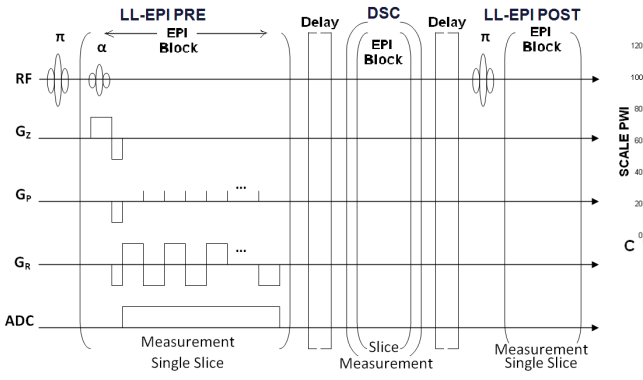

Figure 1*. Timing diagram of the SCALE PWI sequence.*

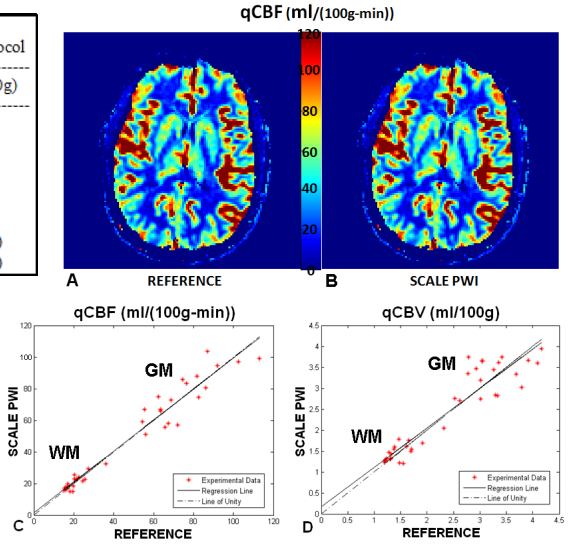

Figure 2*. A and B are representative qCBF images for a brain slice obtained with the REFERENCE protocol and SCALE PWI, respectively. C and D are WM and GM correlation plots for qCBF and qCBV, respectively (The line of unity is shown).*

CONCLUSIONS

We have validated the accuracy of the new sequence for perfusion quantification in healthy volunteers, by comparing it to our reference Bookend protocol, which has been validated through direct comparison with $H_2[O^{15}]$ PET (the "gold standard" for perfusion imaging). Future steps include improving our calibration further by finding a better way to mitigate the T_2* decay effects which cause the T_1 measurements pre- and post-gadolinium to be inaccurate. Completing the online automatic image reconstruction for SCALE PWI is the final goal.

REFERENCES

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