Whole Brain Perfusion Using Dynamic pCASL with Multiband Look-locker EPI

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TARGET AUDIENCE: MR physicists and physicians interested in performing perfusion measurements with Arterial Spin Labelling.

PURPOSE: Dynamic pseudo-continuous Arterial Spin Labelling (pCASL) with Look-Locker (LL) EPI readout can sample the trace kinetic curve at multiple time points after a single labelling pulse. Due to the signal recovery of the labelled blood, the readout slice number is limited. The aim of this study is to apply the multiband (MB) acceleration technique to dynamic pCASL to triple the number of the readout slices in the same measurement time.

METHODS: The MB[1] technique combined with 2-fold in-plane parallel imaging was incorporated into the LL EPI for dynamic sampling of kinetic behaviour following the pCASL labelling scheme. By applying a sinusoidal modulation to a sinc RF pulse, multiple bands in the frequency domain of the RF were determined. The multi-band RF produces multiple clones of the original single band profile each of which has a symmetric frequency offset to simultaneously excite three slices, as in our case. The MB data were reconstructed by the 'Slice-GRAPPA' algorithm[2] suggested by Setsompop et at. The fundamental elements to separate the individual slice from the overlapped signals are distinct sensitivity profiles at each different slice position. To avoid the high g-factor penalty caused by the small differences in the sensitivity profiles at the overlapped area between the simultaneously excited slices, the approach of blipped-controlled aliasing in parallel imaging (blipped-CAIPI)[2] was also used in this work. The performance evaluation of MB and single-band (SB) excitation methods was carried out in 4 healthy subjects using a 32-channel head coil on a 3T Tim-Trio (Siemens, Erlangen, Germany).

For perfusion, MB EPI accelerated dynamic pCASL (MED-pCASL) sequence was developed, which labels blood spins using a pCASL labelling pulse and acquires multiple inversion time information using MB adapted LL-EPI readout. To measure the local arterial input function (AIF) both crushed (c=8cm/s) and non-crushed data were acquired in 7 cycles[3] with crusher gradient in different directions. These crusher gradients suppress the macrovascular signals from flowing blood above 8cm/s. Control-label pairs were acquired in an interleaved manner. Specific sequence parameters were as follows: flip angle/TR/TE/ΔTI/TI_1=35°/4500/27/270/50 ms, bandwidth=1302 Hz, slice acquisition order: ascending, voxel size=3.4×3.4×6 mm^3 with an in-plane matrix size of 64×64. The number of slices/slices distance in the MB (factor of 3) and SB cases were 18/1.2mm and 6/12mm, respectively. The total measurement time of 42 control-label pairs containing 7 crush cycles was 6.23 min. Crushed data were used for the evaluation of tissue signal. Non-crushed data minus crushed data were calculated to be the macrovascular signal. For the macrovascular signal, the subtraction of crushed data from non-crushed data was first thresholded (max(signal) > 0.03*max($signal_{max}$)) to remove noisy pixels. Next, the raw macrovascular signal was fitted to a modified Hrabe-Lewis model[4] which takes the temporal dispersion effect into account. In this study a one-compartment Buxton model was used in fitting the tissue data on a voxel-by-voxel basis. For each brain voxel the previously fitted macrovascular signal of the nearest arterial voxel was used as local AIF. All fitting procedures were performed with nonlinear least squares algorithm as provided by MATLAB.

RESULTS: For comparison, Fig. 1 shows the EPI-based images acquired with SB and MB techniques. One reconstructed image volume from MB technique with MB factor of 3 and in-plane iPAT factor of 2 is presented. After reconstruction using blipped-CAIPI, three simultaneously acquired slices are successfully separated from the MB aliased images. The dynamic perfusion weighted images (Fig. 2) show a slight signal drop in the non-crushed data (-20.8%) but comparable signal level in the crushed data (-13.4%) after using MB acceleration. An initial qualitative comparison of the CBF image from a representative subject reveals a basic similarity (Fig 3). Both the SB and MB-CBF fit well within the colour scale ranging from 0 to 140 mL/100g/min. The histograms of whole-brain CBF from both methods (Fig. 3) show similar Gaussian distributions with the mean value of 56.9 mL/100g/min for SB-CBF and 54.2 mL/100g/min for MB-CBF. After measurements of four young healthy male (24~29 years), the averaged CBF values in grey matter are 52.3 and 53.3 mL/100g/min for SB and MB, respectively. The respective white matter CBF is 26.5 and 33.5 mL/100g/min.

CONCLUSIONS: This study demonstrates results from a quantitative perfusion measurement acquired using pCASL with the MB accelerated LL-EPI. With the help of the MB technique whole-brain CBF can be acquired with a tripled number of slices in the same measurement time as the SB method.

REFERENCES: [1] Moeller S, Magn Reson Med 2009;63:1144–1153. [2] Setsompop K, et al. Magn Reson Med 2012;67(5):1210-1224. [3] Chappell MA, et al. Magn Reson Med 2010;63(5):1357-1365. [4] Ozyurt O, et al. Proceedings of the 18th Annual Meeting of ISMRM, Stockholm, Sweden 2010:4065.

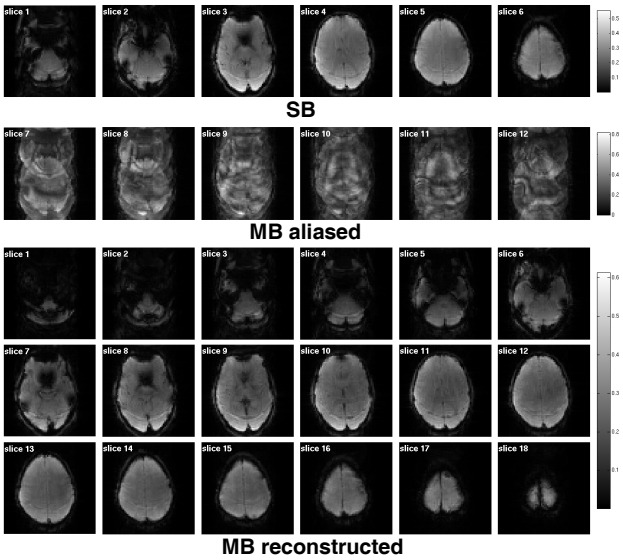

Figure 1. EPI-based images from SB and MB. All the images were reconstructed after 2-fold in-plane parallel imaging. Before and after using MB technique, the slice number was 6 and 18, respectively. Using MB excitation with an MB factor of 3 and blipped-CAIPI, three simultaneous excited slices were folded together with a phase shift. After reconstruction with the 'Slice-GRAPPA' algorithm, the three folded slices were successfully separated and unaliased.

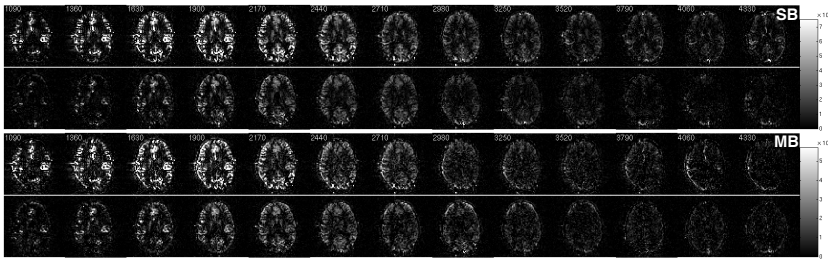

Figure 2. Dynamic perfusion weighted images with no crushing (top row) and with crusher gradients (bottom row) with the method of SB and MB, respectively.

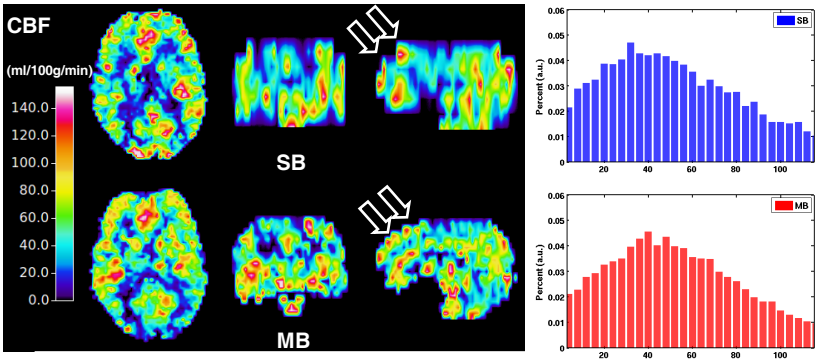

Figure 3. Quantitative CBF ranging from 0 to 140 mL/100g/min after using SB and MB techniques. High resolution along slice direction in sagittal orientation (arrows) was observed with MB method. The corresponding histograms are shown on the right side.