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Heart deformation analysis: The distribution of regional myocardial motion patterns at left ventricle

Kai Lin, MD, MS¹, Leng Meng, MD^{2,*}, Jeremy D. Collins, MD¹, Varun Chowdhary, MD¹, Michael Markl, PhD¹, and James C. Carr, MD¹

¹Department of Radiology, Northwestern University, 737 N Michigan Avenue, Suite 1600, Chicago, IL 60611

²Department of Radiology, Anzhen Hospital, Capital Medical University, Anzhen Li, Chaoyang District, Beijing 100029, China

Abstract

The aim of the present study was to test the hypothesis that heart deformation analysis (HDA) is able to discriminate regional myocardial motion patterns on the left ventricle (LV). Totally 21 healthy volunteers (15 men and 6 women) without documented cardiovascular diseases were recruited. Cine MRI was performed on those subjects at four-chamber, two-chamber, and short-axis views. The variations of segmental myocardial motion indices of the LV, which are measured with the HDA tool, were investigated. Regional displacement, velocity, strain and strain rate were compared between lateral wall and septal wall using t-tests. There are significant variations (CoV = 18.0% to 72.4%) of myocardial motion indices (average over 21 subjects) among 16 myocardial segments. There are significant differences ($p < 0.05$) between displacement, velocity, strain and strain rate measured at lateral and septal areas of the LV. In conclusion, HDA is able to present different regional LV motion patterns from multiple aspects in healthy volunteers.

Keywords

Heart deformation analysis; MRI; myocardial motion pattern; variations

Address for correspondence: Kai Lin (kai-lin@northwestern.edu), Department of Radiology, Northwestern University, 737 N Michigan Avenue, Suite 1600, Chicago, IL 60611, Tel: (312)695-5577, Fax: (312)926-5991.

*KL and LM contributed equally to this work

Conflict of Interest:

One co-author, MPJ, is employee of SIEMENS AG. The other authors have nothing to declare. The data and information of this study are under control by authors who are not SIEMENS employee.

Ethical approval: All procedures performed in studies were in accordance with the ethical standards of the institutional and/or national research committee and with the 1964 Helsinki declaration and its later amendments or comparable ethical standards. The IRM approved this study.

Informed consent: Written informed consent was obtained from all individual participants included in the study.

Compliance with Ethical Standards

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Introduction

Congestive heart failure (CHF) represents the incapability of the ventricles to contract or relax due to advanced cardiovascular disease (CVD). However, at the early stage of CVDs, myocardial damage can involve a limited area instead of the whole ventricle and result in minimal change of the ejection fraction (EF), a major global indicator for the diagnosis of CHF in standard of care. Therefore, regional myocardial motion patterns are expected to sensitively present cardiovascular vulnerability. In previous studies, impaired regional systolic left ventricle (LV) thickening (identified with semi-quantitative methods on echocardiography or magnetic resonance imaging [MRI]) was correlated with high incidence of cardiovascular events (1–3). However, affected by various anatomic and physiological factors, such as anisotropic structure or adjunct ventricular overload, both magnitude and direction of regional myocardial deformation can vary greatly from segment to segment under normal physiological conditions (4–6). Therefore, it is necessary to investigate background motion patterns to judge regional myocardial motion abnormalities. As such, multiple quantitative biomechanical indices, including displacement, velocity, strain and strain rate, should be adopted to comprehensively describe region-specific myocardial motion patterns from various aspects.

Currently, many advanced image tracking techniques in the domains of computer vision and machine learning have been introduced to obtain the information of myocardial motion from cardiac cine MRI acquired with traditional balanced steady-state free precession (bSSFP) techniques (7). Based on deformable imaging registration (DIR), heart deformation analysis (HDA) is a recently developed myocardial motion tracking technique that is able to calculate regional and global myocardial displacement, velocity, strain and strain rate on existing cine images without extra MRI scans (8–10). Using HDA, we measured displacement, velocity strain and strain rate on a per-segment basis (mapped on a standard 16-segment AHA LV model) at 21 healthy volunteers, and investigated the regional distributions of magnitudes for each myocardial index on the LV. The aim of the present study is to test the hypothesis that HDA is able to discriminate regional myocardial motion patterns on the LV from multiple aspects.

Materials and Methods

Description of subjects

This study complied with HIPAA regulations. Following the approval of the institutional review board (IRB), 21 healthy volunteers (15 men and 6 women) without documented history of cardiovascular diseases were recruited (Table 1). All participants provided written informed consent prior to the MRI scans.

cine MRI acquisition protocol

All participants underwent a single MRI examination on a 1.5 T commercial available whole-body scanner (MAGNETOM, Aera, Siemens AG, Germany) with an 18-channel coil. The basic physical conditions, including body weight, heart rate systolic blood pressure

(SBP) and diastolic blood pressure (DBP) of all participants, were routinely recorded before MRI scans.

Firstly, a three-plane fast localization sequence was used for general anatomic orientation. Four-chamber, two-chamber, and short-axis views were then identified with a black-blood half-Fourier rapid acquisition with relaxation enhancement sequence.

For each participant, segmented bSSFP sequences were used to acquire cardiac cine images in the two-chamber, four-chamber and short-axis of the heart. Imaging parameters were as follows: TR/TE = 2.8/1.1 ms; flip angle = 65°, slice thickness = 8 mm, in-plane resolution = $2.1 \times 2.1 \text{ mm}^2$, bandwidth = 930 Hz/pixel, parallel imaging (GRAPPA technique) with reduction factor R = 2. Each myocardial slice was acquired within a breath-hold at end-expiration using retrospective ECG gating (with 25 retrospective constructed cardiac phases). Eight to ten short-axis slices were acquired to cover the entire LV from the apex to base.

Image processing with the HDA tool

The cine MRI datasets, including 2-chamber, 4-chamber and short-axis views were transferred to a dedicated image processing workstation (Dell, STUDIO, SPS 435T) and were analyzed using a prototype software package (TrufiStrain, Siemens Corporation, Corporate Technology, Princeton, NJ) developed in Visual C++ environment. An experienced analyzer (KL, reader #1, with 9 years of experience in cardiovascular imaging) manually loaded the cine image stack. Based on an algorithm which was previously described (11), landmark anatomic structures in the heart, such as left atrium, aortic root, right atrium, could be automatically detected by the software and the LV borders of the LV could be automatically segmented at short-axis slices. Then, a DIR algorithm was applied to calculate motion deformation fields using frame-to-frame elastic image registration (12). Then, a special 2D displacement vector was calculated and assigned to each pixel within the region of deformation fields. Two adjacent images were registered for the displaced pixels of the moving object and the reference object by solving the 2D displacement vectors. Local cross correlation was minimized. Myocardial motion indices, including displacement, velocity, strain and strain rate, could therefore be derived from the deformation fields over time. Next, the in-plane time-resolved regional myocardial motion vectors in radial and circumferential directions were generated for every myocardial pixel and were mapped on a standard 16-segment AHA LV model as a reference. Positive velocities were generally defined for systolic contraction / shortening / clockwise rotation while negative values represented diastolic expansion / lengthening / anticlockwise rotation. See figure 1 for the whole work flow of analyzing regional myocardial motion patterns using our HDA tool.

Since contour drawing and landmark selection for calculation of motion indices were performed automatically by the software, intra- or inter-observer variability seem unlikely to affect the final results. In the present, we only tested the inter-analysis and inter-study variability of the HDA tool. The reader #1 reloaded cine bSSFP images a week later and repeat the same workflow of image analysis for all subjects. Cine datasets from five randomly chosen volunteers who underwent a second cine MRI examination in a different

day were used to test the inter-study variability of segmental myocardial motion indices acquired with the HDA tool.

Data processing and statistical analysis

All continuous variations were represented by mean $\pm$ one standard deviation (SD). The segmental motion indices at radial and circumferential directions, including displacement (Drr and Dcc), velocity (Vrr and Vcc), strain (Err, Ecc and Ess [shear strain, defined as the shearing between the Ecc and Err]) and strain rates (SRr and SRc) in systole and diastole, were recorded and average over 21 subjects. The coefficient of variation (CoV, defined as SD/Mean) was applied to describe the distribution of peak myocardial measurements among 16 segments. Among sixteen myocardial segments on the LV, septal area was defined as segment 2, 3, 8, 9 and 14, while lateral area was defined as segment 5, 6, 11, 12 and 16 (13). The differences in peak segmental variables between different areas (segment groups) were compared using paired *t*-tests. Statistical analysis was performed using SPSS statistical software (Version 13.0, SPSS, Inc, Chicago, IL). Statistical analyses were two-tailed. A *p* value <0.05 was considered statistically significant. A CoV $\geq 20\%$ among myocardial segments was considered as significant variance for individual measurements. Bland-Altman plots were used to demonstrate inter-study variances of myocardial motion indices.

Results

bSSFP cine sequences were successfully run in 21 volunteers. All images were eligible for quantitative analysis and resulted in motion indices on 336 myocardial segments for comparisons.

There are significant variations (CoV = 18.0% to 72.4%) of myocardial motion indices (average over 21 subjects) among 16 segments. Figure 2 and table 2 summarized the discrepancies of motions indices measured at different myocardial segments.

The distribution of segmental motion indices were presented in supporting figure 3. Lateral area (average measures over segments 5, 6, 11, 12 and 16) of the LV have larger magnitudes of Drr, Vrr-sys, Vrr-dia, Err, Ecc, Ess, SRr-sys, SRr-dia, SRc-sys and SRC-dia than septal area (average measures over segments 2, 3, 8, 9 and 14). However, septal segments have larger magnitudes of Dcc, Vcc-sys and Vcc-dia than lateral segments. All differences of motion indices between lateral and septal segments have statistical significance ($p < 0.05$). See table 3.

The re-analysis on 21 cine image datasets generated exactly the same outputs of myocardial motion measures. The inter-analysis variation of the HDA tool does not exist in the present study. The inter-study variations of HDA-derived motion patterns (80 segments of 5 volunteers) were shown in figure 4.

Discussion

In the present study, our data demonstrated significant differences on various HDA-derived indices, including displacement, velocity, strain and strain rate, among 16 myocardial

segments. Myocardial motion indices measured at lateral area of the LV were significantly different from their counterparts measured at septal area.

Although cardiac motion indices have the potential to serve as a cluster of quantitative imaging biomarkers for monitoring the progression of various cardiovascular diseases, comprehensive quantification of myocardial motion remains a challenge because the heart keeps deforming in a non-linear mode. Many MRI techniques have been developed to measure myocardial strain or velocity, such as MRI tagging, tissue phase mapping (TPM) and displacement encoding with stimulated echoes (DENSE) (14–16). However, those MRI methods usually require a time consuming image acquisition and procession procedure. Currently, several advanced image tracking methods have been applied in cardiovascular research to calculate myocardial motion indices from bSSFP cine images. Feature tracking (FT) is an existing method for tracking cardiac motion (17, 18). By using FT, mechanics indices of the regional heart tissue can therefore be calculated based on the trajectory of the selected features during cardiac cycles. However, Morton et al. found that the inter-study reproducibility of FT in measuring myocardial strain could be low in multiple myocardial areas on a per-slice basis (19). Furthermore, Wu et al. found that the intra- and inter-observer of peak strain values measured with FT are not high enough through the LV area (20).

HDA is a recently developed myocardial motion tracking technique based on different algorithms that are used for the FT. Previous studies have proven the capability of HDA in measuring global LV function, mass and regional myocardial velocities (8, 9). Instead of identifying and tracking characteristic geometry or brightness “features” on target images, HDA calculates deformation fields for the whole heart through image frames using DIR algorithms. DIR has been applied to calculate myocardial strains or lung motion in previous studies (21, 22). Combined with other automatic post-scan image procession strategies or segmentation techniques, such as myocardium border detection, HDA represents a robust tool for the comprehensive evaluation of myocardial motion by generating multiple indices automatically. This advantage is valuable in clinical study because multiple myocardial indices are necessary for the diagnosis of some cardiovascular abnormalities. For example, impaired diastolic function need to be identified by jointly using lower velocity and strain rate (23). Based on traditional cine images, we demonstrated the discrepancies of various HDA-derived myocardial motion indices on a per-segment basis. Such diversities of regional myocardial motions patterns in healthy volunteers remain as barriers for defining “normal” segmental myocardial motion patterns in human subjects.

A previous animal study demonstrated regional differences of myocardial fibers shortening in different LV areas (24). To the best our knowledge, no existing results have quantitatively described the LV motion inequality using multiple indices. In the present study, we were able to comprehensively discriminate motion patterns of individual myocardial segments in human subjects using multiple HDA-derived indices. In addition, we also noticed that many other quantitative MRI indices, such as T1 value and extracellular volume fraction (ECV), have inhomogeneous distributions in different LV regions (25, 26). These natural variations of myocardial characteristics among individual LV areas suggest that background segment-specific variations in regional myocardial motion should be taken into account for the interpretation of myocardial motion indices for cardiovascular risk estimation. Furthermore,

our data showed that the affection of the location on individual motion indices are bidirectional. Lateral segments have higher Drr, Vrr-sys, Vrr-dia, Err, Ecc, Ess, SRr-sys, SRr-dia, SRc-sys and SRC-dia than septal segments. Septal segments have higher Dcc, Vcc-sys and Vcc-dia than lateral segments. A complicated model is therefore required to define “normal” motion patterns and to discriminate “abnormal” motion behaviors by taking into account multiple regional myocardial motion indices.

Our study has limitations. First, we did not include a clinical reference to evaluate the accuracy of HDA in quantifying all myocardial motion. However, there is not a single “gold standard” for calibrating displacement, velocity strain and strain rate measures in clinical practice (27). Second, we only studied motion indices on the LV, the regional motion patterns of other cardiac structures, including left atrium (LA) and right ventricle (RV), should be assessed separately in the future. Third, we did not work out “normal ranges” of any motion indices because we did not think those “large-span” ranges for individual myocardial segments are useful for specifically guiding therapeutic managements. Fourth, we did not directly compare HDA-derived motion indices to corresponding measures acquired with existing MRI techniques, such as tagging, or other similar image processing strategies, such as FT. Further outcome studies are warranted to evaluate clinical values of HDA-derived regional myocardial motion in assessing the progression of CVDs or individual responses to cardiovascular treatments.

In conclusion, HDA is able to automatically present different regional LV motion patterns from multiple aspects in healthy volunteers.

Acknowledgments

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List of abbreviations

HDA	Heart deformation analysis
MRI	Magnetic resonance imaging
LVEF	Left ventricle ejection fraction
Drr	Radial displacement
Dcc	Circumferential displacement
Vrr	Radial velocity
Vcc	Circumferential velocity
Err	Radial strain
Ecc	Circumferential strain
Ess	Shear strain
SRr	Radial strain rate

SRc Circumferential strain rate

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Figure 1.

The workflow of HDA for the quantification of regional myocardial motion. The analyzer manually loaded cine images to the HDA tool. Then, the anatomic land marks were automatically detected (yellow crosses) by the software and myocardium borders could be robustly tracked on short-axis cine images for the calculation of deformation field on every time frame using DIR algorithm (A and C). Then, myocardial indices (mapped on 16 segment AHA model) and time-resolved curves were reported on a per-segment basis (B and D).

Figure 2.

Diversities of peak motion indices (average over 21 volunteers) among 16 myocardial segments (SDs of measures among 21 volunteers were also presented).

A The variations of peak segmental displacement at radial and circumferential directions.

B The variations of peak segmental velocity (systolic and diastolic) at radial and circumferential directions.

C The variations of peak segmental strain at radial and circumferential directions.

D The variations of peak segmental strain rate (systolic and diastolic) at radial and circumferential direction

Figure 3.

Segmental distributions (average over 21 subjects) of displacement, velocity, strain and strain rate. Inhomogeneous distributions could be found among 16 segments for all myocardial motion indices.

A Distribution of peak radial displacement D_{rr} (cm) at the AHA LV model

B Distribution of peak circumferential displacement D_{cc} (cm) at the AHA LV model

C Distribution of peak radial velocity in systole V_{rr-sys} (cm/s) at the AHA LV model

D Distribution of peak radial velocity in diastole V_{rr-dia} (cm/s) at the AHA LV model

E Distribution of peak circumferential velocity in systole V_{cc-sys} (cm/s) at the AHA LV model

F Distribution of peak circumferential velocity in diastole V_{cc-dia} (cm/s) at the AHA LV model

G Distribution of peak radial strain E_{rr} at the AHA LV model

H Distribution of peak circumferential strain E_{cc} at the AHA LV model

I Distribution of peak shear strain E_{ss} at the AHA LV model

J Distribution of peak radial strain rate in systole SR_{r-sys} (s^{-1}) at the AHA LV model

K Distribution of peak radial strain rate in diastole SR_{r-dia} (s^{-1}) at the AHA LV model

L Distribution of peak radial strain rate in systole SR_{c-sys} (s^{-1}) at the AHA LV model

M Distribution of peak radial strain rate in systole SR_{c-dia} (s^{-1}) at the AHA LV model

Figure 4.

Bland-Altman plots show that the inter-study variances of HDA-derived segmental myocardial motion indices is low. Totally 80 myocardial segments from 5 volunteers were included.

A Inter-study variances of peak radial displacement (Drr)

B Inter-study variances of peak circumferential displacement (Dcc)

C Inter-study variances of peak radial velocity in systole (Vrr-sys)

D Inter-study variances of peak radial velocity in diastole (Vrr-dia)

E Inter-study variances of peak circumferential velocity in systole (Vcc-sys)

F Inter-study variances of peak circumferential velocity in diastole (Vcc-dia)

G Inter-study variances of peak radial strain (Err)

- H Inter-study variances of peak circumferential strain (Ecc)
- I Inter-study variances of peak shear strain (Ess)
- J Inter-study variances of peak radial strain rate in systole (SRr-sys)
- K Inter-study variances of peak radial strain rate in diastole (SRr-dia)
- L Inter-study variances of peak circumferential strain rate in systole (SRc-sys)
- M J Inter-study variances of peak circumferential strain rate in diastole (SRc-dia)

Table 1

Description of subjects

	Volunteers (N = 21)
Male (%)	15 (71)
Age (years old)	49.7 ± 14.8
Weight (kg)	88.6 ± 18.8
Height (cm)	172.5 ± 10.2
Heart rate (beats/minute)	69.9 ± 9.7
Systolic blood pressure (mmHg)	122.6 ± 18.7
Diastolic blood pressure (mmHg)	77.7 ± 16.3

Table 2

Dispersion of motion indices (peak values) among 16 myocardial segments (average over 21 subjects)

Indices (peak)	Mean value	SD	Range	CoV(%)
Drr (cm)	0.61	0.23	0.87 0.33	29.8
Dcc (cm)	-0.15	0.11	-0.06 -0.27	46.2
Vrr-sys (cm/s)	3.25	1.49	4.57 2.23	22.8
Vrr-dia (cm/s)	-3.82	1.32	-2.48 -5.25	25.8
Vcc-sys (cm/s)	2.15	1.18	1.42 2.99	18.6
Vcc-dia (cm/s)	-1.81	0.61	-2.56 -1.46	18.8
Err	0.34	0.25	0.52 0.11	40.6
Ecc	-0.18	0.13	-0.12 -0.26	21.4
Ess	0.05	0.04	0.12 0.003	72.4
SRr-sys (s^{-1})	1.67	0.91	2.40 0.73	34.4
SRr-dia (s^{-1})	-1.77	1.09	-0.77 -2.7	34.6
SRc-sys (s^{-1})	-1.03	0.48	-0.73 -1.49	21.7
SRc-dia (s^{-1})	0.84	0.32	1.11 0.63	18.0

• Acronyms of cardiac motion indices

Drr Radial displacement

Dcc Circumferential displacement

Vrr-sys Radial velocity in systole

Vrr-dia Radial velocity in diastole

Vcc-sys Circumferential velocity in systole

Vcc-dia Circumferential velocity in diastole

Err Radial strain

Ecc Circumferential strain

Ess Shear strain

SRr-sys Radial strain rate in systole

SRr-dia Radial strain rate in diastole

SRc-sys Circumferential strain rate in systole

SRc-dia Circumferential strain rate in diastole

Table 3

Significant differences on major myocardial motion indices (peak values, 21 pairs of data points) between lateral and septal areas at LV (t-tests). All values are averages over 5 myocardial segments in lateral and septal areas, respectively.

Indices (peak)	Lateral (SD)	Septal (SD)	p values
Drr (cm)	0.80 (0.12)	0.40 (0.12)	< 0.001
Dcc (cm)	-0.11 (0.6)	-0.20 (0.08)	< 0.001
Vrr-sys (cm/s)	4.05 (0.99)	2.61 (0.63)	< 0.001
Vrr-dia(cm/s)	-4.90 (1.07)	-2.74 (0.58)	< 0.001
Vcc-sys(cm/s)	1.72 (0.41)	2.47 (0.65)	0.006
Vcc-dia(cm/s)	-1.61 (0.43)	-1.93 (0.51)	0.002
Err	0.45 (0.08)	0.18 (0.07)	< 0.001
Ecc	-0.20 (0.02)	-0.16 (0.02)	< 0.001
Ess	0.06 (0.03)	0.04 (0.02)	0.004
SRr-sys (s^{-1})	2.08 (0.47)	1.03 (0.27)	< 0.001
SRr-dia (s^{-1})	-2.32 (1.30)	-1.10 (0.51)	< 0.001
SRc-sys (s^{-1})	-1.12 (0.29)	-0.93 (0.23)	< 0.001
SRc-dia (s^{-1})	0.92 (0.39)	0.75 (0.26)	0.002