Interspecies Variability in the Myocardial Fiber Structure Acquired using MR Diffusion Tensor Imaging

L. Healy[1], S. Joshi[1,2], Y. Jiang[3], and E. Hsu[1]

[1]Department of Bioengineering, University of Utah, Salt Lake City, UT, United States, [2]School of Computing, University of Utah, Salt Lake City, Utah, United States, [3]Center for In Vivo Microscopy, Duke University, Durham, NC, United States

Introduction: Precise knowledge of the myocardial fiber structure is essential for accurate understanding of cardiac electrophysiology and mechanics [1,2]. Due to the challenges in obtaining the 3D myocardial fiber structure, anatomical models of the heart exist for only a small number of species. Although scaled models from other species have been used as a substitute when species-specific models are not available [3], to date, little is known regarding the similarity (or variability) of the myocardial fiber structure across different species. MR diffusion tensor imaging (DTI) [4] has emerged as a convenient and viable technique to quantify the myocardial fiber orientation. In this study, we used principal component analysis (PCA) to examine the cross-species variability of DTI-measured myocardial fiber structures among the mouse, rabbit and sheep.

Methods: Three-dimensional DTI datasets of isolated, fixed normal hearts acquired using 9.4, 7.0 and 2.0 T scanners at 100, 250 and 780 μm isotropic resolution, respectively, were obtained for the mouse (n=7), rabbit (n=4), and sheep (n=4) from separate studies [5,6,7]. The cardiac left ventricles were segmented and co-registered via unbiased diffeomorphic deformation [8] to create a template, which was used to determine the long axis and anatomically equivalent points among the specimens. The local cylindrical-coordinate helix angle [9] was used to denote the fiber orientation, and the helix angles from each heart were re-mapped onto the common template for comparison. A previous PCA study [7] has found the mouse datasets to be sufficient in representing the variability of the myocardial fiber structure of the group of normal hearts. Consequently, the vectorized helix angles from each of the rabbit and sheep hearts were projected onto the PCA space obtained from mouse hearts. A normalized distance (divided by 2 times the standard deviation of each principal component) of greater unity on the PCA space is taken as significantly different. To compare between rabbit and sheep hearts, because the relatively low number of specimens available for each species, the datasets were pooled and leave-one-out PCA [10] was performed to test whether the group of hearts formed an inclusive set.

Results: The helix angle volumes for representative mouse, rabbit and sheep hearts are shown in their common coordinate system in Fig. 1. Comparison to the mouse indicates all rabbit and sheep hearts are significantly different when all 6 principal components are evaluated, and 3 of each rabbit and sheep hearts are different for 3 principal components. Comparison within the rabbit-sheep pooled group reveals that none of the hearts is significantly different, when 3 principal components were used and only 1 was different when 6 principal components were used, suggesting that the rabbit and sheep hearts are indistinguishable.

Discussion and Conclusions: The results indicate that whereas the rabbit and sheep myocardial fiber structures may be similar, significant differences were observed between rabbit and mouse, and between sheep and mouse. The dissimilar results suggest that species-to-species comparisons cannot be generalized, and the comparison outcome may depend on factors such as animal, hence heart, sizes. One practical implication of the current findings is that, at least for fiber structure, hearts from larger animals cannot be directly scaled down as substitution for those of small animals.

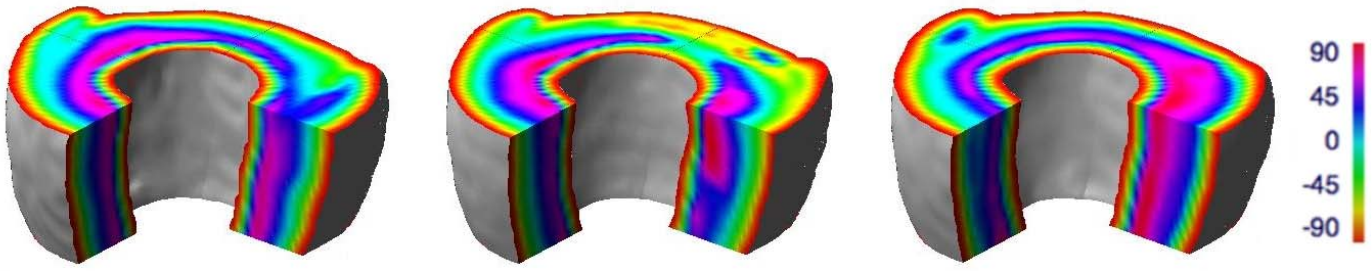

Fig. 1: Fiber orientation helix angle maps of representative mouse (left), rabbit (center), and sheep (right) hearts on co-registered coordinate system.

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