Fiber Tracking of the Human Heart In Vivo

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Introduction

The left ventricle is composed not only of circumferential and longitudinal myocardial fibres but also of obliquely running sheets of fibres that form a double helical spiral from base to apex [1]. The orientation of left ventricular (LV) fibres changes smoothly from a left-handed helix in the subepicardium to a right-handed helix in the subendocardium. This structure contributes significantly to efficient ventricular function and is subject to remodelling and disarray in the presence of disease. Diffusion MRI tractography provides a non-invasive approach for the depiction of the myocardial fibre architecture. Both stimulated echo (STEAM) and spin echo techniques have been used successfully to demonstrate the myocardial fibre architecture in the normal beating heart [2-6] and to depict zone dependant alterations in the presence of disease [4-5]. In this work a stack of five 2D diffusion-encoded MR slices of the heart was acquired in a healthy volunteer using a STEAM single shot EPI technique with the aim of constructing continuous fiber tracts of the human heart in vivo. Images were post-processed to create fractional anisotropy (FA) maps and helix angle fibre tractography maps.

Materials and Methods

The diffusion weighted (DW) STEAM single shot EPI sequence was implemented on a clinical scanner (1.5 T, MAGNETOM Avanto, Siemens AG Healthcare Sector, Germany) equipped with a cardiac 12-element matrix coil. This sequence runs over two heart beats and makes the assumption that the heart is in the same position at both diffusion encoding times (mid systole) on consecutive cardiac cycles as described in [2,3]. The following sequence parameters were used: 6 diffusion encoding directions, b=500 s/mm^2, fat saturation, TR/TE = 1060/28 ms, $\alpha_1 = \alpha_2 = \alpha_3 = 90°$, BW = 2442 Hz/pixel, spatial resolution = 2.7×2.7×8 mm^3, 5 slices, 50% slice distance, 12 averages, 60 breathholds, acquisition time approximately 40 min. The raw data was reconstructed using the product reconstruction algorithms available at the scanner. The Dicom images were resampled and interpolated to produce 17 contiguous slices with isotropic voxels. 2D maps of fractional anisotropy (FA) and 3D tractograms, color coded by fiber helix angle, were constructed using customized software developed in our center.

Results

Figure 1 shows helix angle myocardial fibre tractograms and FA maps of the heart of a healthy volunteer. Although the tracts are generally noisy and the spatial resolution in slice direction is low, the helix angle structure of the left ventricle is clearly depicted. Dispersion in the helix angles over the papillary muscles can be observed and the right ventricle is significantly noisier than the left.

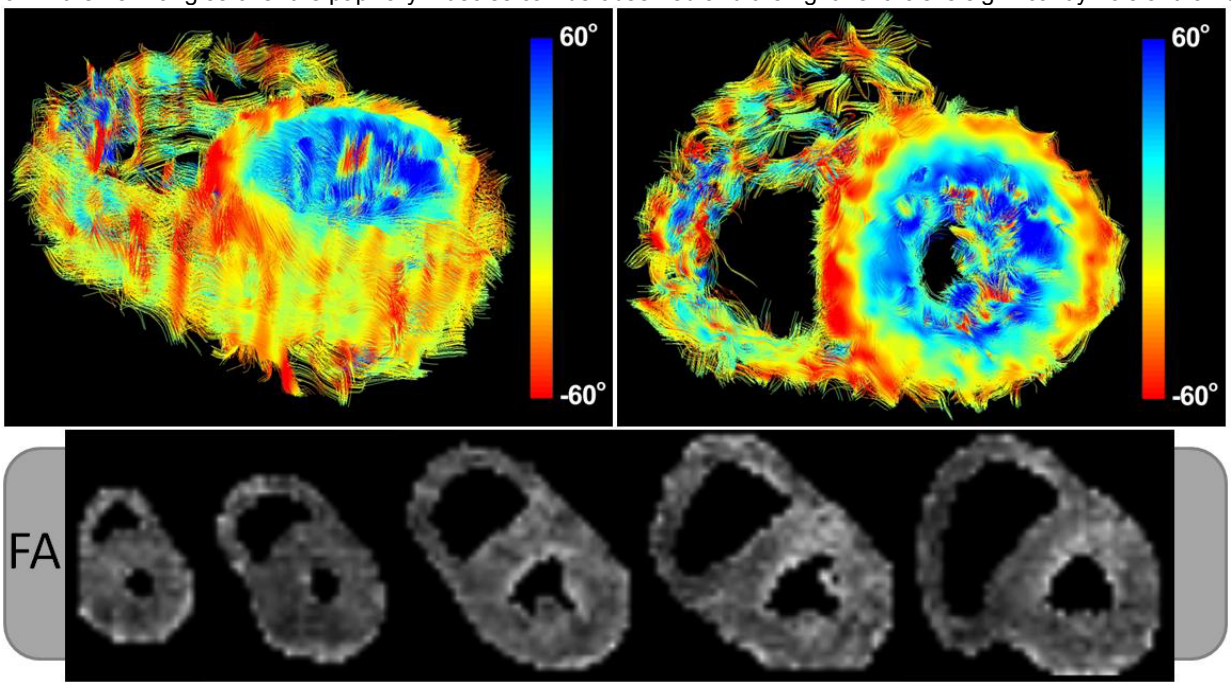

Figure 1. Reformatted views of the helix angle myocardial fibre tractograms and FA maps of the 5 *in vivo* slices.

Discussion

A stack of five 2D slices of the heart of a healthy volunteer was acquired with a DW STEAM single shot EPI sequence on a clinical scanner with a total scan time of about 40 min. The resulting myocardial fibre tractograms clearly depicted the helical structure of the left ventricle. However, the acquisition of this data required multiple breathholds, which can be challenging for patients. Future work will focus on the implementation of motion compensation techniques such as navigators and arrhythmia rejection algorithms. The goal is a free-breathing 3D technique that achieves isotropic voxel coverage of the heart in clinically feasible acquisition times in order to produce continuous 3-dimensional tractograms of myocardial fibre architecture *in vivo*. This could prove to be a powerful tool to characterise the structural remodelling and fibre disarray patterns of diseases such as myocardial infarction and cardiomyopathies, improving the capability of cardiac MRI for diagnosis and therapy follow-up.

Bibliography **1.** Streeter DD. et al. Circ Res 24:339-347(1969) **2.** Edelman RR. et al. MRM 32:423-428(1994) **3.**Reese TG. et al. MRM 34:786-791(1995) **4.** Dou J et al. MRM 50:107-112 (2003) **5.** Wu et al. Circulation 114:1036-1045 (2006) **6.** Gamper U. Et al. MRM 57:331-337(2007)

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