Biological vulnerability to depression: linked structural and functional brain network findings


Background
Patients in recovery following episodes of major depressive disorder (MDD) remain highly vulnerable to future recurrence. Although psychological determinants of this risk are well established, little is known about associated biological mechanisms. Recent work has implicated the default mode network (DMN) in this vulnerability but specific hypotheses remain untested within the high risk, recovered state of MDD.

Aims
To test the hypothesis that there is excessive DMN functional connectivity during task performance within recovered-state MDD and to test for connected DMN cortical gyrification abnormalities.

Method
A multimodal structural and functional magnetic resonance imaging (fMRI) study, including task-based functional connectivity and cortical folding analysis, comparing 20 recovered-state patients with MDD with 20 matched healthy controls.

Results
The MDD group showed significant task-based DMN hyperconnectivity, associated with hypogyrification of key DMN regions (bilateral precuneus).

Conclusions
This is the first evidence of connected structural and functional DMN abnormalities in recovered-state MDD, supporting recent hypotheses on biological-level vulnerability.

Declaration of interest
N.L.N. received funding from the Institute of Mental Health, Nottingham, which enabled him to carry out this research project, and has received financial assistance to attend academic meetings from Janssen-Cilag, AstraZeneca, Servier and Shire. He has also taken part in advisory panels for Janssen-Cilag and Servier. P.F.L. has received honoraria for academic presentations from GlaxoSmithKline, AstraZeneca, Janssen-Cilag, Bristol-Myers Squibb, Eli Lilly and Johnson & Johnson Pharmaceuticals. He has also taken part in advisory panels for Eli Lilly, Pfizer and GlaxoSmithKline. G.W. has received honoraria for academic presentations from Janssen-Cilag. M.L. received a grant from the National Alliance for Research on Schizophrenia and Depression (NARSAD). L.P. has received a travel fellowship from the International Bipolar Disorder Society sponsored by Eli Lilly in 2010.

Patients who have recovered from episodes of major depressive disorder (MDD) remain highly vulnerable to future recurrence and clinical studies put this risk of further MDD episodes at up to 80%, in contrast with the general population lifetime risk of 6.7% (95% CI 4.2–10.1). Although psychological determinants of this risk are well established, relatively little is known about associated biological mechanisms. Functional magnetic resonance imaging (fMRI) studies have provided some early data on the presence of functional brain abnormalities in recovered-state patients with MDD when performing executive tasks. However, there remains no published evidence on brain network functional connectivity or related structure in recovered MDD despite credible recent hypotheses of their importance. The clearest theory concerns the default mode network (DMN); a brain network in which increased levels of activity have well-evidenced associations with internally focused appraisal and that has therefore been considered a potential neural substrate for the ruminative, introspective cognitive patterns of MDD. The DMN is further implicated through convergent findings of increased resting-state functional connectivity between specific DMN regions (namely the dorsomedial prefrontal cortex and precuneus) in both depressed-state MDD and never-depressed, first-degree relatives of patients with recurrent MDD. This has led the authors of a recent review to hypothesise that DMN hyperconnectivity continues within recovered-state MDD, persisting into task-based activity where it acts as a substrate for overly internal processing, interfering with the recruitment of more effective networks and ultimately creating biological-level vulnerability to depression. Recent evidence linking functional connectivity and gyrification of the cortical surface means we might additionally predict that abnormal DMN functional connectivity is associated with abnormal gyrification in key DMN regions. In light of this literature, our aims were first to test the hypothesis that there is excessive task-based DMN functional connectivity within recovered-state MDD; and second to test the hypothesis that there are connected abnormalities in cortical gyrification within anatomical regions of the DMN.

Method

Recruitment and clinical assessment
The recruitment and assessment of this population has been previously reported in detail, but is summarised here. Patients (the MDD group) were recruited through physician referral from general adult psychiatric clinics in Nottingham, UK. The control group were mainly recruited through posters displayed at a general hospital and a community surgery in Nottingham, UK. The control group were mainly recruited through posters displayed at a general hospital and a community surgery in Nottingham, UK. Following complete description of the study, written, informed, capacitous consent was obtained from all participants. The study was approved by the local research ethics committee.

All potential recruits underwent an initial psychiatric assessment by senior clinical psychiatrists (N.L.N., G.W., P.F.L.), including a detailed history of personal and family psychiatric/medical disorder, substance misuse and medication history; followed by the Structured Clinical Interview for DSM-IV Axis I Disorders (SCID-CV); two measures of depressive symptoms, the 17-item Hamilton Rating Scale for Depression (HRSD).
and the Beck Depression Inventory – II (BDI-II); and two measures of personality, the Short Eysenck Personality Questionnaire-revised (EPQ-R) and the Personality Disorders Questionnaire-revised version 4 (PDQ-4+); a measure of IQ, the Ammons Quick Test (Quick); a measure of cognitive function, the Folstein Mini-Mental State Examination (MMSE); a handedness questionnaire (ROC); and an MRI safety questionnaire.

A clinical consensus meeting followed initial screening to determine inclusion/exclusion. Minimum inclusion for the MDD group required at least two previous episodes of DSM-IV major depression, diagnosed through SCID-CV, now in a recovered-state (with normalised function for at least 3 months and HRSD score <8). Exclusion criteria were comorbid Axis I psychiatric disorder (with particular focus on misdiagnosed bipolar II disorder or anxiety disorder); personality disorder; drug or alcohol disorder; untreated medical disorder; any previous or current central nervous system (CNS) disease; or MRI safety issues. In addition to the above criteria, potential controls were excluded if there was evidence of any current or past psychiatric disorder. Patients were followed up over 1 year for evidence of recurrence, current central nervous system (CNS) disease; or fMRI safety issues.

Blood oxygen level-dependent (BOLD) data acquisition: gradient echo-echo planar images were acquired using a Philips 3T system during two separate 10 min sessions of a Go/No-Go (GNG) paradigm. Following $T_2$- image stabilisation, 252 volumes of 36 contiguous descending slices were collected (image matrix $64 \times 64$, voxel size $3 \text{ mm} \times 3 \text{ mm} \times 3 \text{ mm}$, field of view $19.2 \text{ cm}$, echo time $40 \text{ ms}$ and repetition time $2300 \text{ ms}$). All participants received standardised preparation aimed at minimising performance variance and anxiety (including scripted explanation, practice sessions of the task and habituation within the scanner).

The GNG paradigm has been previously reported in detail but is summarised here. Go (x) or No-Go (k) stimuli were presented on a projected screen for 267 ms; interstimulus interval was jittered and pseudorandom between 3100 and 3700 ms, so that each participant had either 159 or 160 stimuli per block of which 32 or 33 were No-Go. Participants were asked to respond as quickly as possible (by a single button press) when shown the letter ‘x’ and to withhold response when shown the letter ‘k’. The only explicit feedback used during task was the message ‘too slow’, shown for correct responses to ‘x’ that were delayed beyond an individually calculated time ceiling, derived from response times in the pre-fMRI practice sessions.

**BOLD data functional connectivity analysis**

First-level analysis

The PAR/REC format data from the 3T Philips system were converted to NIfTI format using the program dci2nii (www.mccauslandcenter.sc.edu/micro/mricron/dci2nii.html) based on MIRion (www.mccauslandcenter.sc.edu/micro/mricron). The converted images were then pre-processed using DPARSFA (www.restfmri.net) based on REST (www.restfmri.net) and SPM8 (www.filion.ucl.ac.uk/spm). During pre-processing, images were reoriented, slice timed, spatially realigned, co-registered, segmented, normalised and smoothed to 8 mm. The MRI time series was then subject to linear detrending and temporal bandpass filtering (0.01–0.08 Hz) before regressing out motion parameters, global mean signal, white matter signal and cerebrospinal fluid signal (aimed at removing spurious fluctuations not involved in specific regional correlations). Following methodology validated in task-based functional connectivity analysis,23,24 transformed correlation coefficients (z-scores) were calculated to generate seed-region based functional connectivity z (FCz) maps in DPARSFA, based on 8 mm radius seeds in the left and right precuneus (essential regional components of the DMN, with coordinates taken from key published literature25). Since the coordinates were initially published in Talairach space, a conversion was made from Talairach to Montreal Neurological Institute (MNI) space for the current analysis, using tal2mni.26 For each participant FCz maps were generated independently for the left and right DMN seeds, each containing the voxel-wise Pearson coefficients of the correlation between the time-series of BOLD variations in the seed region and the rest of the brain.

**Second-level analysis**

This comprised a main analysis, in which single-participant FCz maps were entered into t-tests, using SPM8, to assess whole-brain significance across-group and between-group (controls v. MDD group); a subsidiary analysis, assessing maintenance-phase medication effects, in which single-participant FCz maps were entered into one-factor analyses of variance (ANOVAs) with three levels (unmedicated patients, medicated patients, controls); and a region of interest (ROI) analysis to enable direct comparison of our findings with key literature. The ROI analysis used a small volume correction (SVC) within a 12 mm radius of bilateral dorsomedial prefrontal cortex regions identified by Sheline et al as uniquely important ‘dorsal nexus’ areas within depressed-state MDD exhibiting increased resting-state functional connectivity to several networks including the DMN.15 All between-group tests used age and session as covariates of no interest.

**Significance testing**

In keeping with Chumbley & Friston, significance testing in our main and ROI analysis incorporates spatial extent, reporting clusters surviving correction at false discovery rate-corrected $P (P_{FWE-corr}) <0.05$. Voxels-level statistics are additionally reported where appropriate at family-wise error-corrected $P (P_{FWE-corr}) <0.05$ (for example in the case of extensive clusters crossing anatomically defined regions). Since cluster-level statistics are not provided in SPM8 ANOVA, this part of the subsidiary analysis reports voxel-level $P_{FWE-corr} <0.05$.

For ease of comparison with existing literature, all coordinates have been reported in Talairach space, following conversion from MNI space using the program mni2tal. Significant clusters have been illustrated with Xjview Version 8.11 (www.alivelearn.net/xjview).

**T1 image gyrification analysis**

Surface extraction

Cortical surfaces were reconstructed using FreeSurfer version 5.1.0 on Mac OSX 10.5.8 (http://surfer.nmr.mgh.harvard.edu). Standard procedures were followed, as described by Dale et al. Pre-processing used Schaefer’s method, an extension of Zilles’ gyrification index approach,27 to measure cortical folding patterns for each of the several thousands of vertices across the entire cortical surface. This automated method provides local gyrification indices (LGIs), numerical values assigned in a continuous fashion to each vertex of the reconstructed cortical surface. The LGI of a vertex corresponds to the ratio of the surface area of the folded pial contour (‘buried’ surface) to the outer contour of the cortex (‘visible’ surface) included within a sphere of 25 mm radius drawn around each vertex, in line with previous studies. Thus the
LGI value at each vertex reflects the amount of cortex buried in its immediate locality. Schaer’s index captures both the spatial frequency and the amount of curvature of cortical folds in the locality of each vertex.

Statistical analysis examining the spatial distribution of group differences in gyriﬁcation

A vertex-wise whole brain analysis was performed to localise brain regions showing the most prominent gyriﬁcation differences between groups, assessing gyriﬁcation on a point-by-point basis across the entire brain. The vertex-wise LGI measurement for each participant was mapped on a common spherical coordinate system (fsaverage). A general linear model controlling for the effect of age and gender was used to compute differences in gyriﬁcation between the groups for the right and left hemispheric surfaces, in keeping with published literature. The FreeSurfer version 5.1.0 on Mac OS X 10.5.8 query design estimate contrast (QDEC) tool was used to generate between-group contrasts. To correct for multiple testing we used a permutation method with 10,000 simulations and identified clusters that survived a type 1 error rate of 5% at a cluster inclusion threshold of .05 (whole-brain level)

Results

Participants, clinical and behavioural data

The demographic and clinical data have been previously reported in detail but are summarised here and in Table 1. In total, 42 individuals (20 patients and 22 controls) met the minimum inclusion/exclusion criteria and hence were recruited. Complete migraine_vol2surf option in FreeSurfer to project these DMN nodes onto the reconstructed average cortical surface (fsaverage), alongside the clusters that emerged as significant in the vertex-wise whole-brain gyrification analysis.

| Table 1 Demographic and clinical data for the major depressive disorder (MDD) and control groups |
|-------------------------------------|-----------------|-----------------|
| Control group (n = 20) | MDD group (n = 20) |
| Age, years: mean (range) | 43 (24–63) | 45 (25–63) |
| Male, n (%) | 6 (30) | 7 (35) |
| Estimated IQ (from Quick), mean (range) | 108 (96–130) | 104 (90–120) |
| Baseline Hamilton Rating Scale for Depression, mean (range) | 0.3 (0–1) | 2 (0–7)* |
| Beck Depression inventory-II, mean (range) | 1.8 (0–6) | 8.1 (3–19) |
| Neuroticism (EPQ-R), mean (range) | 2.9 (0–6) | 8.9 (3–12) |
| First-degree relatives with MDD, n (%) | 1 (5) | 14 (70)* |
| Age at first episode of MDD, years: mean (range) | N/A | 27 (14–38) |
| Episodes of MDD, mean (range) | N/A | 4 (2–10) |
| Time since remission, months: mean (range) | N/A | 13 (3–36) |
| Taking any antidepressant, n (%) | 0 | 14 (70)* |
| Group total of antidepressant medication (range) | 0 | 19 (0–2)* |

Quick, Ammons Quick Test; EPQ-R, Short Eysenck Personality Questionnaire – revised; N/A, not applicable.

a. Significant difference between the MDD and control groups, two-tailed t-tests P < 0.05.

b. Significant difference between the MDD and control groups and also within MDD group, with significantly greater amounts of antidepressant medication in the non-recurrence group (two-tailed t-tests P < 0.05).

Demographic data indicated that the control and MDD groups were well matched for age (range 24–63 years), gender, IQ and laterality. The MDD group showed high recurrence (mean of four episodes) but were in stable recovery at the time of data acquisition (mean 13 months).

Paired across-group t-tests (n = 40) showed significantly faster reaction times for error commission trials v. correct response trials (t = 7.11, d.f. = 39, P < 0.001) in keeping with the literature; and significant slowing across-group in reaction times for correct response trials following error commission (t = 6.37, d.f. = 39, P < 0.001), again in keeping with the literature. There were no significant between-group (controls v. MDD group) behavioural differences.

Main task-based functional connectivity analysis (whole-brain level)

Across-group (n = 40) findings

As expected the across-group (n = 40) positive and negative functional connectivity patterns were very similar for the two DMN seed regions in the right and left precuneus (illustrated using results from the right precuneus seed in Fig. 1). Thresholded at t = 5.23, with clusters surviving PFDR-cor < 0.05 (and voxels surviving voxel-level PperiFWE-cor < 0.05), regions of significant positive functional connectivity included bilateral precuneus and posterior cingulate cortex (Brodmann area (BA) 31); bilateral anterior cingulate cortex (BA 10, 32, 24); bilateral medial prefrontal cortex (BA 10); bilateral temporal cortex (BA 21); and bilateral posterior parietal cortex (BA 40). Regions of signiﬁcant negative functional connectivity included bilateral supplemental motor area (BA 6); bilateral inferior orbitofrontal cortex (BA 11); bilateral anterior insula; bilateral precenral gyrus (BA 9); and bilateral dorsolateral prefrontal cortex (BA 10). These results are consistent with the literature.

Between-group findings

At corrected whole-brain cluster-level PFDR-cor < 0.05 there was signiﬁcantly greater functional connectivity for the MDD group > controls from both right and left precuneus seeds to clusters in the right dorsomedial prefrontal cortex (BA 9) with some extension...
into dorsal regions of the right frontal pole (BA 10) (statistics given in Table 2). There was also some evidence of increased functional connectivity (MDD group > controls) to clusters in the left dorsomedial prefrontal cortex (BA 9), when thresholded at \( P < 0.001 \), but this did not survive subsequent whole-brain correction (strongest from the right precuneus seed for the MDD group > controls, cluster extent 20 voxels, cluster-level \( P_{FDR-corr} = 0.054 \) with peak voxel \( t = 4.85 \) at \(-24, 34, 43\)). These findings are illustrated in Fig. 2. There were no cluster-level significant findings for the control > MDD group.

### Subsidiary analysis of medication status (whole-brain level task-based functional connectivity)

Three-group ANOVAs using medicated \( (n = 14) \) and unmedicated \( (n = 6) \) and control \( (n = 20) \) groups investigated the effect of continuing maintenance-phase antidepressant medication (detailed in online Table DS1) on functional connectivity. The ANOVA of left prefrontal seed functional connectivity showed significant main effect of group within a right dorsomedial prefrontal cortex cluster (peak at 30, 36, 39, \( F_{2,75} = 17.44, P_{FWE-corr} = 0.042 \)). Follow-up \( t \)-tests, inclusively masked for a main effect of group at \( P < 0.001 \), were significant for unmedicated patients > controls at whole-brain level (cluster extent 28 voxels, cluster-level \( P_{FDR-corr} = 0.021 \), peak \( t = 5.85 \) at 30, 36, 39). The ANOVA of right prefrontal seed functional connectivity showed main effect that approached significance in the same right dorsomedial prefrontal cortex region (peak at 30, 36, 39, \( F_{2,75} = 16.60, P_{FWE-corr} = 0.075 \)) and given the importance of exploring potential bias through an analysis of potential bias through medication follow-up \( t \)-tests were performed, masked for main effect of group at \( P < 0.001 \), showing whole-brain significance for unmedicated patients > controls (cluster 33 voxels, cluster-level \( P_{FDR-corr} = 0.006 \), peak \( t = 5.76 \) at 30, 36, 39). Figure 3 depicts these main between-group findings, using extracted data from 12 mm radius spheres centred on the peak voxel for main effect within the 3-group ANOVAs.

Prospective follow-up of the MDD group showed that positive medication status was associated with significantly reduced 1-year relapse (relative risk = 0.29, 95% CI 0.10–0.85).

### ROI task-based functional connectivity analysis

A separate ROI analysis assessed the proximity of our whole-brain dorsomedial prefrontal cortex findings to specific bilateral dorsomedial prefrontal cortex ‘dorsal nexus’ regions from the literature (left ROI \(-24, 35, 28\); right ROI \(18, 34, 29\)).\(^\text{11}\) Results of this ROI analysis are presented in Table 3, showing significantly increased task-based functional connectivity, surviving cluster-level correction \( P_{FDR-corr} < 0.05 \), between bilateral prefrontal regions and clusters within a 12 mm radius sphere centred on the bilateral dorsomedial prefrontal cortex ‘dorsal nexus’ regions.

### Gyri/fication analysis

There was significant bilateral hypogyrification (cluster-wise \( P < 0.001 \), permutation corrected for multiple testing, cluster inclusion threshold \( P = 0.05, n = 10000 \)) in the MDD group extending across bilateral medial surface regions incorporating the precuneus. Additionally, there was hypergyrification (cluster-wise \( P < 0.001 \), permutation corrected for multiple testing, cluster inclusion threshold \( P = 0.05, n = 10000 \)) in the MDD group in a more anterior region incorporating the left anterior cingulate cortex. These results are illustrated in Fig. 4.

To assess the effect of medication in this gyri/fication analysis we compared medicated and unmedicated patients at the lenient statistical threshold of \( P = 0.10 \) but did not detect any significant differences. The results of this analysis were unaffected when re-analysed using ICV as an additional covariate.

As shown in Fig. 4, the left prefrontal hypogyrification incorporated the precuneus (DMN) seed used in our functional connectivity analysis and originally identified by Sheline \( et al.\)\(^\text{11}\) Additionally, we mapped Sheline \( et al.\)’s left ‘dorsal nexus’ \((-24, 35, 28\) spherical ROI of 12 mm radius) onto the inflated surface to study the overlap with the gyri/fication maps. The BA 32 part of ‘dorsal nexus’ (but not the BA 8 or BA 9 areas) showed an overlap with the hypergyric anterior cingulate cortex cluster identified here. Task-based functional connectivity analysis based on this hypergyric anterior cingulate cortex cluster (presented in the online data supplement) identified only one significant finding, of hyper connectivity for the control > MDD group within
Biological vulnerability to depression

Discussion

Our data provide the first direct evidence of task-based DMN hyperconnectivity within recovered-state MDD, confirming a recently published hypothesis.10 This adds to resting-state functional connectivity evidence from depressed-state MDD11 and never-depressed, high vulnerability cohorts,9 supporting the idea that DMN hyperconnectivity is a core feature of the highly recurrent disorder of MDD, extending across different states into apparent clinical recovery. Viewed as a biological substrate, the persistence of DMN hyperconnectivity into recovery is consistent with well-established psychological models that have long identified the persistence of psychological-level risk factors into recovered-state MDD.34 More specifically, because of its association with internal focus, DMN hyperconnectivity is a plausible substrate for rumination, observed across states of MDD and described by Beck as involving disproportionate allocation of resources from, ‘the external environment to internal experiences’.35 At a brain network level, ‘the interference hypothesis’ holds that persistence

Table 2 Whole-brain significant functional connectivity from right and left precuneus (default mode network) seeds (+/–7, –60, 21; from Sheline et al8) a

<table>
<thead>
<tr>
<th>MDD group vs control group</th>
<th>Cluster size (voxels)</th>
<th>Region</th>
<th>Brodmann area</th>
<th>Cluster-level P_{FDR-corr}</th>
<th>Peak t score</th>
<th>Peak Z score</th>
<th>Peak coordinates (x, y, z)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Right DMN seed</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Right dmPFC</td>
<td>45</td>
<td>9</td>
<td>0.001</td>
<td>4.45</td>
<td>4.18</td>
<td>30, 40, 34</td>
<td></td>
</tr>
<tr>
<td>Left DMN seed</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Right dmPFC</td>
<td>27</td>
<td>9</td>
<td>0.025</td>
<td>4.46</td>
<td>4.19</td>
<td>30, 40, 34</td>
<td></td>
</tr>
<tr>
<td>Right dmPFC</td>
<td>25</td>
<td>10</td>
<td>0.025</td>
<td>4.57</td>
<td>4.28</td>
<td>21, 56, 14</td>
<td></td>
</tr>
</tbody>
</table>

MDD, major depressive disorder; DMN, default mode network; dmPFC, dorsomedial prefrontal cortex. a. Reports statistics where whole-brain, cluster-level P survived false discovery rate-corrected < 0.05. There were no cluster-level significant findings for the control>MDD group.
of relatively high DMN connectivity into task interferes with adaptive switching to more appropriate goal-oriented brain networks. More recently there have been indications that these networks overlap to an unusual degree within MDD (reviewed in Marchetti et al[38]) and that the most robustly identified hub in our task-based DMN analysis (right dorsomedial prefrontal cortex, BA 9) acts as a ‘dorsal nexus’, strongly connected to several networks within the depressed-state of MDD. Since we have previously shown event-related fMRI hypoactivity within this right ‘dorsal nexus’ region during active processing (for example of error commission) in recovered-state MDD,37 then invoking the ‘interference hypothesis’36 supports the proposition that within recovered-state MDD persistent excessive DMN activity during task, most prominently involving the right ‘dorsal nexus’, interferes with capacity to appropriately switch this dorsomedial prefrontal cortex (BA 9) region to its role in more ‘task positive’ (active) networks; resulting in cognitive and attentional bias that increases the risk of depression.

The functional connectivity findings were associated with bilateral hypogyrification incorporating the precuneus, broadly consistent with the only previous MDD gyrification study that we are aware of, which did not incorporate a functional connectivity analysis but demonstrated hypogyrification in a depressed-state MDD cohort extending bilaterally into posterior cingulate/precuneus areas.37 Our data extend this finding by consistent with the only previous MDD gyrification study that we are aware of, which did not incorporate a functional connectivity analysis but demonstrated hypogyrification in a depressed-state MDD cohort extending bilaterally into posterior cingulate/precuneus areas.37 Our data extend this finding by

<table>
<thead>
<tr>
<th>MDD group &gt; control group</th>
<th>Cluster size voxels</th>
<th>Region Brodmann area</th>
<th>Cluster-level ( P_{\text{corrected}} )</th>
<th>Peak ( t ) score</th>
<th>Peak ( z ) score</th>
<th>Peak coordinates ( x, y, z )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Right precuneus</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Right dmPFC</td>
<td>20</td>
<td>9</td>
<td>0.002</td>
<td>4.10*</td>
<td>3.88</td>
<td>24, 39, 28</td>
</tr>
<tr>
<td>Left precuneus</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Right dmPFC</td>
<td>10</td>
<td>9</td>
<td>0.040</td>
<td>4.04*</td>
<td>3.83</td>
<td>27, 36, 29</td>
</tr>
<tr>
<td>Left dmPFC</td>
<td>15</td>
<td>9</td>
<td>0.006</td>
<td>3.70*</td>
<td>3.54</td>
<td>21, 31, 29</td>
</tr>
</tbody>
</table>

MDD, major depressive disorder; DMN, default mode network; dmPFC, dorsomedial prefrontal cortex.

*Voxel-level significance \( P_{\text{corrected}} < 0.05 \).

Limitations

We acknowledge the potential bias introduced by maintenance-phase antidepressant medication in the MDD group. However, additional targeted analyses did not find any association between either task-based functional connectivity or gyrification and positive medication status. Indeed, where there was any association with medication status (in task-based functional connectivity), this was most abnormal (from both DMN seeds) in patients who had stopped maintenance-phase medication prior to scanning. Although we could not find any indication that maintenance-phase antidepressant medication caused the observed differences in DMN functional connectivity or gyrification, we should remain cautious that this part of the analysis (relying on relatively small groups) may have been underpowered to detect real differences.

Additionally, we have presented a seed-region DMN functional connectivity analysis using task-based data, following on from extensive literature indicating the validity of this approach (for example Rissman et al,23 Hampson et al,24 Fair et al40), and evidence of persisting, although relatively attenuated DMN activation during a range of tasks, including externally focused activity.40,41 Although this approach has been shown to provide qualitatively similar results to the analysis of resting-state functional connectivity data, caution should be exercised in the quantitative differences that may exist between these approaches.40 This issue is likely to be most problematic when making within-group task-based v. resting-state functional connectivity comparisons and should be much less problematic in the analysis presented here, where we made between-group comparisons focused purely on task-based DMN functional connectivity (i.e. not making experimental comparisons with resting-state). We should also remain conscious of this issue in considering resting-state and task-based studies from the literature; different approaches that often retain mutual relevance, as here.9,11

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Table 3 Results of the region of interest analysis based on coordinates for the dorsomedial prefrontal cortex ‘dorsal nexus’ regions given in Sheline et al[8,9]

<table>
<thead>
<tr>
<th>Region of Interest</th>
<th>Cluster Size (Voxels)</th>
<th>Brodmann Area</th>
<th>Cluster-level ( P_{\text{corrected}} )</th>
<th>Peak ( t ) Score</th>
<th>Peak ( z ) Score</th>
<th>Peak Coordinates ( x, y, z )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Right precuneus</td>
<td>20</td>
<td>9</td>
<td>0.002</td>
<td>4.10*</td>
<td>3.88</td>
<td>24, 39, 28</td>
</tr>
<tr>
<td>Right dmPFC</td>
<td>10</td>
<td>9</td>
<td>0.040</td>
<td>4.04*</td>
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<td>0.006</td>
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</tr>
</tbody>
</table>

DMN, default mode network; dmPFC, dorsomedial prefrontal cortex.
Strengthes
We present the first data on DMN connectivity (task-based) in recovered-state MDD and provide the first multimodal analysis relating functional connectivity findings in MDD to cortical gyrification. These data test a specific and important hypothesis coming out of the MDD literature.

Implications
Within apparent clinical recovery from MDD there are significant and apparently linked abnormalities in DMN structure (identified through hypogyrification of key hubs) and function (identified through task-based DMN hyperconnectivity). These new findings strengthen our knowledge of the biological-level vulnerability to MDD by confirming and extending an important hypothesis based on previous research. When assessed alongside event-related fMRI evidence, it seems possible that the identified cortical gyrification abnormalities.

Further research is needed to confirm the more limited findings that DMN functional hyperconnectivity is greatest in patients with MDD who have discontinued maintenance-phase medication; and the theory that this networked brain activity may represent a more dynamic indicator of MDD vulnerability linked to relatively stable cortical gyrification abnormalities.

References
17 Hyler SE. Personality Diagnostic Questionnaire (PDQ-4+). New York State Psychiatric Institute, 1994.
Table DS1 Maintenance-phase antidepressant medication taken within the patient group, grouped by non-recurrence, recurrence or loss to follow-up over 1 year

<table>
<thead>
<tr>
<th></th>
<th>Non-recurrence patient group (n=11)</th>
<th>Recurrence patient group (n=7)</th>
<th>Lost to follow-up (n=2)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number Taking Drug</td>
<td>Average Dose (mg)</td>
<td>Number Taking Drug</td>
</tr>
<tr>
<td>Venlafaxine</td>
<td>4</td>
<td>225</td>
<td>2</td>
</tr>
<tr>
<td>Mirtazapine</td>
<td>1</td>
<td>15</td>
<td>1</td>
</tr>
<tr>
<td>Fluoxetine</td>
<td>1</td>
<td>20</td>
<td>0</td>
</tr>
<tr>
<td>Sertraline</td>
<td>2</td>
<td>100</td>
<td>0</td>
</tr>
<tr>
<td>Citalopram</td>
<td>1</td>
<td>50</td>
<td>0</td>
</tr>
<tr>
<td>Trazodone</td>
<td>1</td>
<td>250</td>
<td>0</td>
</tr>
<tr>
<td>Dosulepin</td>
<td>1</td>
<td>225</td>
<td>0</td>
</tr>
<tr>
<td>Lithium</td>
<td>3(^b)</td>
<td>733</td>
<td>0</td>
</tr>
<tr>
<td>Lamotrigine</td>
<td>1(^b)</td>
<td>50</td>
<td>0</td>
</tr>
</tbody>
</table>

n/a, not applicable.

a. Overall, 14 patients took 19 medications (at a maximum of two medications each); and 6 patients were not on any antidepressant medication.
b. All psychiatric medication was prescribed for unipolar major depressive disorder, with lithium and lamotrigine prescribed as augmenting agents to relieve previous episodes of unipolar depression, and continued thereafter as maintenance-phase medication to reduce recurrence risk.

Data supplement

We conducted a functional connectivity analysis based in the hypergyric left anterior cingulate cortex cluster identified in the gyrification analysis using an 8 mm seed region (as in the main default mode network analysis) centred on the peak coordinate for hypergyrification (−5, 30, 9). Across-group (n=40) findings, thresholded as in the main functional connectivity analysis (T=5.23), showed positive connectivity with rostral and ventral extensions of the anterior cingulate cortex (BA 24 and BA 32), medial prefrontal cortex (BA 10) and with the posterior anterior cingulate cortex (BA 31). There was no significant hyperconnectivity in the patient group > controls, either at whole-brain level or within a small volume correction of the ‘dorsal nexus’ sites. There was one significant area of hyperconnectivity for controls > patients at whole-brain cluster-level, within a left posterior temperoparietal area incorporating the supramarginal gyrus (cluster 33 voxels, cluster-level \(P_{FDR-corr}=0.005\), peak \(T=4.24\) at −45, −48, 27).
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