Characterization of Skeletal Muscle Fascicle Arrangements Using Diffusion Tensor Tractography

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Introduction

Accurate characterization of the arrangement of fascicles within muscle is essential for understanding muscle function. Fascicle arrangements can be complex and vary widely across skeletal muscles. Most estimates of human muscle fascicle arrangements are based on cadaveric measurements [7]; however, *in vivo* approaches are needed to characterize fascicle arrangements in more representative subject populations. Ultrasound techniques have been used to characterize *in vivo* fascicle orientations and lengths [4]; however, they are limited to planar measurements and can only be used to study superficial muscles. The goal of this work is to establish a framework for characterizing the *in vivo* three-dimensional arrangements of skeletal muscle fascicles, by using diffusion tensor imaging and MR tractography. We present results from measurements in the soleus muscle (a short-fibered pennate muscle) and tibialis anterior muscle (a long-fibered parallel muscle).

Methods

We acquired diffusion-weighted images in the calf of a healthy human female subject (age 30). A single-shot echo-planar sequence was used to acquire axial slices for two b-values, b = 0 and $b = 4000 \text{ s/mm}^2$ along 12 diffusion directions, in a 1.5T GE Signa LX scanner. The subject was positioned supine with the ankle and knee in the neutral position. We used the standard head coil in order to cover the whole extent of the calf. To minimize B_0 inhomogeniety and gradient non-linearity effects on the diffusion measurements, we collected the images in three separate acquisitions, with each covering 28 of the 84 total slices. The images were acquired using a 20*cm* by 20*cm* FOV, 128 by 128 matrix size, and a 4.5*mm* (skip 0.5*mm*) through-plane resolution, and 15 acquisitions were collected and averaged for each slice. We also collected 3D-SPGR images at the same axial locations (256 by 256, 20*cm* by 20*cm* FOV, 5*mm* slices) to identify anatomical structures.

The boundaries of the soleus and tibialis anterior muscles were manually segmented from the SGPR images, and we verified the registration between the SPGR and DTI acquisitions by overlaying the segmented boundaries on the DT images (Fig. 1A,B). The reconstructed diffusion tensor data and segmented muscle regions were imported into an interactive fiber tractography exploration software system [1,6]. Using the tractography query software, we identified all possible pathways within each muscle volume. The pathways were generated with the STT streamline tracking algorithm [3,5], which traces paths that follow the principle diffusion direction. The termination conditions for each path were (*i*) if the fractional anisotropy fell below a threshold value, and (*ii*) if the path exited the specified muscle volume. We interpreted the pathways as representative fascicles trajectories within the muscle.

Results

The fascicle trajectories (Figs. 1C and D) were consistent with geometry observed in anatomical specimens. The soleus displayed short fascicles that were angled with respect to the muscle aponeurosis and the tibialis anterior displayed long fascicles that were parallel to its aponeurosis. The lengths of representative fascicles for the soleus varied from 1-5*cm*, and from 8-22*cm* for the tibialis anterior. These average fascicle lengths compare well with previous cadaveric measurements [7].

Discussion

We present initial *in vivo* measurements of the three-dimensional arrangements of skeletal muscle fascicles. Further optimization in the image acquisition will be to condition the diffusion gradients to better resolve slight angular deviations in direction of the muscle, and, in the tracking algorithms, to minimize artificial pathway switching.



Until now, our understanding of muscle architecture has been based on simplified two-dimensional representations and measurements of cadaveric muscle. By combining the fascicle arrangement measurements presented here with three-dimensional models of muscle [2], we will enhance our understanding of normal muscle architecture and function. Moreover, these *in vivo* techniques can be used to identify alterations in muscle architecture in persons with muscular pathologies.

References

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