Regional microstructural differences of the corpus callosum using cytoarchitectural parcellation and DT-MRI

Y-P. Chao[1], K-H. Cho[1], C-H. Yeh[2], K-H. Chou[3], J-H. Chen[1], and C-P. Lin[2,4]

[1]Department of Electrical Engineering, National Taiwan University, Taipei, Taiwan, [2]Institute of Biomedical Imaging and Radiological Sciences, National Yang-Ming University, Taipei, Taiwan, [3]Institute of Biomedical Engineering, National Yang-Ming University, Taipei, Taiwan, [4]Institute of Neuroscience, National Yang-Ming University, Taipei, Taiwan

Introduction

The function of the corpus callosum (CC) is to distribute perceptual, motor, cognitive, learned, and voluntary information between the two hemispheres of the brain. Accurate parcellation of the CC according to fiber composition and fiber connection is of upmost important. Recently, tractography technique with diffusion magnetic resonance imaging (dMRI) has been employed for distinguishing vertical segments of CC and for revealing the topographical distribution of fiber connections to the cortex [1]. The segmented result may serve as a brain landmark for sub-regional analyses of the CC. Such relationship between regional microstructural differences of the CC and diffusion anisotropy indices has been proposed in several reports [1-2]. In this study, population-based probabilistic connection topographies of the CC, in the standard MNI space, were estimated by incorporating anatomical cytoarchitectural parcellation with high angular resolution diffusion imaging (HARDI) tractography. Using q-ball imaging (QBI) with MFACT algorithm [3-4], a more detailed CC subdivision according to 27 selected Brodmann's areas (BAs) was demonstrated. Further, it allowed an assignment of the quantitative distribution of fractional anisotropy (FA) values derived from diffusion tensor imaging (DTI) data of 20 normal healthy subjects to evaluate the correlation with neural composition in distinct CC regions explored by Abotitiz in 20 postmortem human brains [5].

Materials and Methods

Imaging: ***QBI part:*** In vivo healthy human brain QBI (n=12, 19-26 years of age; 7 females) were acquired in a GE Healthcare Signa 1.5T Excite scanner by spin-echo EPI (SP-EPI) sequence with 162 diffusion-encoding directions (4-folds tessellated icosahedrons) at a b-value of 3000 s/mm^2. Each QBI study consisted of 46 transverse sections was acquired parallel to the AC-PC line to cover the entire cerebrum with TR/TE = 17000/91.2 ms, FOV = 256 × 256 mm^2, matrix size = 128 × 128, yielding voxel size = 2 × 2 × 2.2 mm^3. ***DTI part:*** The DTI data (n=20, 22-31 years of age, 10 females) were performed on the whole brain (70 transverse slices) in the same scanner using a single shot diffusion SP-EPI sequence with b=0 s/ mm^2 image and 13 images with diffusion gradients applied in 13 noncollinear encoding directions at b-value of 900 s/mm^2, TR/TE = 17000/68.9 ms, FOV= 26 × 26 cm, thickness = 2.2 mm, matrix size = 128 × 128, and NEX of 6.

Cytoarchitectural parcellation of the CC: First, reconstruction of fiber diffusion orientation distribution function (ODF) within each voxel was based on the spherical harmonic approach with harmonic series order =12 [6], and then fiber orientations were determined by estimating the local maximum of ODF. Second, for extracting the CC fiber trajectories, CC shapes were outlined from the eight mid-sagittal planes by two experienced physicians in native T1 anatomy space. From selected CC voxels of individual subjects, around 1400 seed voxels, were defined to extract the complex neural tracts. Fiber tracking was performed using the MFACT algorithm with a length threshold of ODF (ODF_{td}) 0.8 and a tract-turning angle threshold (TTA) of 45 degrees. Third, for normalizing the reconstructed tracts of all subjects from individual spaces to a common space, a tract-based transformation approach was employed to transfer the extracted tracts from each subject into the MNI coordinate system [7]. Fourth, in order to archive a reliable identification of fiber bundles, fiber bundles were clustered and labeled using the cytoarchitectonic subdivisions derived from the BAs template provided with MRIcro (software by C. Rorden). Finally, a population–based probabilistic connection map of the CC to 27 selected BAs was created according to Park's approach [8].

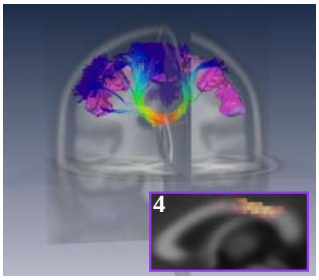
Regional microstructural differences of the CC: All DTI calculations (including determining the elements of diffusion tensor and calculating the FA values) were performed with an in-house program developed in C++. The DTI b=0 image was registered to standard MNI space using FLIRT with trilinear interpolation. The FA map of each subject was subsequently registered to the MNI space using the same transform function obtained from the previous step. And then, according to the above probabilistic connection map of the CC, the mean and standard deviation of FA values of 27 subdivisions were calculated. Regional differences were evaluated for significance (Statistical Package for the Social Sciences, SPSS Inc.) using one-way ANOVA combined with a Post-hoc test (Least significant difference (LSD) for multiple comparisons).

Results

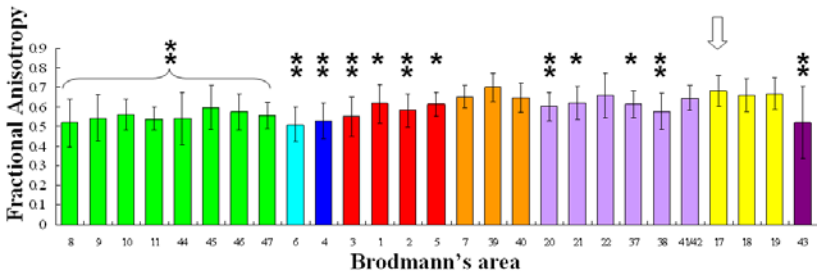
Fig. 1 presented an example of extracted fiber bundles which passed through primary motor area (BA 4) in a subject and the generated probabilistic connection map of the CC to BA 4 in the MNI space. Fig.2 showed the mean FA values across subjects over the parcellated CC regions. Our results were highly consistent with the previous results [1], high FA values in parietal lobes (BA 7, 39 and 40) and occipital lobes (BA 17, 18, and 19) and low FA values in BA4 and premotor and supplementary motor areas (BA 6). The mean FA value of the callosal occipital region (BA 17) was significantly different to those in all other regions ($P < 0.01$ or $P < 0.05$) except for the parietal segments (BA 7, 39 and 40) and two temporal regions (BA 22 and 41/42).

Discussions

The measured FA may be possible to evaluate the histological evidences in the human CC. Several neurobiological features contribute to FA, such as the thickness of myelin sheaths covering the axons, cell-packing density, fiber diameter, and directional coherence. Using light and electron microscopy, fiber compositions in the human CC between midbody (thick, myelinated, and sparse fibers) and genu and splenium of the CC (thin, un-myelinated and dense fibers) have been evaluated [5]. Associated the results with our topography, localization of regions with high FA values are in accordance with the posterior portions of the CC, which are associated with parietal and occipital lobe. Comparing with the genu of the CC, even though thin fibers were also found, lower FA values than that in the splenium may be due to the fewer number of fiber bundles (about twelve millions) and the existence of fewer non-parallel, obliquely oriented axons. Moreover, the regions with high density of thin fibers in the genu and splenium are the major distributions where fibers propagate to frontal areas (BA 9, 10, 11, 45, 46, and 47) and high-order processing areas of the temporal (BA 20, 21, 37, and 41/42), parietal lobe (BA 7, 39, and 40) and occipital lobe (BA 17, 18, and 19). In these cortical regions, processing time may be long enough to make the delay produced by interhemispheric transfer through smaller diameter fibers irrelevant [5].



◄◄**Fig. 1** An example of extracted fiber trajectories passed through BA 4 in single subject and the generated probabilistic CC topography of 12 subjects.



◄**Fig. 2** Mean FA within the clustered CC regions averaged across subjects. $P < 0.01$ and $P < 0.05$ were marked with double and single asterisk respectively.

References

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