Associations between hemispheric asymmetry and schizophrenia-related risk genes in people with schizophrenia and people at a genetic high risk of schizophrenia

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Background
Schizophrenia is considered a polygenic disorder. People with schizophrenia and those with genetic high risk of schizophrenia (GHR) have presented with similar neurodevelopmental deficits in hemispheric asymmetry. The potential associations between neurodevelopmental abnormalities and schizophrenia-related risk genes in both schizophrenia and those with GHR remains unclear.

Aims
To investigate the shared and specific alternations to the structural network in people with schizophrenia and those with GHR. And to identify an association between vulnerable structural network alternation and schizophrenia-related risk genes.

Method
A total of 97 participants with schizophrenia, 79 participants with GHR and 192 healthy controls, underwent diffusion tensor imaging (DTI) scans at a single site. We used graph theory to characterise hemispheric and whole-brain structural network topological metrics. For 26 people in the schizophrenia group and 48 in the GHR group with DTI scans we also calculated their schizophrenia-related polygenic risk scores (SZ-PRSs). The correlations between alterations to the structural network and SZ-PRSs were calculated. Based on the identified genetic–neural association, bioinformatics enrichment was explored.

Results
There were significant hemispheric asymmetric deficits of nodal efficiency, global and local efficiency in the schizophrenia and GHR groups. Hemispheric asymmetric deficit of local efficiency was significantly positively correlated with SZ-PRSs in the schizophrenia and GHR groups. Bioinformatics enrichment analysis showed that these risk genes may be linked to signal transduction, neural development and neuron structure. The schizophrenia group showed a significant decrease in the whole-brain structural network.

Conclusions
The shared asymmetric deficits in people with schizophrenia and those with GHR, and the association between abnormal asymmetry and SZ-PRSs suggested a vulnerability imaging marker regulated by schizophrenia-related risk genes. Our findings provide new insights into asymmetry regulated by risk genes and provides a better understanding of the genetic–neural pathological underpinnings of schizophrenia.

Keywords
Structural network; brain asymmetry; polygenic risk score; genetic susceptibility; schizophrenia.

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Background
Schizophrenia is a highly heritable disorder with neurodevelopmental deficits – characterised by a failure to integrate neural processes as a result of an abnormal brain network.1–3 These brain network deficits can occur years before the illness appears through disruptions of normal neuro-maturational processes. Furthermore, family studies reported a tenfold increased risk of developing schizophrenia in unaffected relatives of people with schizophrenia,4 and polygenic risk score (PRS) analysis was estimated to explain 7% of the variance in liability.5 Identifying these potential imaging features could help explain the multilevel genetic–neural underpinnings of the development of schizophrenia.

Hemispheric asymmetry and schizophrenia
Neurodevelopmental researchers have suggested that brain asymmetry is a core metric of both neurodevelopment in healthy individuals5,6 and in numerous developmental disorders.6,8,9 Previous post-mortem and neuroimaging studies in schizophrenia have repeatedly shown the condition to be associated with an anomalous pattern of hemispheric asymmetry.10–13 Crow and colleagues undertook a series of studies14,15 and proposed an influential theory: schizophrenia, which stems from the failure of normal hemispheric asymmetry in the temporal lobe region can be explained by genes.13 Furthermore, Crow et al indicated that hemispheric asymmetry in schizophrenia was unrelated to episode progression, and the anatomical asymmetry occurred during development.16 These neurodevelopmental alterations in hemispheric asymmetry were found both in brain structure and function, such as white matter architecture, cortical thickness and functional activation.

White matter
White matter plays a pivotal role in modulating communication and the functional integrity of the brain. A brain network study found that reduced communication capacity and altered functional brain dynamics in schizophrenia may be caused by a selective...
disruption of brain connectivity among central hub regions of the brain.\textsuperscript{16} Anomalous white matter integrity has been associated with neurodevelopmental abnormalities of myelination, axonal growth and synaptic plasticity in schizophrenia.\textsuperscript{17,18} Pathological turbulences of the brain are rarely focused on a single brain region, as deficits often spread via axonal pathways to affect other regions.

Using diffusion tensor imaging (DTI), we can virtually reconstruct white matter tracts and model the human brain as a complex network/graph. Graph theoretical analysis can provide a powerful new way to evaluate the topological organisation of the constructed human brain white matter network. Multiple topological metrics can be used to assess white matter network connectivity by graph theoretical analysis,\textsuperscript{19,20} which is a relatively novel technique to understand the neuropathology in neural disease. Neuroimaging evidence indicates a global efficiency decrease in the topological metric of brain anatomical networks in schizophrenia.\textsuperscript{21} Although some studies have focused on abnormal topological metrics of the whole-brain network, few studies have investigated alterations to topological metrics of hemispheric asymmetry and the whole-brain network within the context of the same study in schizophrenia.

### Benefits of studying populations at genetic high risk for developing schizophrenia

Abnormalities of hemispheric asymmetry and the whole-brain network have also been found in individuals without psychosis but with genetic high risk for developing schizophrenia (GHR).\textsuperscript{20,22} Thus, GHR populations can be used to identify liabilities expressed across a range of phenotypes, presumably reflecting vulnerability. Studies of morphology and the white matter network in neonates at genetic risk of schizophrenia indicated that this risk would induce lower efficiency both in the white matter network and grey matter structural associations.\textsuperscript{23} Furthermore, recent studies found that people with schizophrenia and their unaffected siblings showed disrupted asymmetry of inter- and intrahemispheric functional connectivity.\textsuperscript{24} A similar pattern was also found in prefrontal, occipitoparietal cortical regions compared with healthy controls.\textsuperscript{25,26} Particularly, left-sided language dysfunctional asymmetry was considered to be the result of familial heritable outcomes.\textsuperscript{27,28} Evidence shows that people with schizophrenia and their unaffected monozygotic co-twins present with decreased language asymmetry; however, the asymmetry was not associated with the severity of psychosis, which suggested that asymmetry was a result of genetic risk, rather than a state-related trait.\textsuperscript{29} However, few studies have focused on evaluating white matter structural network topological metrics at the hemispheric level in people with schizophrenia and their unaffected relatives.

### Value of using PRSs

Although family association studies have confirmed genetics contributes significantly to schizophrenia risk, these studies have resulted in few replicated findings. It is difficult to find research on the latent genetic architecture of schizophrenia using individual single nucleotide polymorphisms (SNPs). This is because the disease is highly polygenic and has many common genetic variants facilitating the disease.\textsuperscript{30} Genome-wide association studies (GWASs) could identify millions of SNPs across the entire genome associated with psychosis, which suggested that asymmetry was a result of genetic risk, rather than a state-related trait. In schizophrenia, however, the asymmetry was not associated with the severity of psychosis, which suggested that asymmetry was a result of genetic risk, rather than a state-related trait.\textsuperscript{29} However, few studies have focused on evaluating white matter structural network topological metrics at the hemispheric level in people with schizophrenia and their unaffected relatives.

### Aims

To the best of our knowledge, this is the first study to investigate the shared and specific alterations in topological metrics of hemispheric asymmetry and the whole-brain structural network in people with schizophrenia and those with GHR. We combined genetic imaging data (genetic variable × white matter structural network in hemispheric asymmetry and whole brain) to explore a vulnerability imaging marker regulated by schizophrenia-related risk genes. The primary aim of this study was to identify an association between shared white matter structural network alteration and schizophrenia-related risk genes in people with schizophrenia and those with GHR, and investigate the functions of these risk genes through bioinformatics enrichment analyses. Secondly, our aim was to reveal a core deficit in the white matter structural network related to pathology in schizophrenia.

### Participants

A total of 368 individuals participated in this study, including 97 people with schizophrenia, 79 with GHR and 192 healthy controls, aged 18–54 years. Detailed inclusion and exclusion criteria are described in the Supplementary Material available at https://doi.org/10.1192/bjp.2021.47. Symptom severity was measured using the 17-item version of the Hamilton Rating Scale for Depression (HRS-D–17),\textsuperscript{39} the Hamilton Rating Scale for Anxiety (HRS-A),\textsuperscript{40} and the Brief Psychiatric Rating Scale (BPRS).\textsuperscript{41} All participants gave written informed consent. This research was approved by the Medical Research Ethics Committee of the China Medical University and in accordance with the Declaration of Helsinki.

### Magnetic resonance imaging (MRI) data

#### MRI acquisition

All MRI scans were performed using a 3.0 T GE Sigma system (General Electric, Milwaukee, USA) with a standard eight-channel head coil at the First Affiliated Hospital of China Medical University, Shenyang, China. The parameters of \( T_1 \) images and DTI are described in the Supplementary Material. Two neuro-radiologists with more than 3 years of experience interpreting neuroradiology images checked image quality.

#### Data preprocessing and network construction

The DTI data-set was preprocessed using PANDA.\textsuperscript{42} Briefly, data preprocessing included (a) brain extraction (b) correction for eddy-current distortion and simple head motion, (c) correction...
for b-matrix, and (d) computation for diffusion tensor and fractional anisotropy. The construction of the white matter network was implemented by PANDA. The procedures used for the white matter network construction are described in the Supplementary Material.

Network analysis

Graph theory was used to characterise the topological metrics of the white matter structural networks derived above. In the current study, both nodal metrics and global network metrics were computed. We characterised a single nodal metric by computing the nodal degree ($D_{nodal}$) and nodal efficiency ($E_{nodal}$). The global metrics of the network were computed for the global efficiency ($E_{glob}$) and local efficiency ($E_{loc}$). GRETNA (https://www.nitrc.org/projects/gretna/) was used to calculate network metrics. Brief descriptions and formulas are provided in Supplementary Table 1.

Asymmetry index analysis

White matter structural network asymmetry of topological metrics ($D_{nodal}$, $E_{nodal}$, $E_{glob}$ and $E_{loc}$) was estimated using the asymmetry index ($AI$): $AI(X) = 100 \times \frac{|X(L) - X(R)|}{X(L) + X(R)}$, where $X(L)$ and $X(R)$, respectively, represent the network metrics of the left and right hemispheres. $AI$ provides the differences between the left and right hemispheres, by incorporating the relative network metrics over both hemispheres in one value.

Genetic data

Genotyping and imputation

Whole blood samples were withdrawn into EDTA (ethylenediaminetetraacetic acid) anticoagulant tubes, with samples taken between 10:00 h and 15:00 h and stored at −80°C until it was assayed. Genomic DNA was extracted from whole blood using standard protocols. Illumina Global Screening Array-24 v1.0 BeadChip was used to screen genome-wide variants for 74 participants (26 in the schizophrenia group, 22 in the GHR group, and 26 in the healthy control group). Detailed demographic and clinical data are provided in Supplementary Table 2 for the 74 participants included in the genetic analysis. This array provides data for 642,824 fixed genetic variants, addition to 53,411 customised variants. Detailed exclusion criteria relating to data and genotype imputation are described in the Supplementary Material.

Calculation of PRSs

The latest international GWAS results published by the Psychiatric Genomics Consortium were used as discovery samples, and our imputed genotyping data were used as a target sample. In the paper by the Bipolar Disorder and Schizophrenia Working Group of the Psychiatric Genomics Consortium, the specific genetic factors contributing to schizophrenia were analysed in 33,426 people with schizophrenia and 32,541 controls. A total of 843,107 ambiguous variants were excluded. PRSs were generated using PRSice software (www.PRSice.info). P-value-informed clumping was performed with a cut-off of $r^2 \geq 0.1$ in a 250 kb window. Twelve PRSs at different P-value thresholds (0.0001, 0.001, 0.01, 0.02, 0.03, 0.04, 0.05, 0.1, 0.2, 0.3, 0.4 and 0.5) were derived for each study participant. The number of variants for 12 PRSs were 91,521, 2523, 6376, 8055, 9185, 10,102, 10,846, 13,638, 17,339, 20,086, 22,299 and 24,268, respectively.

Bioinformatics enrichment analyses

All the SNPs in SZ-PRSs under a certain P-value threshold were extracted and transformed into the corresponding genes where they were located based on the dbSNP database. A gene list was obtained and uploaded to the online tool DAVID Bioinformatics Resources v6.8 (https://david.ncifcrf.gov/) for the Gene Ontology and the Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analyses. The functions of genes were annotated with three Gene Ontology terms: biological process, cellular component and molecular function. Multiple testing corrections were performed with the Bonferroni method (significance level at 0.01).

Statistical analysis

ANOVA(s) (analyses of variance) or chi-square tests were used to examine participants’ demographic characteristics (age and gender) and clinical characteristics (duration of illness, first episode and medication status). ANCOVA (analyses of covariance) was implemented to evaluate differences between white matter network topological metrics for the asymmetry index and the entire brain among the three groups, with gender and age as covariates. Least significant differences post hoc analyses were performed to detect significant group effects in the ANCOVA. Bonferroni correction was applied for multiple comparisons (90 tests), and significance was set to a corrected $P < 0.05$. Partial correlation analyses, with age and gender as covariates, were performed to investigate the relationships between asymmetry index metrics and entire brain network metrics with S-Z PRSs in the schizophrenia and GHR groups. Significance was set at $P < 0.05$ (two-tailed) for all tests. All analyses were performed using SPSS 22.0.

Results

Demographics and clinical scales

No significant between-group differences were found in age and gender. The effect of diagnosis on HRSD, HRSA and BPRS scores was significant (see Table 1), with significantly higher HRSD, HRSA and BPRS scores in the schizophrenia group compared with the healthy control group, and higher HRSD scores in the GHR group compared with the healthy control group. There was no significant difference between the GHR and healthy control groups in HRSA and BPRS scores.

Asymmetry index among the schizophrenia, GHR and healthy control groups

Significant group effects were observed in AI-$E_{nodal}$ of the right orbital superior frontal gyrus in the three groups. Post hoc analysis revealed significant increases in the schizophrenia and GHR groups compared with the healthy control group. There was no statistical difference between schizophrenia and GHR (details in Fig. 1(a) and Supplementary Table 3). ANCOVA showed significant between-group effects in AI-$E_{glob}$ and AI-$E_{loc}$ among the schizophrenia, GHR and healthy control groups. Comparisons of the healthy control, schizophrenia and GHR groups increased in AI-$E_{glob}$ and AI-$E_{loc}$, but did not differ from each other (details in Fig. 1(b) and Supplementary Table 3). No significant group effect was found in AI-$D_{nodal}$ after Bonferroni correction among the schizophrenia, GHR and healthy control groups.

$D_{nodal}$ and $E_{nodal}$ of whole brain among the schizophrenia, GHR and healthy control groups

A significant difference was observed in $D_{nodal}$ left postcentral gyrus, and post hoc analyses revealed that compared with the healthy control and GHR groups, the schizophrenia group showed a decrease in $D_{nodal}$. Significant group differences in the $E_{nodal}$ of the right middle frontal gyrus, right opercular
inferior frontal gyrus, left superior occipital gyrus, left postcentral gyrus, right inferior parietal angular gyrus and left angular gyrus were observed. Post hoc analyses revealed that compared with the healthy control and GHR groups, the schizophrenia group showed a decrease in $E_{\text{nodal}}$. But there was no significant difference in $D_{\text{nodal}}$ and $E_{\text{nodal}}$ between the GHR and healthy control groups (details in Fig. 1(d), 1(f) and Supplementary Table 3).

$E_{\text{glob}}$ and $E_{\text{loc}}$ of whole brain among the schizophrenia, GHR and healthy control groups

Significant differences were found in $E_{\text{glob}}$ and $E_{\text{loc}}$ among the three groups. Compared with the healthy control and GHR groups, the schizophrenia group showed a decrease in $E_{\text{glob}}$ and $E_{\text{loc}}$, but there was no significant difference between the GHR and healthy control groups (Fig. 1(g) and Supplementary Table 3).

Correlation between SZ-PRS and AI-$E_{\text{loc}}$ in the schizophrenia and GHR groups

We excluded participants who failed to evaluate SZ-PRS, and demographic and clinical data for participants in the correlation analysis are provided in Supplementary Table 2. According to the aims of our study, we performed partial correlation analyses to investigate the relationships between asymmetry index metrics and entire brain network metrics using SZ-PRS rather than using a gene-based association test to find specific risk genes influencing development of hemispheric asymmetry. AI-$E_{\text{loc}}$ was significantly positively correlated with SZ-PRS at $P$-value thresholds of 0.05 (PT_0.05), which has the smallest $P$-value in the association analysis with AI-$E_{\text{loc}}$. In total, 10,729 SNPs and 4070 genes were extracted and identified in SZ-PRSs at PT_0.05. Thirty-five Gene Ontology terms were identified in SZ-PRSs (Fig. 2a).

For biological process, terms were enriched in signal transduction, neural development, neuron structure and calcium signaling pathways. Thus, we were able to link our imaging findings to potential pathways involved in the molecular pathophysiology of schizophrenia.

With regard to cellular components, neuron structure was among the significant aspects, containing several terms (cell junction, plasma membrane, postsynaptic density, postsynaptic membrane and cytoskeleton).

Calcium ion binding was the most significant term in molecular function. Additionally, we obtained eight significantly enriched pathways (Fig. 2b) based on the KEGG database, including calcium signaling pathway, axon guidance, focal adhesion, glutamatergic synapse, Rap1 signaling pathway and oxytocin signaling pathway.

### Discussion

**Main findings**

To our knowledge, this is the first combined genetic imaging study (genetic variable × white matter network in hemispheric asymmetry and the entire brain) to investigate shared and specific alterations in hemispheric asymmetry and the whole-brain structural network among people with schizophrenia, those with GHR and healthy controls, to estimate the possible effects of genes on the white matter network, and to explore SZ-PRS bioinformatics enrichment. There were shared alterations in network topological asymmetry (right orbital superior frontal gyrus of $E_{\text{nodal}}, E_{\text{glob}}$ and $E_{\text{loc}}$) in the schizophrenia and GHR groups. The implication of this is that genetic susceptibility to schizophrenia potentially regulated abnormalities in the cerebral hemispheres. Furthermore, we found $E_{\text{loc}}$ of hemispheric asymmetry was associated with SZ-PRSs in both the schizophrenia and GHR groups, and bioinformatics enrichment analyses revealed that genes driving the SZ-PRS interaction were involved in signal transduction, neural development, neuron structure and calcium signaling pathways. Thus, we were able to link our imaging findings to potential pathways involved in the molecular pathophysiology of schizophrenia.

In the schizophrenia group, we observed decreased $D_{\text{nodal}}$ (left postcentral gyrus), $E_{\text{nodal}}$ (right middle frontal gyrus, right opercular inferior frontal gyrus, left superior occipital gyrus, left postcentral gyrus, right inferior parietal angular gyrus and left angular gyrus), $E_{\text{glob}}$ and $E_{\text{loc}}$ of the entire brain, compared with the GHR and healthy control groups.

**Interpretation of our findings and comparison with findings from other studies**

The human brain is structurally and functionally asymmetrical – the left cerebral hemisphere is typically associated with language ability, and the right hemisphere is typically associated with non-verbal functions. Although the cerebral hemispheres are similar in weight and volume, there is a difference in brain tissue distribution. The right hemisphere protrudes anteriorly beyond the left, and the left hemisphere extends posteriorly beyond the right. In
Fig. 1  (a) AI-eNodal among the schizophrenia, GHR and healthy control groups. (b) AI-eGlob and AI-eLoc among the schizophrenia, GHR and healthy control groups. (c) Three-dimensional representations of the Dnodal in the entire brain among the schizophrenia, GHR and healthy control groups. (d) Dnodal in the entire brain among the schizophrenia, GHR and healthy control groups. (e) Three-dimensional representations of the Enodal in the entire brain among schizophrenia, GHR and healthy control groups. (f) Eglobal in the entire brain among schizophrenia, GHR and healthy control groups. (g) Eglobal and Elocal in the entire brain among schizophrenia, GHR and healthy control groups.

AI, asymmetry index; ANG.L and Angular_L, left postcentral gyrus; Dnodal, nodal degree; Eglob, global efficiency; Eloc, local efficiency; Elocal, nodal efficiency; Frontal_Sup_Orb_R, right superior frontal gyrus, orbital part; IFGoperc.R and Frontal_Inf_Oper_R, right inferior frontal gyrus, opercular part; IPL.R and Parietal_Inf_R, right inferior parietal angular gyrus; HC, healthy control; GHR, genetic high risk of schizophrenia; PoCG.L and Postcentral_L, left postcentral gyrus; SOG.L and Occipital_Sup_L, left superior occipital gyrus; MFG.R and Frontal_Mid_R, right middle frontal gyrus; SZ, schizophrenia. ***P < 0.001; **P < 0.01; *P < 0.05.
addition, the right hemisphere is significantly more efficient and interconnected than the left, whereas the left hemisphere has more central/indispensable regions for whole-brain structural network function.56

These results are in line with brain functional principles: the left hemisphere may demand specialised networks for processes such as language and motor actions, whereas the right hemisphere is more efficient and interconnected for more general processes such as integrating information. Patients with schizophrenia do not show these patterns of right-more-than-left efficient global integration that are observable in healthy control participants. Consistent with this result, our study found that patients with schizophrenia and those with GHR have higher asymmetry index scores in $E_{glob}$ and $E_{loc}$ ($AI = L-R/L+R$), implying that in both schizophrenia and those with GHR there is abnormal lateralisation at the ‘whole-hemisphere’ level. Furthermore, those with schizophrenia demonstrated lower global and local efficiency in the whole brain and higher asymmetry index scores in the ‘whole hemisphere’. These findings suggest that there may be right hemisphere impairments of efficient connection in schizophrenia.

We also found local network efficiency of asymmetry to be positively correlated with SZ-PRSs. This finding suggested that schizophrenia-related risk genes may influence aberrant alterations in hemispheric asymmetry. This finding is also in line with a previous study, in which higher SZ-PRSs were associated with a steeper decline in the white matter network in older age.53 Although enormous studies have illustrated functional and structural network differences in the two hemispheres and genetic risk factors have contributed to the development of abnormal lateralisation, post-mortem studies have failed to find hemisphere discrepancies of gene expression in cerebral cortex.52,53 Due to the lack of availability of post-mortem tissue samples, these studies have small sample sizes (four mid-fetal brains and two adult brains, respectively). There may still be significant lateralised expression differences, particularly because it is likely that multiple genes interact to influence neuronal and circuit properties. Overall, our PRS findings may help to identify intermediate brain phenotypes that are fundamental or common in the development of schizophrenia neuropathology.

Interestingly, we conducted bioinformatics enrichment analyses to identify the functions of schizophrenia-related polygenic risk that influenced aberrant alterations in hemispheric asymmetry. We found genes driving the SZ-PRS interaction were involved in functions such as signal transduction, neural development, neuron structure and calcium signalling pathways. One study has found that brain asymmetry was regulated by genes, and this asymmetrical genes expression was involved in signal transduction, neural development, neuron structure and calcium signalling pathways. One study has found that brain asymmetry was regulated by genes, and this asymmetrical genes expression was involved in signal transduction, neural development, neuron structure and calcium signalling pathways. One study has found that brain asymmetry was regulated by genes, and this asymmetrical genes expression was involved in signal transduction, neural development, neuron structure and calcium signalling pathways. 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the white matter structural network of the whole brain between the GHR and healthy control groups in this study. The specificity of the whole-brain structural network deficits in the schizophrenia group indicates that these deficits relate to the disorder.

**Limitations**

There were several limitations in this study. First, most of the patients with schizophrenia were taking psychotropic medications at the time of study participation. Second, a moderate sample size was used for association analyses between SZ-PRSs and abnormal asymmetric changes (total 74 participants including participants with schizophrenia and those with GHR) in this study. Further study is needed, in a larger, unmedicated sample to confirm our results. Additionally, environmental risk factors could also influence the development of abnormalities in hemispheric asymmetry and the whole-brain structural network in schizophrenia. Therefore, future studies are needed to evaluate how specific genes and their interactions with environmental risks may contribute to the alterations in asymmetry found in schizophrenia.

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**Fig. 2** (a) Significant Gene Ontology enrichment analysis for risk genes of schizophrenia-related polygenic risk scores (SZ-PRSs). (b) Significant Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment analysis for risk genes of SZ-PRSs.

cGMP-PKG, cyclic guanosine monophosphate-protein kinase G.
Implications

The shared deficits of hemispheric asymmetry in patients with schizophrenia and those with GHR suggested that anomalous asymmetry may be potential susceptibility markers of the disease. The significant association between altered hemispheric asymmetry and schizophrenia-related risk genes indicate a vulnerability imaging marker regulated by schizophrenia-related risk genes. These risk genes are also involved in signal transduction, neural development, neuron structure and calcium signalling pathways. These specific alterations to the white matter structural network of whole brain in people with schizophrenia largely relate to the neuropathologic features of the disorder. Our findings provide new insights into asymmetry regulated by risk genes and provide a better understanding of the genetic–neural pathological underpinnings of schizophrenia.

Supplementary material

Supplementary material is available online at https://doi.org/10.1192/bjp.2021.47.

Data availability

The data that support the findings of this study are available from the corresponding author (Y.T.), upon reasonable request.

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Author contributions

Y.T. and F.W. designed the study. Y.Z., S.W. and X.J. enrolled participants. S.W., Y.Q., S.Z., C.L., P.Z., X.G. and G.G. acquired the data X.G. and F.W. did the analysis plan. Y.Z., S.W. and Y.Q. analysed the data. Y.Z. and E.K.E. wrote the paper.

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Declaration of interest

The authors declare that they have no conflict of interest.


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