AN INTEGRATED PENCIL-BEAM PROBE FOR ASSESSING THE ARTERIAL INPUT FUNCTION IN QUANTITATIVE 3D MYOCARDIAL PERFUSION IMAGING

Lukas Wissmann[1], Johannes F.M. Schmidt[1], Robert Manka[1,2], and Sebastian Kozerke[1]

[1]*Institute for Biomedical Engineering, University and ETH Zurich, Zurich, Switzerland,* [2]*Department of Cardiology, University Hospital Zurich, Zurich, Switzerland*

Introduction: Assessment of whole-heart myocardial perfusion using three-dimensional dynamic contrast-enhanced magnetic resonance imaging (DCE-MRI) has significantly evolved in the recent past [1-3]. However, robust quantification of perfusion from 3D data remains to be accomplished. Most quantification methods employ deconvolution of the tissue response curve from the myocardium with an arterial input function (AIF) extracted from the left ventricular (LV) blood pool in the image [4,5]. The accuracy of the quantification process is highly dependent on the dose of the gadolinium-based contrast agent and the timing of the saturation recovery imaging sequence [6]. While high dose and a long delay between saturation pulse and imaging sequence are beneficial for signal-to-noise in the myocardium, the accuracy of the AIF acquisition may be compromised due to signal saturation [7]. To address this issue, the AIF may be acquired separately at a reduced delay after the saturation pulse prior to the actual imaging module [6].

In the present work a pencil-beam probe is proposed to efficiently sample the AIF at flexible delays relative to the saturation pulse prior to the single-shot 3D *k-t* imaging module. It is demonstrated that the pencil-beam probe allows addressing AIF saturation effects while preserving the benefits of high dose contrast agent injection and long saturation delays.

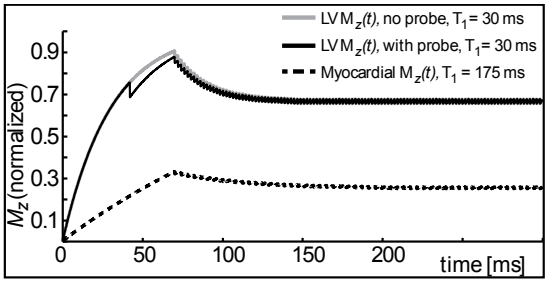

Figure 1. Simulation of longitudinal magnetization in the LV (solid) and myocardium (dashed) during one repetition of the imaging experiment.

Methods:

Data acquisition: The pencil-beam probe was implemented using a 2D selective spiral excitation pulse with jinc amplitude weighting and integrated into a 10x *k-t* PCA 3D single-shot sequence [3]. Data were acquired in healthy subjects on a 3T Philips Ingenia system (Philips Healthcare, Best, The Netherlands) with a 28-element anterior and posterior coil array, using a saturation-recovery gradient echo sequence. Imaging parameters were TR: 2.02 ms, TE: 0.65 ms, flip angle: 15°, slice thickness: 5 mm, in-plane spatial resolution: 2.3x2.3 mm^2. Net acceleration based on 10-fold nominal undersampling was 7.0 when taking into account the densely sampled training data. The pencil-beam probe was placed in the LV blood pool perpendicular to short-axis orientation. The pencil-beam diameter was 20 mm and the axial field-of-view 256 mm, sampled along 256 points resulting in 1 mm axial resolution. DCE-MRI was performed using Gadovist (Bayer Schering Pharma, Germany) at 0.1 mmol/kg dose, followed by a washout period of 20 minutes and a second bolus of 0.05 mmol/kg.

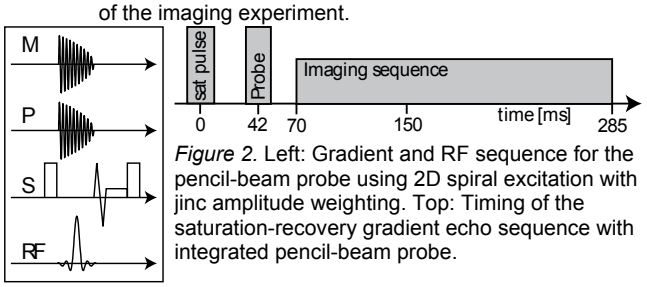

Figure 2. Left: Gradient and RF sequence for the pencil-beam probe using 2D spiral excitation with jinc amplitude weighting. Top: Timing of the saturation-recovery gradient echo sequence with integrated pencil-beam probe.

Computer simulations: Sequence timing was optimized assuming *T1* = 30 ms for the LV and *T1* = 175 ms for the myocardium during peak contrast enhancement [6]. Figure 1 demonstrates the effect of partial saturation introduced by the pencil-beam probe given a pencil-beam excitation angle of 25°. The probe sequence setup and timing are displayed in Figure 2.

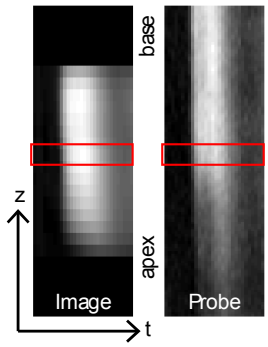

Figure 3. LV signal vs. time in the image for all 16 slices (left) and the pencil-beam probe (right). FOV: image: 16 cm, probe: 25.6 cm. Red areas were used for AIF extraction, cf. Figure 4.

Postprocessing: The pencil-beam data were zero-filled to account for 62.5% partial Fourier sampling and subsequently Fourier transformed. Signal-intensity (SI) curves from both the pencil-beam probe and the image data were extracted for comparison using manual segmentation of the LV. Tissue response curves were extracted from six myocardial sectors of nine slices for quantitative analysis. Comparison of flow rate quantification with probe and image AIF was done using model-independent deconvolution [5].

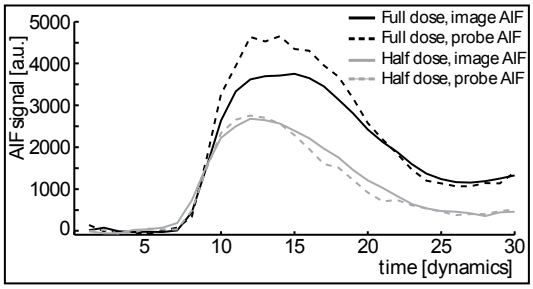

Figure 4. Baseline-corrected SI curves of one volunteer from full (0.1 mmol/kg) and half (0.05 mmol/kg) dose DCE-MRI extracted from the red areas in Figure 3. The image AIF (solid) is partially saturated, the pencil-beam probe AIF (dashed) shows higher peak enhancement.

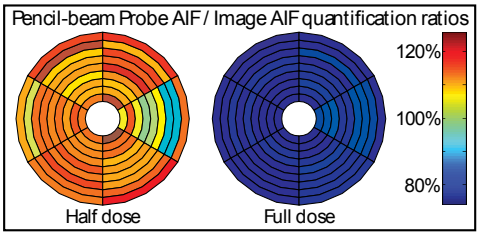

Figure 5. Bull's eye plots of MBF probe to image ratios computed using model-independent deconvolution of the myocardial SI curves for 6 myocardial sectors in 9 slices.

Results: Figure 3 shows the pencil-beam probe data and a *z-t* plot extracted from the image and adjusted to the pencil-beam size. Good agreement between the image and the pencil-beam probe data was found. Image and probe AIFs are plotted in Figure 4 for 0.05 and 0.1 mmol/kg dose. Image and probe data agree very well for half dose. The full dose imaging AIF is partially saturated around the peak. This saturation effect is not visible in the probe AIF. Figure 5 shows bull's eye plots of the ratios of myocardial blood flow (MBF) computed using probe and image AIF, respectively, for half and full dose. For half dose the probe AIF MBF is 12.5 ± 5.9% higher than the image AIF MBF. In contrast, the full dose probe MBF is 19.2 ± 1.0% smaller than the full dose image MBF. While the differences for half dose are wide-spread and not reflected in the AIFs in Figure 4, the full dose ratios are more homogeneous and a direct consequence of underestimation of the image AIF due to signal saturation, which leads to overestimation of myocardial flow.

Discussion: It has been demonstrated that a pencil-beam probe to assess the left-ventricular arterial input function is feasible and allows to circumvent signal saturation effects of the AIF during high dose 3D myocardial perfusion imaging. The timing of the probe and the imaging sequence can be optimized individually for best LV and myocardial signal. Comparison of myocardial blood flow values yielded good agreement, but further investigation in a large study cohort is required.

References: [1] Shin, JCMR 2008;**10**:57-66; [2] Manka, JACC 2010;**3**:710-7; [3] Vitanis, MRM 2011;**65**:575-87; [4] Jerosch-Herold, Med. Phys. 1998;**25**:73-84; [5] Jerosch-Herold, Med. Phys. 2002;**29**:886-97 ; [6] Gatehouse, JMRI 2004;**20**:39-45; [7] Utz, JMRI 2007;**25**:1131-35.