

Meeting abstract

Open Access

I 107 Quantification of left ventricular strain using turbo field echo produces less variable data than using fast field echo

Ulrika S Pahlm-Webb*, Erik Hedstrom, Einar Heiberg, Erik Bergvall, Helen Sonesson and Hakan Arheden

Address: Lund University Hospital, Department of Clinical Physiology, Lund, Sweden

* Corresponding author

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):A232 doi:10.1186/1532-429X-10-S1-A232

This abstract is available from: <http://jcmr-online.com/content/10/S1/A232>

© 2008 Pahlm-Webb et al; licensee BioMed Central Ltd.

Background

Evaluation of regional wall function is of importance for diagnosing cardiac disease, as well as for evaluation of treatment. Qualitative assessment of wall function is however highly variable between observers. Using velocity-encoded magnetic resonance imaging (VE-MRI), wall function may be assessed quantitatively in terms of strain. Different velocity-encoding techniques have been used to acquire the images needed to calculate strain. Fast field echo (FFE) has been validated but has several disadvantages to the faster Turbo Field Echo (TFE) which has not yet been validated for strain measurement. TFE would be more suitable in clinical routine since it is faster and offers improved image quality (Figure 1). We hypothesized that there is a good agreement between TFE and FFE strain and that TFE strain is reproducible between observers.

Methods

VE-MRI images from 10 healthy volunteers (5 male and 5 female) were obtained in 2-, 3-, and 4-chamber projections. The TFE echo train length was 5. The myocardium was manually outlined by two independent and blinded observers in end-diastole in TFE images, and by one observer in both TFE and FFE images. In-house developed software <http://segment.heiberg.se> was used for automatic tracking of the myocardium and calculated strain for each of the 17 AHA left ventricular segments. Maximum left ventricular strain over the cardiac cycle was determined, and intra- and interobserver variability for each of the 17 sections were determined.

Results

Bland-Altman analysis showed no systematic difference in strain between TFE and FFE images (bias -0.01 ± 0.19) (Figure 2). Interobserver variability regarding strain in TFE images (-0.03 ± 0.10) was smaller than the intraobserver variability between TFE and FFE images (Figure 3).

Discussion

There was a good agreement between TFE and FFE strain, and TFE strain was reproducible between observers. It takes a relatively long time to acquire the FFE sequence, and the patient is unable to hold their breath for that time. Breathing artifacts make the images difficult to interpret. TFE is a faster image acquisition method that makes it possible to acquire the images in one breathhold, which leads to fewer breathing artifacts, and therefore makes the images easier to interpret. TFE would therefore be a better choice for clinical routine. The in-house developed software <http://segment.heiberg.se> automatically tracks the myocardium and calculates strain for each of the 17 AHA segments within seconds.

Conclusion

Strain acquired by TFE VE-MRI shows good agreement with FFE strain, and low interobserver variability. Both the acquisition and the evaluation method for strain measurement by TFE VE-MRI are very fast, and therefore suitable for clinical use.

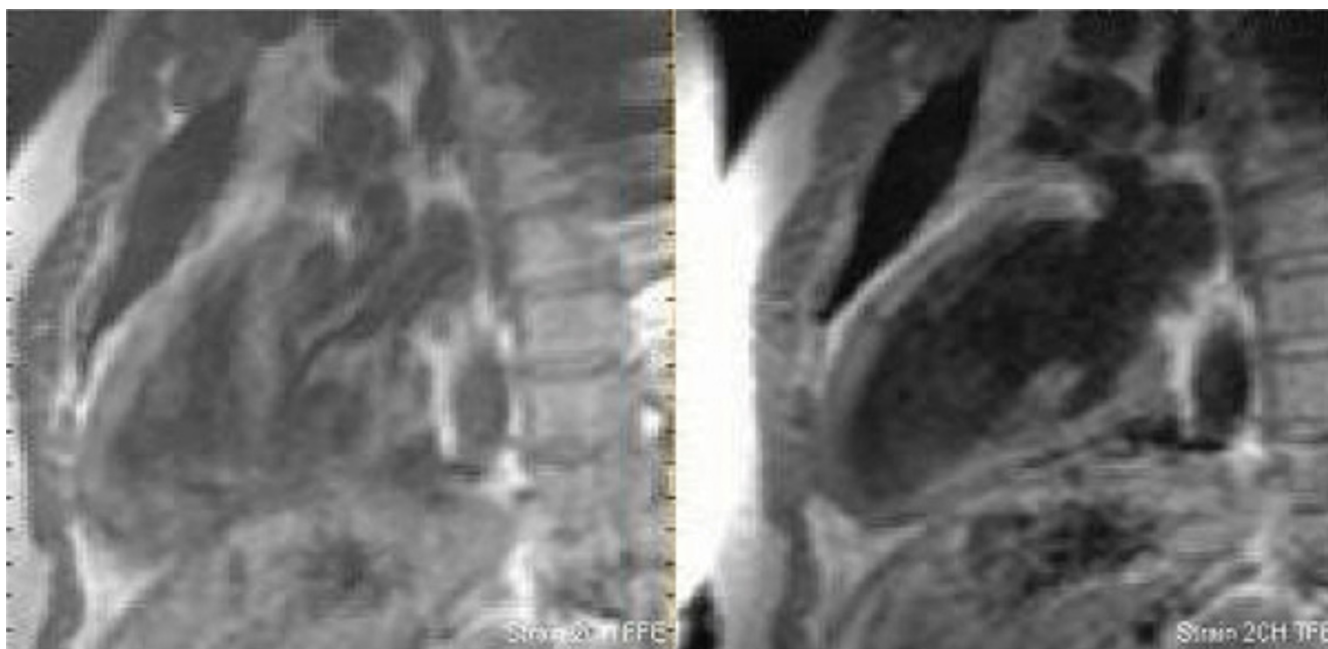


Figure 1
Image quality in 2-chamber FFE (left) and TFE (right), used for delineation of the left ventricle to measure strain.

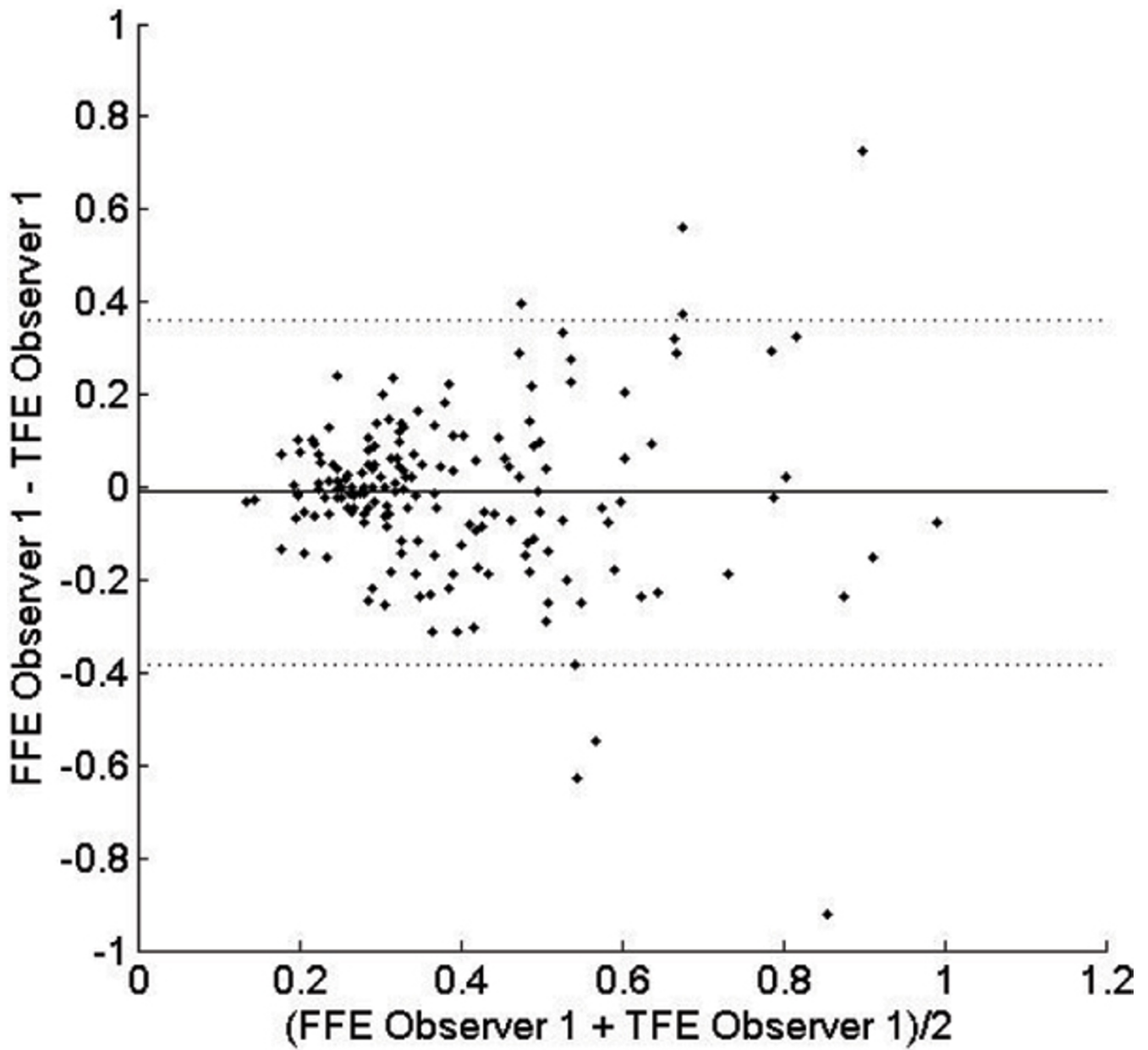


Figure 2
Bland-Altman showing good agreement between TFE and FFE strain.

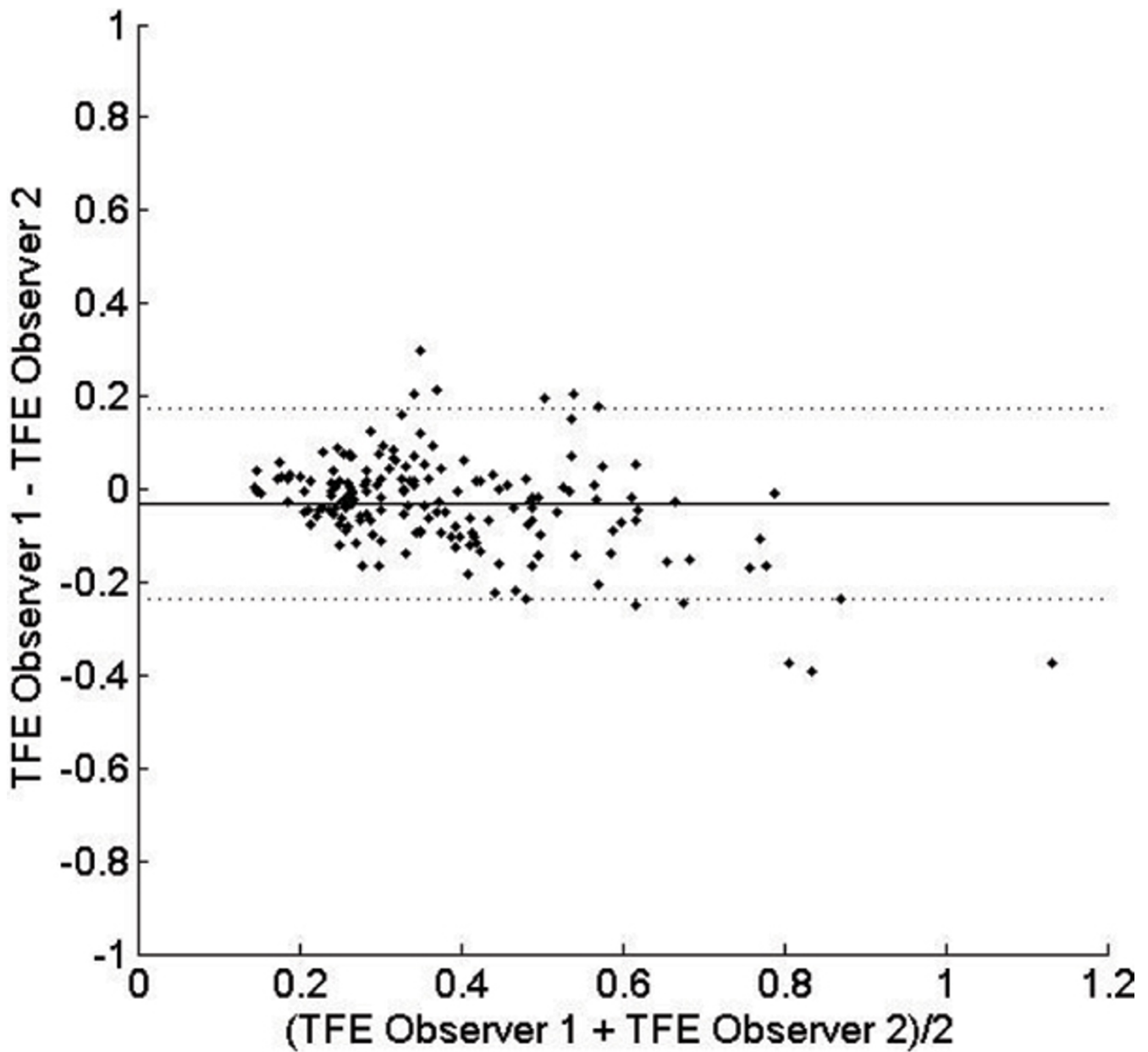


Figure 3
Bland-Altman showing low interobserver variability for TFE strain.

Publish with **BioMed Central** and every scientist can read your work free of charge

"BioMed Central will be the most significant development for disseminating the results of biomedical research in our lifetime."
Sir Paul Nurse, Cancer Research UK

Your research papers will be:

- available free of charge to the entire biomedical community
- peer reviewed and published immediately upon acceptance
- cited in PubMed and archived on PubMed Central
- yours — you keep the copyright

Submit your manuscript here:
http://www.biomedcentral.com/info/publishing_adv.asp

