Journal of Cardiovascular Magnetic Resonance

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Meeting abstract

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2067 Scan-rescan reproducibility of left ventricular mass with 3D Cardiac Image Modeling (CIM)

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from 11th Annual SCMR Scientific Sessions
Los Angeles, CA, USA. 1–3 February 2008

Published: 22 October 2008

Journal of Cardiovascular Magnetic Resonance 2008, **10**(Suppl 1):A336 doi:10.1186/1532-429X-10-S1-A336

This abstract is available from: http://jcmr-online.com/content/10/S1/A336

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Introduction

Cardiac MRI intra- and inter-observer errors are routinely calculated to quantify analysis variability. Scan-rescan variability is a more stringent test where subjects are scanned and analyzed on two separate occasions. This incorporates variability due to patient positioning, EKG lead placement, scout and cine image placement, and changes in scan parameters, in addition to the variability in the analysis. This represents the true variability associated with determining patient disease progression or treatment effect in a clinical trial.

Due to the difficulty of controlling loading conditions and their effect on end-diastolic and end-systolic volumes, scan-rescan variability is best determined using left ventricular mass (LVM) which can reasonably be expected to be constant between scans. As this is a difference measurement between both the endocardial and epicardial surfaces it is also particularly sensitive to errors in the placement of these contours.

Purpose

To determine the scan-rescan variability of cardiac MRI analyzed with the 3D model based reconstruction technique CIM [1].

Methods

25 patients with asymptomatic moderate-severe mitral regurgitation due to mitral valve prolapse were scanned at a two week interval using an SSFP protocol (TE~1.7 msec, FOV~360 mm, slice thickness 7–8 mm, pixel size~1.5 × 1.5 mm, and with ~24 reconstructed frames), as part of a crossover trial investigating the acute effects of Metoprolol (mean dose 119 mg, range 23.75–195 mg/day) on regurgitant volume. The assumption was made that due to the short duration of treatment that changes in LVM were unlikely and there were no major medical events which could be expected to change LVM. Reduced heart rate on treatment was expected.

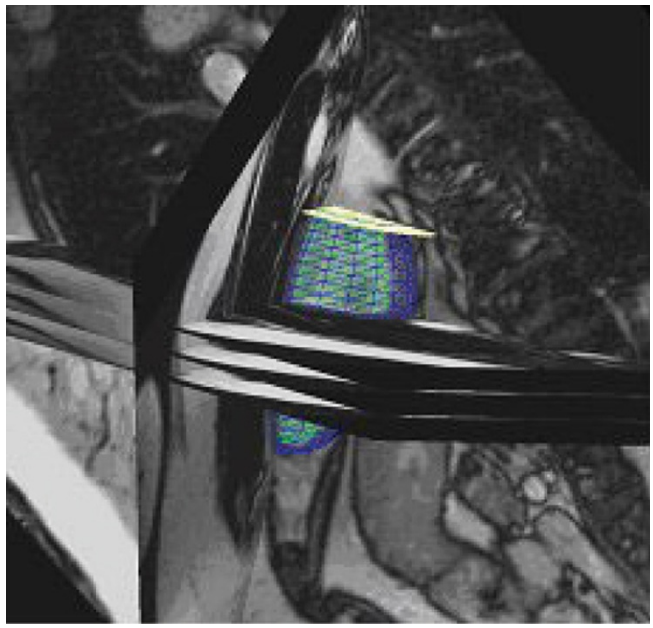

Figure 1
Model based representation of the left ventricle from CIM.

Analyses were performed using guide-point modeling where a 3D mathematical model (Figure 1) was adaptively optimized to fit each subject's images (CIM version 4.5, Auckland MRI Research Group). The model was interactively fitted to guide-points provided by the user, and image derived data points provided by an image processing algorithm. The method correctly accounted for the motion of the base of the heart, by tracking the insertion of the mitral valve leaflets and volume was calculated up to but not through this moving plane. Papillary muscles were included with the blood pool.

All cases were independently analyzed by two experienced observers. Cases with discrepancies in LVM of >5% were independently reanalyzed. The final result was calculated as the average of the two analysts (where there was a reanalysis, the results from each analyst with closest agreement in LVM were chosen for averaging). All analyses were randomized and blinded to patient identity, first or second scan, previous results and results from the other analyst.

Results

Baseline heart rate was 65/min and this fell by 10/min ($p < 0.0001$) on Metoprolol. As a group, the average mass on first scan was 183.4 g and on the second scan 186.3 g (difference 1.1 g or 0.6%). Individually, the average difference between the first and second scans was 4.1 g (2.2%), with a standard deviation of 5.7 g. The maximum single difference in one case was 16.4 g (8.2%). A Bland-Altman plot (Figure 2) shows that the errors are not related to ventricular size.

Conclusion

Scan-rescan variability with SSFP and 3D CIM reconstruction is excellent with an average difference between scans of only 0.6%. Heart rate change did not affect the results.

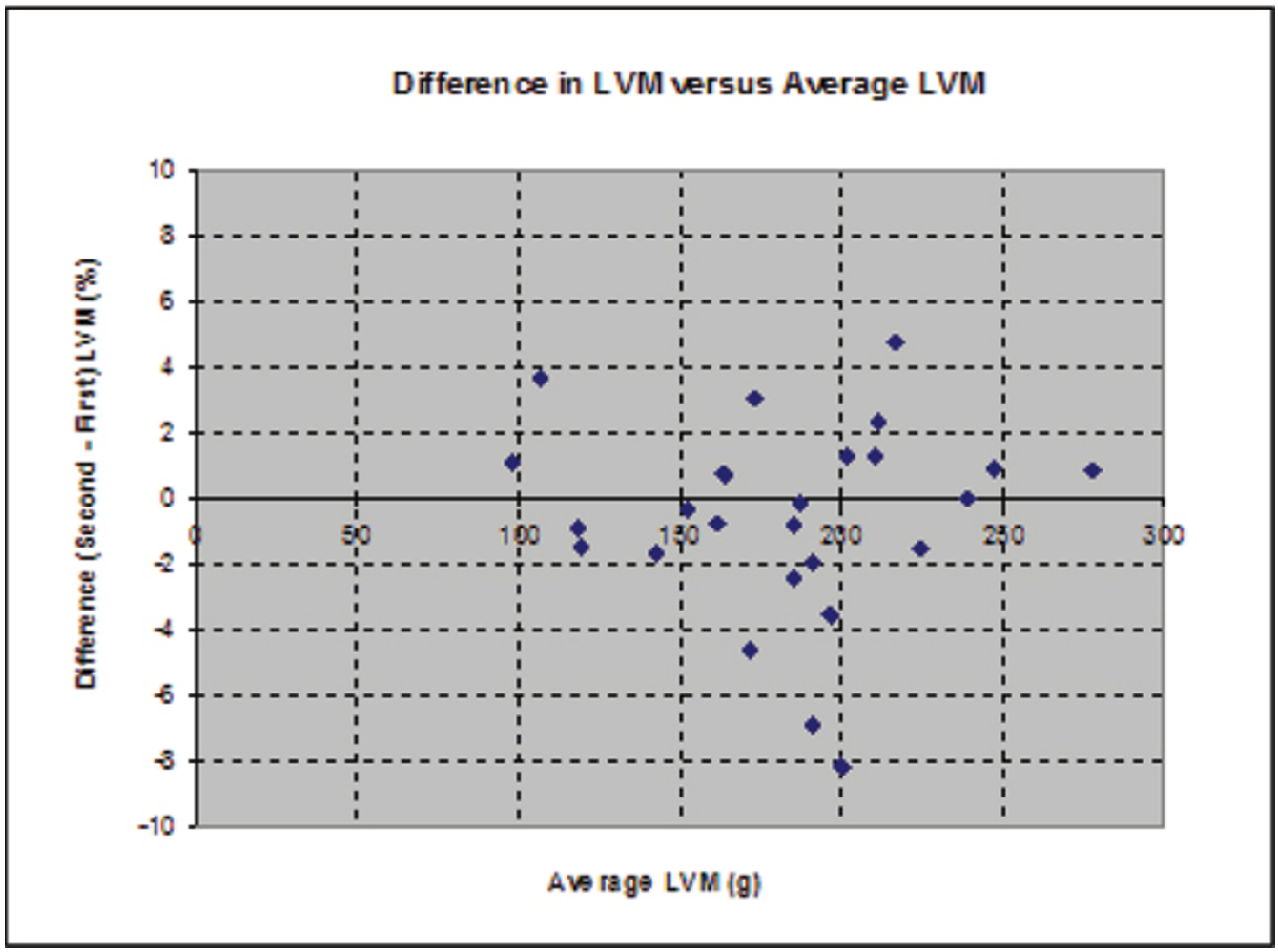

Figure 2
Bland-Altman plot of the difference in LVM between the first and second scan versus average LVM.

This confirms that smaller sample sizes may be used in trials with primary endpoints of change in LVM.

References

1. Young AA, *et al.*: *Radiology* 2000, **216:**597-602.

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