3D first-pass myocardial perfusion imaging at 3T: towards complete left ventricular coverage

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Introduction: Conventional 2D multi-slice myocardial perfusion imaging (MPI) is not capable of evaluating the extent of perfusion defect due to incomplete coverage of the left ventricle (LV). Accelerated 2D multi-slice imaging can achieve more complete coverage [1], but suffers from suboptimal slice profiles and possible inter-slice signal contamination. 3D MPI is an attractive alternative due to its contiguous coverage, higher signal-to-noise ratio (SNR) efficiency, and greater capacity for parallel imaging acceleration, and has been demonstrated at 1.5T [2]. In this work, we demonstrate 3DFT GRE first-pass MPI with complete LV coverage at 3T in healthy volunteers, and perform semi-quantitative perfusion analysis.

Methods: Our pulse sequence consisted of an adiabatic BIR-4 saturation RF pulse followed by 3DFT GRE acquisition. Slab excitation was achieved with a RF pulse having a time-bandwidth-product of 4. Data acquisition occurred only during diastole and was triggered by ECG or plethysmography. 2D TSENSE acceleration of rate 3 and 2 were used along the phase and partition encoding axes, respectively [3,4]. Imaging parameters include T_{SR}= 130ms, TR=2.3 ms, TE=0.9 ms, flip angle= 10°, spatial resolution= 3.0x4.5x10 mm^3, FOV=30x30x10 cm^3, acquisition time per heart beat = 303.6 ms. A proton-density-weighted (PDW) data set was obtained using 4° flip angle with the saturation pulse turned off at the beginning of the scan. Experiments were performed on three healthy volunteers using a GE Signa Excite 3 Tesla scanner with 40 mT/m gradient amplitude and a slew rate of 150 T/m/s. An eight-channel cardiac phased array coil was used for signal reception. Contrast media (0.1 mmol/kg Gd-DTPA, Magnevist®) was injected at a rate of 5 ml/s followed by 20 ml saline flush at the same rate. Subjects were instructed to hold their breath as long as possible. Raw perfusion images were normalized by PDW images to remove variations in the receiver coils. Corrected images were then segmented into six (basal and mid-short axis levels) or four (apical level) myocardial sectors. Within each myocardial sector, time intensity curve (TIC) was generated and the corresponding upslope value was computed by linear fitting of the data during signal enhancement. CNR values were calculated by the method described in [5], where noise standard deviation is computed from the difference of two images.

Results: Fig. 1 shows representative perfusion images at pre-contrast, RV enhancement, LV enhancement, and myocardium enhancement. Overall image quality is excellent, clearly showing the arrival and the passage of contrast agent. Superimposed colormap visualization of TIC upslopes in the first nine slices is shown in Fig. 2. The average upslope value of the whole myocardium is scaled to 100%. As expected, the upslope values are all within normal range for these healthy volunteers. Average CNR values for the first eight slices, were 24.1, 24.7, 31.1, 29.5, 29.1, 29.0, 13.4 and 14.4.

Discussion: High quality perfusion images covering whole LV can be achieved using 3D MPI with 3.0x4.5x10 mm^3 spatial resolution. We expect to perform perfusion experiments on patients with known coronary artery disease. Spatial resolution may be insufficient in apical slices, and higher acceleration will be explored by adding total variation constraint to the SENSE reconstruction [6]. 3D encoding is advantageous to image registration due to its volumetric acquisition, and can potentially correct for breathing motion.

References: [1] Köstler H et al. JMRI 2003; 18: 702-708. [2] Kellman P et al. ISMRM2004: 310. [3] Kellman P et al. MRM 2001; 45: 846-852. [4] Weiger M et al. Magma 2002; 14: 10-19. [5] Reeder SB et al. MRM 2005; 54:748-754 [6] Block KT et al. MRM 2007; 57:1086-1098

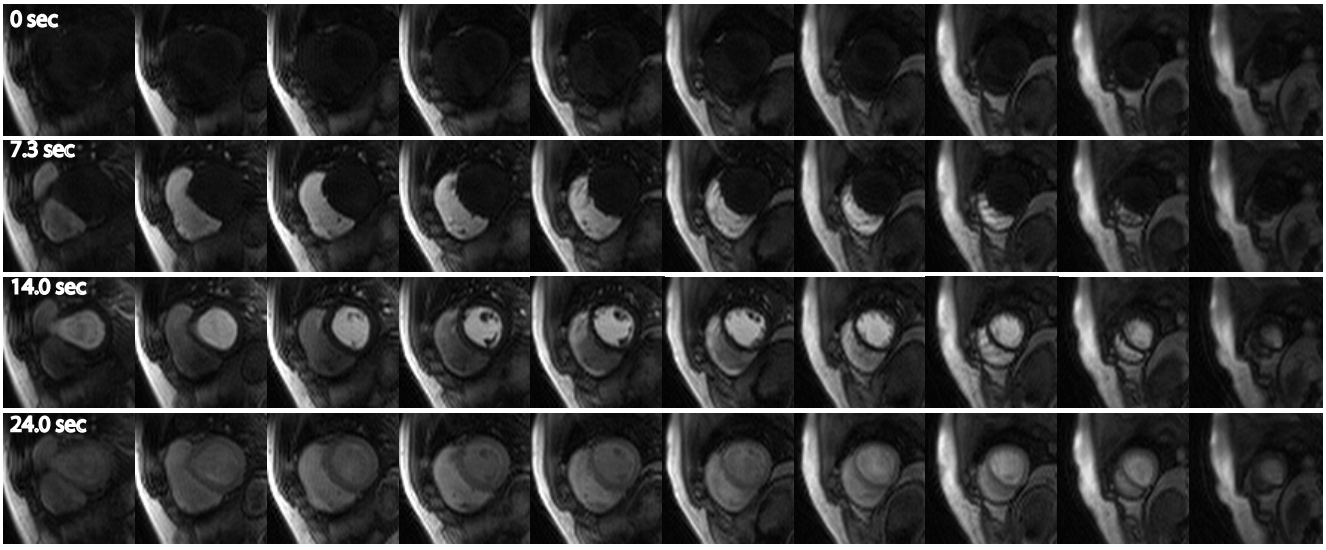

Fig. 1. Representative perfusion images at pre-contrast, RV enhancement, LV enhancement, and myocardium enhancement.

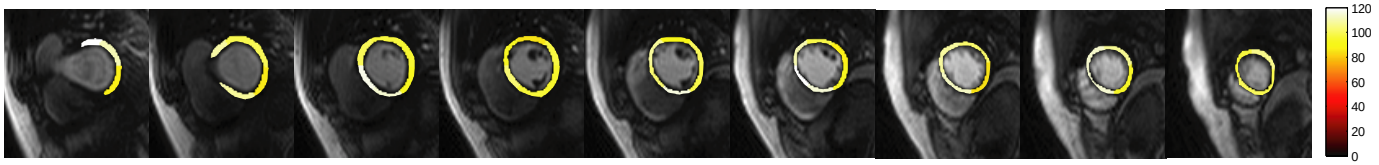

Fig. 2. Maps of time-intensity curve (TIC) upslope in a healthy volunteer.