Effect of Tracer Delay on CBF Determination by DSC-MRI: Comparison with Positron Emission Tomography

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Introduction:

Dynamic susceptibility contrast enhancement magnetic resonance imaging (DSC-MRI) can estimate brain perfusion in acute stroke setting. Cerebral blood flow (CBF) can be determined by deconvolution with an arterial input function (AIF)[1,2], however, the accuracy of CBF remains controversial. To investigate the feasibility of DSC-MRI for CBF quantification, we compared CBF determined by MRI-DSC (MRI-CBF) with that by positron emission tomography (PET-CBF) for 7 healthy men. In the study, we paid attention to the regional differences of tracer arrival timing in MR perfusion study, which could cause underestimation of CBF by singular value decomposition (SVD) deconvolution[2,3].

Methods:

Perfusion MRI and PET were performed in 7 healthy men between ages 20 and 22 years. All MR scans were performed by 1.5T Siemens scanner. Structural MRI and MRA were normal in all subjects. The perfusion data were measured with 1-second interval using a gradient echo EPI sequence. After the start of perfusion scanning, 10 mL of Gd-DTPA contrast agent were injected into the antecubital vein by a power injector. The matrix size was 128×128 and the measured data were smoothed by 3×3 uniform filter. CBF values were calculated by SVD-deconvolution using AIF measured in MCA region[2]. To determine the tracer arrival delay in each pixel, we utilized non-linear least square fitting. After time-shifting of measured tissue curve in each pixel, the delay corrected CBF was calculated by SVD-deconvolution. Finally, we obtained CBF images with and without the correction. All MRI-CBF images were processed by Gaussian smoothing with 10-mm FWHM to match the spatial resolutions of MRI and PET. All PET measurements were performed by Shimadzu Headtome-V scanner. PET-CBF were determined by $H_2{}^{15}O$ bolus injection and dynamic analysis using non-linear least square fitting. PET-CBF images were registered to T2 weighted MR images using SPM99. Regions of interest (ROIs) were drawn on PET-CBF and MRI-CBF images. CBF values of cerebral cortex (MCA territory), basal ganglia, and thalamus were normalized to that of white matter (centrum semiovale).

Results:

Averages and standard deviations of CBF for 7 healthy men are shown in Fig.1. Normalized MRI-CBFs, 3.5±0.6 (cerebral cortex), 3.0±0.5 (basal ganglia), and 2.5±0.5 (thalamus), were larger than normalized PET-CBFs, 2.1±0.3, 2.2±0.4, and 2.1±0.4, respectively. In MR perfusion study, the tracer arrival timings in white matter and thalamus were delayed 0.5 second compared with that in cerebral cortex and basal ganglia (Fig.2). By applying the tracer delay correction, MRI-CBF increased by about 20 % in white matter and thalamus, therefore, normalized MRI-CBF with the correction decreased by about 20 % in cerebral cortex and basal ganglia. Normalized MRI-CBFs with the delay correction, 2.9±0.4 (cerebral cortex), 2.5±0.3 (basal ganglia), and 2.6±0.3 (thalamus), were still larger than that of PET-CBF although the differences between MRI-CBF and PET-CBF were reduced in cerebral cortex and basal ganglia. In all brain regions, standard deviations of MRI-CBF with the correction were smaller than that without the correction.

Conclusion:

The regional differences of tracer arrival timing in DSC-MRI introduce inaccurate CBF estimation when SVD deconvolution is used. We have demonstrated that the delay correction reduces the differences between MRI-CBF and PET-CBF, although still exist. The tracer delay correction will enable us to estimate more accurate CBF with less intersubject variability.

References:

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[3] Calamante F et al.; *Magn. Reson. Med*. 44, 466-473 (2000).

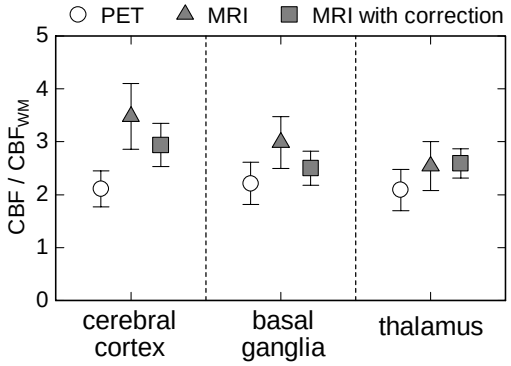

Figure.1 PET-CBF and MRI-CBF normalized to white matter CBF.

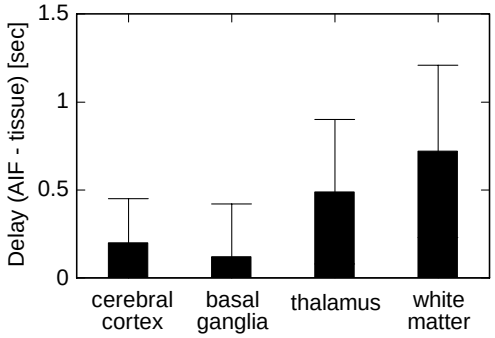

Figure.2 Tracer arrival delay to AIF.