Connectivity-based parcellation of the midsagittal corpus callosum in human brain using diffusion probability tractography

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Introduction: The corpus callosum is the main commissure of the human brain. It is well known that cortical regions project to corresponding regions (homotopic projections) or to different regions (heterotopic) in the contralateral hemisphere. The precise topography of these fibres in the human brain, however, is largely unknown. The aim of the present study is to parcellate the midsagittal corpus callosum (MCC) on the basis of its connectivity. Therefore, we used diffusion probability tractographic tracking in order to analyse the connection distributions between the MCC and seven cortical regions (1, 2), which are known to send projections through the corpus callosum.

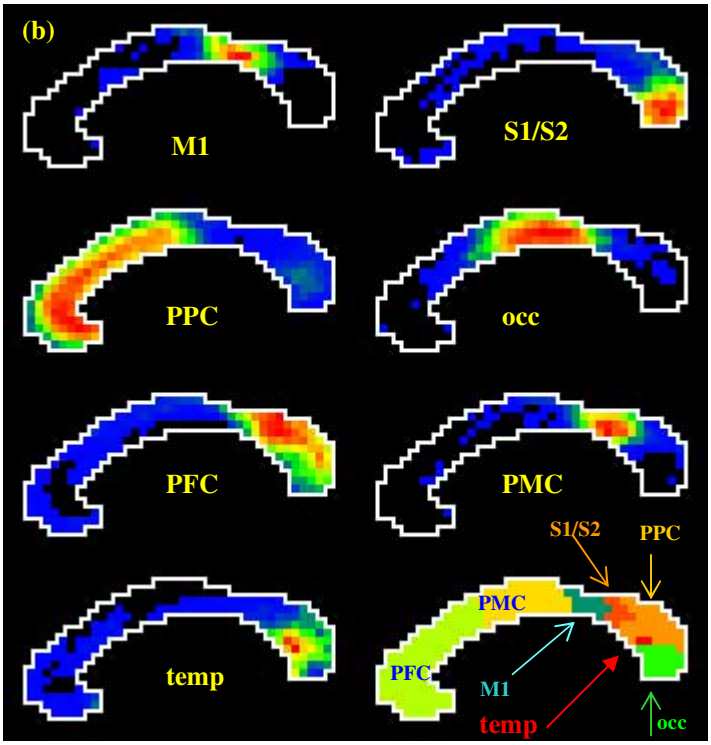
Methods: All MRI data were acquired on 15 participants using a Siemens Sonata 1.5T MR scanner with an 8-channel phased array coil (GRAPPA reconstruction scheme with acceleration factor 2). Anatomical reference images (isotropic 1mm^3) were acquired using the T1-weighted MP-RAGE sequence with the following parameters: TR/TE= 2200/3.93ms, FA=15^o, matrix size 256x256, FOV=256 x 256mm^2, slice thickness=1mm, BW=130Hz/px, 160 slabs, the number of the reference lines for GRAPPA was 70. Diffusion-weighted data (isotropic 1.8mm^3) were acquired with the following parameters: TR/TE=12000/92ms, b=800s/mm^2, BW=1502Hz/px, FOV=230x216mm^2, slice thickness=1.8mm, matrix size 128x120, slice thickness=1.8mm. For each scan, sixty-seven volume datasets (60 volumes with b = 800 DWIs and 7 volumes with b = 0 or without diffusion weighting) were acquired. The sixty diffusion gradient directions were implemented in an icosahedra scheme (3) to reduce error propagation. In order to improve SNR, the measurement was repeated four times for subsequent averaging. The total acquisition time was around 20 minutes per scan.

Tracts were seeded from regions-of-interest within the MCC (Fig. a). They were classified according to the termination of the tracks in the specified cortical region. We generated two types of connectivity-based probability parcellation maps for the MCC, the connectivity-based probability map (CPM) corresponding to the specified cortical region, and the maximum probability map (MPM) assigning the voxel within MCC with the highest connectivity probability. Tractographic tracking was performed automatically from a seed mask to target masks without the need to make a deterministic decision at each step. The target areas are the following seven cortical regions (1, 2): prefrontal (PFC), premotor (lateral and medial) (PMC), primary motor (M1), primary and secondary somatosensory (S1/S2), temporal (temp), posterior parietal (PPC), and occipital (occ) (Fig. b). Probability maps were calculated for each region which quantifies the overlap in the sample of 15 data sets.

The algorithm employed in this work is based on Markov Chain Monte-Carlo (MCMC) model (2) implemented in the FSL/FDT software package (www.fsl.ok.uk). It enables to one to calculate diffusion probability tractography and allows us to obtain information about connectivity distribution and tissue structure. Multi-directional DW-EPI datasets were used to perform the diffusion probability tractographic tracking from MCC to the target areas (the seven cortical regions) and the connectivity distribution was calculated in the diffusion space which was followed by transformation in ICBM/ MNI152 standard space. The above procedures were performed using the FMRIB's diffusion toolbox (FDT) included in software package of FSL (4).

The brain mask in diffusion space was extracted from the b = 0 images using the brain extraction tool (BET). High-resolution MP-RAGE images serve as a reference for anatomical structure. Individual anatomical images were normalized to ICBM/MNI152 standard space (Fig. 1a). The MCC mask was outlined from the group-averaged brains in standard space (Fig. 1a). Data were transformed into anatomical (from MP-RAGE images) and diffusion spaces using the linear registration tool (FLIRT). The transform matrices among the three spaces (anatomical space, diffusion space and standard space) were calculated. Diffusion probability tractographic tracking was performed on FDT.

Results and Discussion: The CPMs for MCC according to its connectivity distribution with the seven cortical regions are shown in Fig. 1b. We found similar results across subjects for the location, size, and ordering of MCC subdivisions, which reflect the topological structure of the analyzed cortical regions. The parcellation results were reproducible and stable across the 15 subjects. Our data show that fibres of the MCC form clusters dependent on their target in one of the seven cortical regions. The parcellation scheme shows a reasonable topological organisational distribution of callosal fibres. It agrees with data of post-mortem human studies and non-human primates (6). Extending and supplementing earlier DTI based studies (5), where the MCC was parcellated by means of the connectivity between MCC and the six planes with different orientations, the present study presents more detailed parcellation results. Moreover, tractographic tracking was performed automatically from the seed mask to the target masks with no need for a deterministic decision at each step.
We conclude that the method presented here can potentially be utilized as a new tool to investigate callosal morphology, including the structural changes in MCC and connectivity changes between MCC and cortical regions.



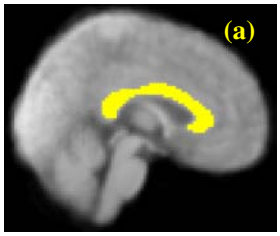


Fig.1 Group-averaged connectivity-based parcellation maps of MCC.
(a) The seed area (MCC) of the group-averaged human brains is chosen (yellow colour) in the standard space.
(b) Group-averaged connectivity probability maps (CPMs) of MCC for the specified cortical regions (the colours from blue-green-yellow-orange-red indicate the density of voxels in MCC connected to the specified cortical region); and the group-averaged of the maximum probability map (MPM) is obtained by selecting the voxels in MCC with the largest connectivity probability in the seven cortical regions (lower right).

References:
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