3D muscle fibre arrangement derived from diffusion-tensor imaging: a validation study

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***Abstract*—Diffusion-tensor imaging (DTI) enables the reconstruction of the 3D arrangement of fibre bundles (FB) within a muscle, however, validation of DTI generated muscle FB data is limited. This study compared the 3D muscle FB arrangement (pennation angle (PA) and fibre bundle length (FBL)) within a human masseter generated through DTI to manual digitization. While agreement was found in PA, generated FBLs were generally longer in DTI. This muscle FB orientation data can ultimately be integrated to improve the representation of physiologic muscle loading in patient specific finite element modelling.**

***Keywords*—Diffusion tensor imaging, 3D muscle modelling, fibre tracking, muscle fibres directionality**

I. Introduction

THREE dimensional (3D) finite element (FE) models are widely used to investigate the behaviour of musculoskeletal structures. In particular, FE modelling of craniomaxillofacial (CMF) behaviour requires representation of complex geometries, material property distributions and physiologic loading patterns. Computed Tomography (CT) imaging data can provide robust skeletal geometry and material property information, but is limited in representing soft tissues key to loading. Simplified loading conditions (no muscle loads or muscle loading represented by one dimensional links between origins and insertions [1]) are widely used, but may not represent physiologic conditions. To accurately represent muscle loading requires both the 3D geometry and the arrangement of fibre bundles within each muscle [2]-[6]. Fibre bundle (FB) tracking algorithms applied to magnetic resonance based diffusion-tensor imaging (MR-DTI) enables the reconstruction of the 3D arrangement of FB within a muscle. However, to date there is only limited validation of DTI generated muscle FB data [7]. As such, prior to the integration of muscle FB directionality data into CMF FE models, experimental validation of DTI based fibre tracking in the muscles of mastication is required. The specific aim of this work is to evaluate the ability of DTI based fibre tracking to represent the spatial organization of FBs in the human masseter.

II. Material and Methods

A single cadaveric specimen (female, 6 months of age) was used in all acquisitions and analyses. Research Ethics Board approval was received from Sunnybrook Research Institute and the University of Toronto.

A. Image acquisition

A CT scan was acquired on a Toshiba Aquilion 320 machine (120 kVp, 100 mA, voxel size 0.62×0.62×0.3 mm). MRI was conducted on a 3T scanner (Achieva, Philips Medical Systems, Best, Netherlands) with a 16-channel SENSE XL torso coil. DTI with fat suppression was acquired using diffusion-weighting factor, b of 1200 s/mm^2 (11 repetitions) and a built-in 32-direction sampling scheme in addition to a non-diffusion-weighted scan (FOV=350 mm FH ×200 mm AP ×300 mm RL, 2 mm isotropic resolution, TR=190 s, TE=72 ms, flip angle=90°, diffusion time 23.4 ms, acquisition time 38.5 h). A high resolution proton density-weighted structural scan with fat suppression was also acquired (TR=9.9 s, TE=10 ms, flip angle=90°, the same FOV as the DTI, but 0.5 mm isotropic resolution, acquisition time 4.8 h).

B. Image processing

Imaging data were first co-registered. The CT scan was segmented (using thresholding and manual refinement) to extract the bone surface. The boundaries of the right masseter were manually segmented on the MRI structural image volume. This generated mask was resampled to be applied to the DTI volumes. The DTI data were separated into their respective gradient directions, averaged among the repetitions and filtered to reduce noise. The diffusion tensor, the eigenvalues and the associated eigenvectors were computed at each voxel. Based on the first eigenvector, the masseter fibre pathways were reconstructed using a streamline tracking algorithm. A fractional anisotropy below 0.01 was chosen as a stop criterion for fibre tracking. All analyses were performed within the Amira software environment (Amira Dev. 5.5, Visualization Imaging, San Diego, CA).

C. Manual digitization

One hundred eighty-one FBs of the masseter were serially microdissected, and digitized using a MicroScribe MX Digitizer (0.05 mm accuracy Immersion Corporation, San Jose, CA). FBs were delineated on the surface of the muscle, digitized and excised. This process was repeated until the entire muscle was digitized.

D. Comparison of muscle architectural parameters

Muscle architecture from DTI and manual digitization was compared in terms of pennation angle (PA) and fibre bundle

length (FBL). Each FB was reconstructed using a Catmull-Rom cubic spline using the original data points resampled to an equal-spacing. To determine the PA of each FB, first the tangent vectors were computed for the terminal 20% of the length of the FB and then averaged [8], [9]. Next, the line of action of the masseter was determined by averaging the orientations of all the FBs [8], [9]. Finally, the PA for each FB was calculated as the angle between the FB and the overall line of action. Each FBL was determined by first calculating the Euclidean distance between adjacent points along the FB, and next the lengths of all segments were summed to obtain the total length[8].

E. STATISTICAL ANALYSIS

The PA and FBL distributions were tested for normality (Kolmogorov-Smirnov test). The Mann Whitney test was used to evaluate correspondence between the two methods (SPSS 20, SPSS Inc., IBM, Chicago, IL, USA).

III. RESULTS

A final set of 193 DTI-derived FBs were analysed in comparison to the 181 FBs digitized. Some DTI-derived FBs were found to be anatomically unrealistic, terminating in the proximal portion of the masseter or with a very short length (minimum FL 2.5 mm). These spurious FBs may have due to an additional stop criterion for tracking during muscle segmentation [7], [10]. As such, FBs that terminated too proximally and those shorter than the minimum length of the digitized FBs were removed prior to analysis (SelecLines module, Amira; Matlab, MathWorks, MA, USA).

A. *PA RESULTS*

Both the DTI-derived PA distribution and that derived from digitization were not normally distributed ($p<0.0001$). In Table I median, standard deviation (SD), first (Q1) and third (Q3) quartiles for PA measurements are reported. There was no significant difference in the PA measurement between the two methods (Mann Whitney test, $p=0.411$).

TABLE I
PENNATION ANGLE AND FIBER BUNDLE LENGTH

PA°	*DTI (193 fiber bundles)*	*Manual Digitization (181 fiber bundles)*
Median	13.1	12.6
SD	9.7	10.7
Q1	8. 1	7.8
Q3	19.7	20.2
FL (mm)	*DTI (193 fiber bundles)*	*Manual Digitization (181 fiber bundles)*
Median	19.7	17.8
SD	4.6	3.1
Q1	16.3	16.3
Q3	23.6	19.5

Median, SD, first (Q1) and third (Q3) quartiles for PA and FBL distributions from the masseter muscle via DTI and digitization methods.

B. FBL RESULTS

While the FBL distribution derived from the digitization data was not normally distributed ($p<0.002$), the DTI-derived FBL distribution was statistically normal ($p=0.09$). In Table I median, standard deviation, Q1 and Q3 quartiles for PA measurements are reported. Significant difference in the FBL measurement between the two methods was found (Mann Whitney test, $p<0.01$).

IV. DISCUSSION

Whereas PA estimated through DTI data showed a strong correlation with the digitization-derived PA, a lack of agreement between the two methods was observed for the FBL. The lack of FBL agreement may depend on the tractography stopping criterion that can determine an early termination (e.g. before reaching the aponeurosis) of the tracts. This may lead to more variability in length for the DTI-derived fibres compared to digitization [11], and represents a challenge in DTI based fibre length estimation [10].

V. CONCLUSIONS

Manual digitization of muscle fibre data is a laborious task that is not practical for larger scale applications including patient specific FE model generation. Image based methods which can yield fibre data may be used to improve the physiologic representation of muscle loading in patient specific CMF FE models. This works represents a first attempt to validate the 3D fibre arrangement derived from DTI in the human masseter muscle.

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