Appendix 1 Supplementary methods

Imaging parameters

Whole-brain T1-weighted anatomical images were acquired using the following volumetric 3D magnetization-prepared rapid gradient-echo (MP-RAGE) sequence. Scan parameters were as follows: repetition time (TR) = 1900 ms, echo time (TE) = 2.95 ms, flip angle = 9°, slice thickness = 1 mm, slices = 160, field of view (FOV) = 230 × 230 mm^2, matrix size = 256 × 256 and voxel size = 1 × 1 × 1 mm^3.

Diffusion tensor imaging (DTI) data were obtained using spin echo planar imaging sequence. Parameters were as follows: TR = 9800 ms, TE = 95 ms, FOV = 256 × 256 mm^2, number of excitations (NEX) = 1, matrix = 128 × 128, slice thickness = 2 mm and slice gap = 0 mm. Diffusion gradients were applied in 30 non-collinear directions with a b factor of 1000 s/mm^2 after an acquisition without diffusion weighting (b = 0 s/mm^2) for reference.

Besides, whole brain resting-state functional MR imaging (rs-fMRI) data were gained with an echo-planar imaging (EPI) sequence. During scanning, all participants were instructed to stay awake, keep their head still, relax with their eyes closed, and not think of anything in particular. Scan parameters were as follows: TR = 2000 ms, TE = 21 ms, flip angle = 90°, FOV = 256 × 256 mm^2, in-plane matrix = 64 × 64, slice thickness = 3 mm, number of slices = 35, no slice gap, voxel size = 3 × 3 × 3 mm^3 and total volumes = 240.

MRI data preprocessing

DTI data preprocessing steps included brain extraction, realignment, eddy current and motion artifact correction, fractional anisotropy (FA) calculation, and diffusion tensor tractography. All these steps were performed using the PANDA toolbox based on FMRIB Software Library. Deterministic fiber tracking was applied to construct white matter (WM) structural brain networks. The fiber tracking was performed using Continuous Tracking algorithm. The FA threshold was set to 0.2, and the turning angle threshold was set to 45° for the fiber assignment. The quality controls and analyses of magnetic resonance images were performed by an experienced imaging scientist (Min Wang, with 10 years of experience in MRI data analysis).

The preprocessing of rs-fMRI data was performed using the Data Processing Assistant for rs-fMRI (DPARSF) based on Statistical Parametric Mapping (SPM). Removed the first 10 time points to reduce transient signal changes caused by unstable magnetic field and to permit subjects to be accustomed to the scanning circumstance. Afterwards, preprocessing included standard slice timing, head motion correction, realignment, spatial normalization by diffeomorphic anatomical registration through exponentiated lie algebra (DARTEL; voxel size [3, 3, 3]), smoothing at 6 mm full-width half maximum (FWHM), temporal band-pass filtering (0.01-0.08 Hz) and nuisance signals regression (including six head motion parameters, average WM, cerebrospinal fluid and global signals). Finally, individuals with more than 2.0 mm or 2-degree cumulative translation or rotation head motion were excluded from our study.

Construction of brain networks

To construct WM structural networks, each brain was parcellated into 116 regions of interest (ROIs) using Anatomical Automatic Labeling (AAL) atlas (including the cerebellum), which were defined as 116 nodes. The parcellation process was performed in the native space. Actually, T1-weighted images of each participant were firstly registered with their corresponding b = 0 image with an affine transformation. Afterwards, the individual transformed T1-weighted images were registered to the ICBM152 T1 template (Montreal Neurological Institute, Montreal, Canada) by a non-linear transformation. Finally, the inversed transformation parameter of each individual was applied to the AAL atlas to generate corresponding AAL regions in individual space. Each AAL region was considered as a node, and interconnections between brain regions (interconnected WM fiber numbers in this study) were considered as the edges of the structural network. Finally, a symmetrically structural connectivity matrix (116 × 116) for each individual was obtained.

Functional networks were constructed using the GRETNA toolbox. Same as before, AAL116 atlas was chosen as the parcellation scheme. Then, A 116 × 116 temporal correlation matrix was assembled by computing Pearson's correlation coefficient between the residual time series of each pair of the 116 nodes for each participant. For each ROI, the mean

https://dx.doi.org/10.21037/qims-22-351

time series were obtained by averaging the fMRI time courses over each ROI. The values of the interregional correlation coefficients were taken as the weights of the edges. Finally, we performed the Fisher's r-to-z transformation to improve the normality of the correlation.

Structural-functional coupling analysis

First, all non-zero connectivities of the structural networks were selected. Second, these connectivity values were rescaled to a Gaussian distribution. Finally, the corresponding connectivities of the functional networks were also extracted and correlated with the structural counterparts selected forehead. And this resulted in a single structural-functional coupling value for each subject (67,68).

References

67. Hagmann P, Sporns O, Madan N, Cammoun L, Pienaar R, Wedeen VJ, Meuli R, Thiran JP, Grant PE. White matter maturation reshapes structural connectivity in the late developing human brain. Proc Natl Acad Sci U S A 2010;107:19067-72.
68. Honey CJ, Sporns O, Cammoun L, Gigandet X, Thiran JP, Meuli R, Hagmann P. Predicting human resting-state functional connectivity from structural connectivity. Proc Natl Acad Sci U S A 2009;106:2035-40.

https://dx.doi.org/10.21037/qims-22-351