Linking Myocardial Function and Structure through Tagged MRI and Diffusion Tensor Imaging

Carla S Gil[1], Stephen D Meredith[1], Adrianus J Bakermans[2], Bastian J Nierop [2]Gustav J Strijkers [2]Hans C van Assen [3]Niall C Colgan [4]and Kathleen M Curran [1]
[1]*School of Medicine & Medical Science, University College Dublin, Dublin, Ireland,* [2]*Biomedical NMR, Department of Biomedical Engineering, Eindhoven University of Technology, Eindhoven, Netherlands,* [3]*Biomedical Image Analysis, Department of Biomedical Engineering, Eindhoven University of Technology, Eindhoven, Netherlands,* [4]*College of Medicine, Swansea University, Wales, United Kingdom*

Introduction

To understand the functional consequences of myocardial disease, one needs to have thorough understanding of the healthy heart's function and structural organization. Diffusion tensor imaging (DTI) provides a method to study the 3-dimensional myofiber architecture, while tagged MRI can provide important insights in the local and global mechanics of myocardial contraction. However, the link between cardiac structure and function is still rather poorly understood. The **aim** of this study was therefore to combine tagging MRI with DTI in order to improve knowledge on the structure-function relations of the healthy rat heart, which in the future may serve to better understand cardiac dysfunction due to pathological remodeling of myofiber architecture.

Methods

(1) Tagged MRI: In-vivo scans of 9 Wister rats were measured at 6.3T (Bruker BioSpec, Germany). First, a fast low angle shot (FLASH) sequence (**Fig.1 A**) was used (FOV= 40x40 mm, matrix size = 256x256, spatial resolution = 156.25 µm/pixel, slice thickness = 1 mm, TE = 2.9 ms, TR = 8.1 ms, no slice gaps). Then, the tagged acquisition was performed using complementary spatial modulation of magnetization (CSPAMM, tagged period = 1 mm) (**Fig.1 B, C**).
(2) DTI: After the in-vivo acquisition, the rats were sacrificed in order to obtain ex-vivo DTI scans. 9 Wistar rat hearts were measured at 6.3T (same scanner used for tagged measurements) (FOV=32x16x16 mm^3, matrix size = 128x64x64, spatial resolution = 250 µm/pixel, TR/TE = 1000/25 ms, NSA = 1). Diffusion weighting parameters: gradient separation time Δ = 14 ms, gradient duration δ = 6 ms, b-value = 900 s mm^{-2}. Diffusion was measured in 10 different directions.
(3) Image Analysis: The tagged MRI data was analyzed using the HARP method for image filtering and a multi-scale optical flow algorithm[1]. The left ventricle was segmented semi-automatically using cine images. Then, the optical flow was computed for a mid-ventricular slice for the 9 datasets. From the flow field, the circumferential, radial, shear and principal strains were computed (see **Fig. 2**). The DTI data was preprocessed using MATLAB routines for tensor reconstruction and background filtering. Fractional anisotropy, mean diffusivity and normalized helix angle maps were constructed.

Results

We have chosen a short-axis view of a mid-ventricular slice to illustrate our results, but the same method can be applied from apical to basal slices. We present the results for one of the datasets. The in-vivo measurements were acquired first and then the hearts were arrested close to an end-diastole phase. The tagged frame that most closely matches the ex-vivo heart geometry (diastole) was chosen for comparison. **Fig. 1 D)** represents the diffusion tensors, where the RGB color code corresponds to x, y (in-plane) and z (out-of-plane) directions. The myocardium fiber architecture can be better described in terms of its helix angle, which is the angle between the principal eigenvector and equatorial plane (**Fig. 1 E**). From Fig. 1 D) and E) one can see that the in-plane myocardium fibers (helix angle from 0 to 0.4) are circumferential and out-of-plane fibers are present in the endocardium and papillary muscles (helix angle from 0.6 to 1). In order to analyze the tagged data, the left ventricle was segmented and strains were computed. Initial qualitative observations show that the circumferential strain (**Fig. 2 A**) is stronger (-0.15) for in-plane fibers and when principal DT eigenvector is y-oriented (**Fig. 1 D**). The radial strain (**Fig. 2 B**) seems to be correlated with the x-orientation of the tensors (red), shear strain and principal strain E1 (**Fig. 2 C) and D)**) are almost negligible. Principal strain E2 (**Fig. 2 E**) shows a positive correlation with in-plane fibers (helix angle 0 to 0.4) and the x and y principal eigenvector orientation. However, these are preliminary observations relating tagged MRI with fiber architecture. In order to investigate if strains are homogenously distributed throughout the healthy heart we need to perform voxel by voxel analysis to derive strains along the helically organized myofibers .

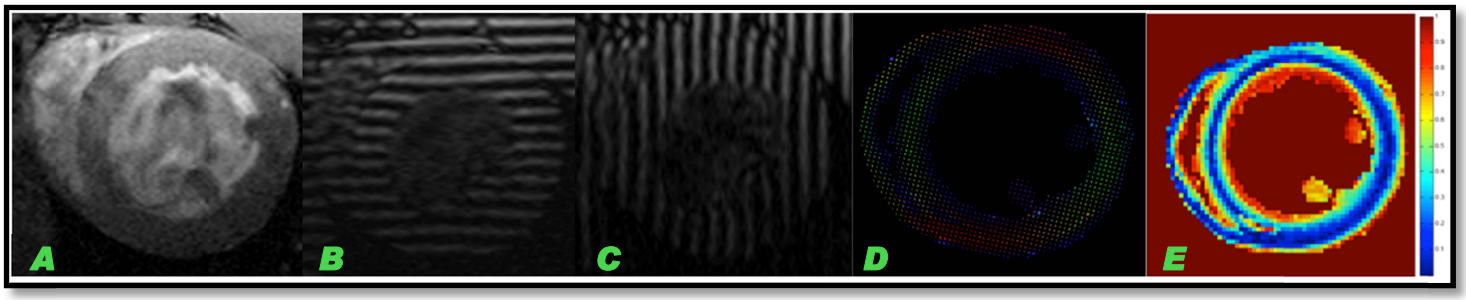

Figure 1. Short axis-view of a mid-ventricular slice: A) Cine MRI. B) Horizontal tagged image. C) Vertical tagged image. D) DTI. E) Fibers helix angle.

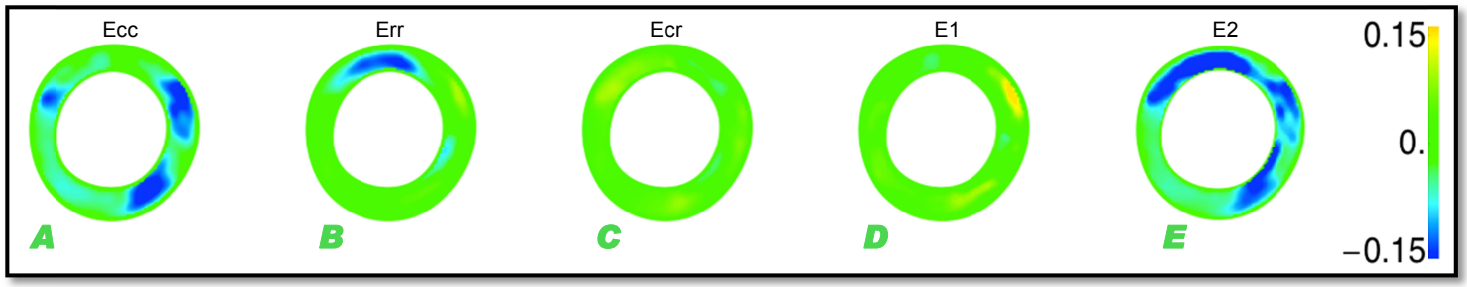

Figure 2. A) Circumferential Strain (Ecc). B) Radial Strain (Err). C) Shear Strain (Ecr). D) and E) Principal strains (E1, E2).

Conclusion

The combination of functional and microstructural imaging of the heart is a powerful tool for the diagnosis of cardiac pathologies. Our preliminary analysis shows a correlation between left ventricular deformation and fiber architecture for normal datasets. In-plane fibers with helix angles of 0 to 0.4 show strong correlations with circumferential and principal strains E2 (-0.15). We plan to extend this study by registering the strain maps to the diffusion maps and perform a more detailed statistical study by segmenting the left ventricle and calculating the average strain per segment.

References

1) van Assen, H.C. MICCAI 2008.