Comparison of Quantitative Cerebral Blood Flow Measured with Bolus Tracking Perfusion MRI and $H_2{}^{15}O$ PET in the Porcine Model

Elias Kellner[1], Irina Mader[2], Michal Mix[3], Marco Reisert[1], Katharina Förster[4], Thao Nguyen-Thanh[2], Daniel Nico Splitthoff[1], Peter Gall[1], and Valerij G. Kiselev[1]
[1]*Department of Radiology, University Hospital Freiburg, Freiburg, Germany,* [2]*Section of Neuroradiology, University Hospital Freiburg, Freiburg, Germany,* [3]*3Department of Nuclear Medicine, University Hospital Freiburg, Freiburg, Germany,* [4]*4Department of Cardiovascular Surgery, University Hospital Freiburg, Freiburg, Germany*

TARGET AUDIENCE: Developers of methodology for perfusion measurements, clinicians searching for advanced methods.

PURPOSE: We recently presented a method for the quantitative determination of the arterial input function (AIF)[1]. Verification in the porcine model demonstrated a good accuracy of the AIF regarding the cardiac output and the cerebral blood volume. In this work, we present CBF values obtained with the new method in comparison with Positron-Emission-Tomography (PET) in 13 animals.

METHODS: The sequence was an extension of the standard EPI-based DSC MRI sequence[1]. In between each slice acquisition in the brain, a slice in the neck was excited. The AIF was quantified using the apparent shift of the arteries induced by the contrast agent. The tracer concentration in the brain was quantified using the model by Yablonskiy and Haacke[2]. From these quantitative tracer concentration time courses, CBF values were calculated using Tikhonov regularisation. 13 pigs were measured with the following parameters: ***MRI:*** 25 mL @ 5 mL/s of 0.5mol/L Gd-DTPA contrast agent (Multihance, Bracco, Italy). EPI parameters: 9 slices, $TE_{GE}/TE_{SE}/TR$=20/86/1590 ms, resolution 2.62x2.62mm^3. Parameters for the AIF slice: gradient strength 1mT/m, TR=176ms, bandwidth 38.2 Hz/mm, TE=0.7ms. ***PET:*** Philips Gemini TF 64, voxel size: 4mm^3 injection of 320 MBq $H_2{}^{15}O$, AIF determined in carotid arteries with partial volume correction.

RESULTS: Based on the T1 reference image (Fig. 1), gray and white matter masks were segmented using SPM (Wellcome Department, University College London). MRI CBF was evaluated separately for gray matter (GM) and white matter (WM) with the group mean 21.8 mL/(100g min) and 13.6 mL/(100g min). Application of these masks to co-registered PET images does not result in any difference in the PET CBF between GM and WM. Hence, the PET evaluation was performed using whole brain masks (group mean CBF 23.5 mL/(100g min)). Comparison between the tissue-specific MRI CBF and the whole brain PET CBF is shown in Fig. 2. The proportionality coefficients between the MRI CBF and the PET CBF are 0.95 (correlation coefficient = 0.72) and 0.60 (0.84) for GM and WM, respectively.

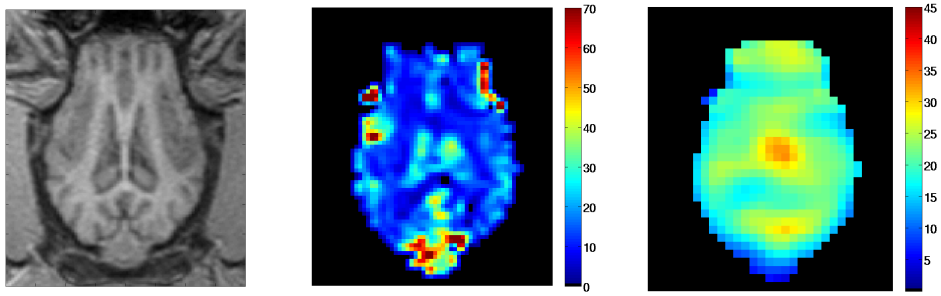

Fig 1: T1 and CBF Maps of the same slice for MRI and PET in an animal. The high resolution in MRI allows for separation of gray and white matter.

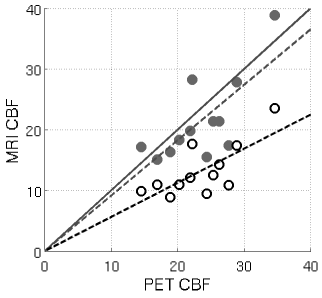

Fig 2: Correlation between PET and MRI for all animals. Gray: GM, White: WM. The lines are identity (solid), and the fitted proportionality for GM and WM (dashed)

DISCUSSION: Resolution of PET imaging is too coarse to discriminate between GM and WM in the small porcine brain. The group mean of 23 mL/(100g min) should be interpreted as the weighted mean between the two corresponding values. In this view, the good agreement between the MRI and PET for GM (Fig. 2) should not be given too much credit. PET CBF in GM and WM can be estimated as 29 mL/(100g min) and 18 mL/(100g min), respectively, using the known volumes of GM and WM and the same proportion as for MRI CBF. This indicates an underestimation of MRI CBF as compared with PET. This is expected due to the dispersion of the tracer bolus and the smoothing effect of the deconvolution. The CBF values in both methods are lower than the known GM and WM values, also in comparison with other works[3]. Note the significant difference in the MRI technique between the present study and other works[3], in particular the absence of any empirical normalisation coefficient applied previously[3].

Determination of a proportionality line rather than a general linear regression presumes no effect for zero CBF in both methods. This limits the proportionality coefficient which would be less precise otherwise. Manipulating the CBF should be performed for a better sampling of the CBF in a larger range, as it was done in study[3].

CONCLUSIONS: The presented MRI perfusion measurement does not involve any adjustable or normalising parameters, which creates a basis for truly quantitative comparison. Note that the PET data processing includes a significant partial volume correction of the AIF. The comparison between MRI and PET is not straightforward due to the unmatched image resolutions and, more deeply, due to differences in both the tracer kinetics and the physical principles of tracer detection. Present results create a quantitative basis for further investigation.

References: 1. Kellner E et al. Arterial input function measurements for bolus tracking perfusion imaging in the brain. MRM 2012;DOI: 10.1002/mrm.24319 **2.** Yablonskiy D and Haacke M. Theory of NMR Signal Behavior in Magnetically Inhomogeneous Tissues: The Static Dephasing Regime. MRM 1994;32:749-763. **3.** Østergaard L et al. Absolute cerebral blood flow and blood volume measured by magnetic resonance imaging bolus tracking: Comparison with positron emission tomography values. J Cerebl Blood Flow and Metab 1998;8:425-432