Meeting abstract

237 MRI myocardial perfusion quantification: effects from contrast dose, imaging plane and sequence

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This abstract is available from: http://jcmr-online.com/content/10/S1/A98

Introduction

The quantification of myocardial perfusion using MRI is a sensitive method for detecting ischemia. The limitations of myocardial perfusion quantification include artifacts, sequence dependence, and saturation effects associated with high contrast agent concentration in the LV. The dual bolus method solves the blood signal saturation problem by using two contrast injections to acquire low contrast dose imaging of LV blood, followed by high contrast dose imaging of myocardium. The objective of this study was to determine whether the resting perfusion quantification using the dual bolus approach is dependent on the MRI pulse sequence or imaging plane orientation.

Methods

Fourteen volunteers (7 male, age: 59 ± 10) without a clinical history of coronary artery disease underwent informed consent before enrollment in this study with institutional IRB approval. In each case, imaging was performed in four slices per RR interval (one short-axis (SX) slice from mid-ventricle, three long-axis (LX) views, including 4-chamber, 2-chamber and LVOT view) using saturation recovery segmented gradient echo (EPI), True-FISP (TFI) and TurboFLASH (TFL) sequences, with 20-minute washout. Typical sequence parameters for the TrueFISP were: TR/TE/TI/FA = 2.6 ms/1 ms/90 ms/50°, rectangular field-of-view 21 × 34 cm^2, bandwidth (BW) per pixel 980 Hz and voxel spatial resolution 3.5 × 2.6 × 8 mm^3. Temporal and spatial resolution for EPI and TFL perfusion sequence were kept similar. Gadodiamide (Omniscan, GE Healthcare, Princeton, NJ) was injected at doses of 0.005 mM/kg mini dose (MD) followed by 0.05 mM/kg high dose (HD), with a Spectris MR power injector (Medrad, Indianola, PA) at a rate of 6 ml/s. First pass breath-hold Perfusion imaging was obtained over 50 cardiac cycles. Using MASS (Medis Medical Systems, Leiden, Netherlands) software, epicardial and endocardial contours were manually traced on an image from each slice with good contrast between blood pool and myocardium. The contours were then propagated through the whole perfusion series in that slice, with manual correction to compensate for respiratory motion when needed. The myocardium was divided equally into six segments for each imaging plane. Segmental myocardial average signal intensity over time was used for the quantitative analysis. A Fermi deconvolution model implemented in Matlab was used to generate regional perfusion in ml/g/min. A total of 252 myocardial segments on long and 84 segments on short axis images for each sequence were quantified and their correlation was analyzed using ANCOVA.

Results

As shown in Table 1, LX and SX with each sequence show good agreement (p = 0.96). Depending on the sequence used, measurements using a standard dose of contrast agent (0.05 mM/kg) produced absolute perfusion more than twice those from dual bolus corrected measurements.

Table 1: Mean myocardial resting perfusion ± sd (ml/g/min) measured by three sequences using MD and HD, in LX and SX (n = 252 for LX and n = 84 for SX). Myocardial rest perfusion quantification results are sequence dependent, and overestimate perfusion at widely used dosage of 0.05 mM/kg. Long and short axis perfusion values are comparable regardless of contrast dose or sequence.

	MiniDose LX	MiniDose SX	HighDose LX	HighDose SX
EPI	0.69 ± 0.14	0.65 ± 0.10	1.73 ± 0.36	1.88 ± 0.59
TFL	0.74 ± 0.26	0.65 ± 0.10	1.59 ± 0.41	1.59 ± 0.43
TFI	0.72 ± 0.26	0.69 ± 0.29	2.51 ± 0.61	2.44 ± 0.68

Conclusion

Mini bolus MRI normal rest perfusion (at 0.005 mM/kg) values are similar to PET values. Results with 0.05 mM/kg, which is widely used, overestimate perfusion. They are sequence dependent. Long and short axis perfusion values are comparable regardless of contrast dose or sequence.