Cingulate networks associated with gray matter loss in Parkinson's disease show high expression of cholinergic genes in the healthy brain

Arlin Keo1,2 | Oleh Dzyubachyk3 | Jeroen van der Grond3 | Anne Hafkemeijer,3,4,5 | Wilma D.J. van de Berg6 | Jacobus J. van Hilten7 | Marcel J.T. Reinders1,2 | Ahmed Mahfouz1,2,8

1Leiden Computational Biology Center, Leiden University Medical Center, Leiden, The Netherlands
2Delft Bioinformatics Lab, Delft University of Technology, Delft, The Netherlands
3Department of Radiology, Leiden University Medical Center, Leiden, The Netherlands
4Department of Methodology and Statistics, Institute of Psychology, Leiden University, Leiden, The Netherlands
5Leiden Institute for Brain and Cognition, Leiden University, Leiden, The Netherlands
6Department of Anatomy and Neurosciences, Amsterdam UMC, location VUmc, Amsterdam, The Netherlands
7Department of Neurology, Leiden University Medical Center, Leiden, The Netherlands
8Department of Human Genetics, Leiden University Medical Center, Leiden, The Netherlands

Correspondence
Ahmed Mahfouz; Leiden University Medical Center, Research Building, Einthovenweg 20, 2333 ZC, Leiden, The Netherlands.
Email: a.mahfouz@lumc.nl

Funding information
The Netherlands Technology Foundation (STW); The Dutch Research Council (NWO); Alzheimer Netherlands; LECMA; Amsterdam Neuroscience; Dutch Research council (ZonMW); Stichting Parkinson Fonds; Alzheimer association; MJ Fox foundation and Rotary Aalsmeer-Uithoorn

Abstract
Structural covariance networks are able to identify functionally organized brain regions by gray matter volume covariance across a population. We examined the transcriptomic signature of such anatomical networks in the healthy brain using postmortem microarray data from the Allen Human Brain Atlas. A previous study revealed that a posterior cingulate network and anterior cingulate network showed decreased gray matter in brains of Parkinson's disease patients. Therefore, we examined these two anatomical networks to understand the underlying molecular processes that may be involved in Parkinson's disease. Whole brain transcriptomics from the healthy brain revealed upregulation of genes associated with serotonin, GPCR, GABA, glutamate, and RAS-signaling pathways. Our results also suggest involvement of the cholinergic circuit, in which genes NPPA, SOSTDC1, and TYRP1 may play a functional role. Finally, both networks were enriched for genes associated with neuropsychiatric disorders that overlap with Parkinson's disease symptoms. The identified genes and pathways contribute to healthy functions of the posterior and anterior cingulate networks and disruptions to these functions may in turn contribute to the pathological and clinical events observed in Parkinson's disease.

KEYWORDS
Allen Human Brain Atlas, brain imaging, neuroinformatics, spatial transcriptomics, structural covariance networks

Edited by: Dr. Yolanda Smith
1 | INTRODUCTION

Parkinson’s disease (PD) is a neurodegenerative disorder characterized by the impairment of diverse motor and nonmotor symptoms that get progressively worse over time (Goedert et al., 2012). The decline in clinical performance has been associated with changes in morphological properties of structural and functional neuroimaging networks (Lucas-Jiménez et al., 2016; de Schipper et al., 2017; Wang et al., 2016). In turn, studies have investigated the relationship between imaging networks and genetic risk factors associated with PD to provide new insights into the pathogenesis of PD (Aarsland et al., 2017; Sampedro et al., 2019; van der Vegt et al., 2009; Winder-Rhodes et al., 2015). However, less is known about the functions that underlie the spatial organization of brain regions contributing to PD. To identify the molecular mechanisms underlying changes in structural and functional networks in PD, imaging data have been integrated with brain-wide healthy gene expression from the Allen Human Brain Atlas (AHBA) (Arnatkevičiūtė et al., 2019; Hawrylycz et al., 2015). Regional brain atrophy in PD patients was correlated with the expression of genes implicated in trans-synaptic alpha-synuclein transfer (Freeze et al., 2018), and a loss of regional connectivity in PD patients was correlated with the regional expression of MAPT in the healthy brain (Rittman et al., 2016). These studies showed that combining imaging data in PD and gene expression from the healthy brain can shed light on the molecular mechanisms underlying the morphological differences between PD and controls.

Structural covariance networks (SCNs) identify brain regions that covary in gray matter volume across a population and can reveal functional network organizations (Alexander-Bloch et al., 2013). SCNs have been shown to be dysregulated in different neurological disorders (Alexander-Bloch et al., 2013; Coppen et al., 2016; Huang et al., 2017; Liu et al., 2019; Spreng & Turner, 2013), and gray matter variations in SCNs can be explained by transcriptomic similarity and structural connectivity (Romero-Garcia et al., 2018; Yee et al., 2018). Hafkemeijer et al. (Hafkemeijer et al., 2014) identified nine SCNs based on gray matter variation among healthy middle-aged to older adults. Gray matter volume in four of these nine networks was negatively associated with age: a subcortical network, sensorimotor network, posterior cingulate networks, and anterior cingulate network. Two of these networks were found to show loss of gray matter volume in PD patients beyond the effects of aging: the posterior cingulate network and anterior cingulate network (de Schipper et al., 2017). Atrophy within these two networks was also associated with cognitive impairment and daytime sleepiness, respectively. Together, these studies revealed how brain networks change in aging and PD, but the molecular mechanisms contributing to the relevant SCNs remain unclear.

Here, we investigated the transcriptomic signatures of the anterior and posterior cingulate networks within the healthy brain. By integrating the nine SCNs with spatial gene expression data from the Allen Human Brain Atlas, we showed that genes highly expressed in the posterior and anterior cingulate networks were associated with multiple neurotransmitter signaling pathways as well as with memory-related, pain-related, and neuropsychiatric disorders. In addition, both networks showed high expression of cholinergic marker genes that are known to act as regulators of extracellular signaling. Our results provide new insights into the molecular processes underlying anatomical network function and aids in better understanding the selective progression of PD.

2 | MATERIALS AND METHODS

2.1 Transcriptomic data preprocessing

To understand transcriptomic signatures of nine anatomical networks of the healthy brain, we analyzed gene expression data from the AHBA, a postmortem microarray data set of 3,702 anatomical brain regions from six nonneurological individuals (5 males and 1 female, mean age 42, range 24–57 years) (Hawrylycz et al., 2015). For two out of six donors, samples were available for two hemispheres, while for the remaining four donors there were only samples from the left hemisphere. We analyzed both hemispheres simultaneously whenever this was possible; otherwise, we used data from one hemisphere. Normalized gene expression from the AHBA was downloaded online (http://human.brain-map.org/). To filter and map probes to genes, the data were concatenated across the six donors. We removed 10,521 probes with missing Entrez IDs, and 6,068 probes with low presence as they were expressed above background in <1% of the samples (PA-call containing presence/absence flag) (Hawrylycz et al., 2015). The remaining 44,072 probes were mapped to 20,017 genes with unique Entrez IDs using the collapseRows-function in R-package WGCNA v1.64.1 (Langfelder & Horvath, 2008) as follows: (a) if there is one probe, that one probe is chosen, (b) if there are two probes, the one with maximum variance across all samples is chosen (method=”maxRowVariance”), (c) if there are more than two probes, the probe with the highest connectivity (summed adjacency) is chosen (connectivityBasedCollapsing=TRUE).

For visualization of gene expression in heatmaps, data were Z-score normalized across all samples for each brain donor separately. Heatmaps were plotted using R-package ComplexHeatmap v2.0.0 (Gu et al., 2016). Genes were clustered using complete linkage with Euclidean distances. The same color scale for gene expression was used for all heatmaps.
2.2 Mapping AHBA samples to SCNs of the healthy brain

We focused on anatomical networks that were previously defined in an MRI study based on whole brain gray matter volume covariation in 370 middle-aged to older adults between 45 and 85 years (51.9% females) (Hafkemeijer et al., 2014). All subjects in this MRI study did not have a history of psychiatric or neurodegenerative disorders. Written informed consent was obtained from all participants in accordance with the Declaration of Helsinki. The Medical Ethical Committee of the Leiden University Medical Center approved the study. Nine networks were defined and named according to the presence of the main structures: thalamus (Network A), lateral occipital cortex (Network B), posterior cingulate cortex (Network C), anterior cingulate cortex (Network D), temporal pole (Network E), putamen (Network F), and cerebellum (Networks G, H, and I). The same networks were previously investigated for loss of integrity in 159 PD patients from the same age range (36.5% females) (de Schipper et al., 2017). PD patients were recruited from the outpatient clinic for Movement Disorders of the Department of Neurology of Leiden University Medical Center (LUMC) and nearby university and regional hospitals. Written consent was obtained from all participants, and the Medical Ethics Committee of the LUMC approved the study. Samples from each one of the six donors were combined by meta-analysis of the Leiden University Medical Center approved the study. The between-brain variance (tau²) was estimated for all 20,017 genes. Genes were differentially expressed within the posterior cingulate network or the anterior cingulate network compared to the other networks combined when the absolute FC > 1 and the BH-corrected p-value < .05. To assess the reproducibility of the differentially expressed genes, we calculated the differential stability of all 20,017 genes in our dataset. This value was calculated as the average Pearson's correlation between all 15 possible pairs of six donors from the AHBA. The individual correlations for each pair of donors were calculated across samples that were shared between two donors.

2.4 Functional enrichment analysis

Pathway analysis was done with the ReactomePA R-package version 1.28 using the function enrichPathway searching for human pathways. All 20,017 genes in the AHBA dataset were set as background genes. Pathways with a minimum size of 10 genes and BH-corrected p < .05 were considered significant. An additional functional enrichment test for GO-terms was done with clusterProfiler R-package version 3.18.1. The same background genes were used as before and GO-terms with BH-corrected p < .05 were considered significant.

2.5 Cell-type marker enrichment

Gene markers for 28 cell-types were downloaded from the NeuroExpresso database (http://neuroexpresso.org/) using markers from all brain regions. These have been identified in a cross-laboratory dataset of cell-type specific transcriptomes from the mouse brain (Mancarci et al., 2017). To assess their expression, Entrez IDs of the mouse cell-type specific markers were converted to human homologs (homologene R-package version 1.4) and filtered for genes present in the AHBA dataset (Table S1). Two markers with different mouse gene IDs (14,972, H2-K1, microglial, and 15,006, H2-Q1 serotonergic) were converted to the same human gene ID (3,105, HLA-A) and therefore removed before analysis. For cell-type enrichment, we assessed which cell-type markers were over-represented among the differentially expressed genes. For 17 cell-types that had at least six markers (astrocyte, Bergmann, cerebellar granule, dentate granule, ependymal, GabaRKN, hypocretinergic, microglia, activated microglia, deactivated microglia, noradrenergic, oligo, purkinje, serotonergic, spinal cord cholinergic, spiny, and thalamus cholinergic), we assessed the significance with the hypergeometric test and p-values were corrected for all 17 cell types (BH-corrected p < .05).
We performed an additional functional enrichment test with expression weighted cell-type enrichment (EWCE) analysis (Skene & Grant, 2016) that makes use of single-cell transcriptome data to estimate the probability of a gene list being associated with a cell-type. For this purpose, we processed cell-type data from the NeuroExpresso database and selected gene markers for 28 cell-types that were proposed by NeuroExpresso. BH-corrected p-values < .05 were considered significant.

2.6 | Enrichment of disease-associated genes

Differentially expressed genes were also assessed for the over-representation of disease-associated genes from DisGeNET (Piñero et al., 2017). A table of 628,685 gene-disease associations was obtained from DisGeNET version 6.0 (July 2019) from http://www.disgenet.org/ website. A hypergeometric test was used to assess the significance of overlapping genes (p < .05), and p-values were BH-corrected for 24,166 diseases. The odds ratio (OR) for cell-type and disease enrichment was calculated using the DescTools R-package.

3 | RESULTS

3.1 | Transcriptomics of the posterior and anterior cingulate networks

We analyzed the transcriptomes of healthy subjects across nine anatomical networks defined by structural covariance of gray matter volume among healthy middle-aged to older adults (Hafkemeijer et al., 2014). For this we used the AHBA microarray dataset of spatial gene expression in postmortem brains of six nonneurological donors and samples were mapped to each one of the nine Networks A- I (Table 1) based on their spatial location (Figure 1). We focused on the posterior cingulate network (Network C) and the anterior cingulate network (Network D) that showed loss of gray matter in PD patients (Figure 2a,b) (de Schipper et al., 2017) and characterized their transcriptional signatures by comparing them to the remaining seven networks together.

Whole genome differential expression analysis showed a large overlap of genes that were differentially expressed in the same direction in the two networks. We found that 73 genes in Network C and 39 genes in Network D were downregulated, of which 25 genes overlapped between both networks (Figure 2c,d and Tables S2 and S3). Furthermore, 200 genes in Network C and 269 genes in Network D were upregulated, for which 144 genes overlapped (Tables S4 and S5). To find out whether our significant genes have reproducible expression across the six donors, we assessed the differential stability, which is the average Pearson’s correlation between all 15 possible pairs of the six donors, an approach that has previously been applied to the same dataset (Hawrylycz et al., 2015). Most differentially expressed genes (>92%) were among the top decile of all 20,017 genes corresponding to a differential stability value >0.73 (Figure S1). Among the differentially expressed genes in the posterior and anterior cingulate networks, no PD-implicated genes were found that arise from familial and genome-wide association studies (Bonifati, 2014; Chang et al., 2017; Nalls et al., 2014).

For functional interpretation of the differentially upregulated genes, we further assessed the enrichment of genes associated with biological pathways in the Reactome Pathway Database (see Methods, Table S6). As both Networks C and D shared many differentially expressed genes, they also shared similar pathways: transcriptional regulation by MECP2, GPCR (G protein-coupled receptor) signaling, voltage gated potassium channels, and neurotransmitter receptor and postsynaptic signal transmission (Figure 2e). For better interpretation, we assessed the hierarchical relationships between enriched pathways based on the ontology of the Reactome Pathway Database. Pathways that describe more general biological functions are found at the top of the hierarchy (closer to the root) and were enriched for both Networks C and D.

<table>
<thead>
<tr>
<th>Donors</th>
<th>Network</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
</tr>
<tr>
<td>Donor 9,861</td>
<td>72</td>
</tr>
<tr>
<td>Donor 10,021</td>
<td>79</td>
</tr>
<tr>
<td>Donor 12,876</td>
<td>37</td>
</tr>
<tr>
<td>Donor 14,380</td>
<td>38</td>
</tr>
<tr>
<td>Donor 15,496</td>
<td>34</td>
</tr>
<tr>
<td>Donor 15,697</td>
<td>49</td>
</tr>
<tr>
<td>Total</td>
<td>309</td>
</tr>
</tbody>
</table>

Note: A: Thalamus; B: Lateral occipital cortex; C: Posterior cingulate cortex; D: Anterior cingulate cortex; E: Temporal pole; F: Putamen; G, H, I: Cerebellum.
that describe more specific biological functions are lower in the hierarchy and were enriched for either Network C or Network D. Network C was additionally related to more specific pathways such as lysosphingolipid and LPA receptors, GABA receptor activation, RAS-signaling mediated by NMDA receptors, glutamate binding, activation of AMPA receptors and synaptic plasticity, and long-term potentiation. Network D was additionally associated with serotonin receptors. To verify our results, we performed another functional analysis and assessed the enrichment of Gene Ontology (GO) terms. Again, Network C and Network D shared similar functional terms, for example, potassium ion transport, GPCR signaling pathway, and regulation of neurotransmitter receptor activity. Overall, we found GO terms that were similar to the pathways identified with Reactome (Table S7 and S8).

3.2 Cholinergic cell markers are highly expressed within cingulate networks

The composition of specific cell-types can shape the transcriptomic features of anatomical networks. Therefore, we analyzed whether genes differentially expressed in the posterior and anterior cingulate networks were enriched for cell-type specific marker genes from the NeuroExpresso database (Mancarci et al., 2017). To assess the expression of cell-types, we averaged the expression of marker genes associated with a cell-type. Both Network C and Network D showed high expression of marker genes for brainstem cholinergic cells, GabaSSTReln, GabaVIPReln, glutamatergic, and pyramidal cells (Figure 3 and Figure S2).

Among the differentially upregulated genes in Network C and Network D, we found 10 marker genes representing six cell-types: astrocyte, Bergmann, GabaVIPReln, hypocretinergic, pyramidal, and thalamus cholinergic (Table 2). Markers that were significantly upregulated in Network C were also significantly upregulated in Network D. In both networks, the 10 markers were highly expressed in cortical regions, including the cingulate gyrus and lowly expressed in limbic regions (Figure 4 and Figure S3).

Cell-type enrichment analysis revealed that only markers for thalamus cholinergic cells were significantly over-represented among genes that were upregulated in Network D (OR = 17.12 and \( p = 2.01 \times 10^{-2} \)). The responsible markers \( NPPA, SOSTDC1, \) and \( TYRP1 \) showed high expression within Network D, as well as in most parts of Network C (Figure 4). An additional enrichment analysis that makes use of single cell transcriptome data (EWCE) revealed that genes upregulated in both Networks C and D were significantly enriched for thalamus cholinergic cells (Figure 5). Interestingly, while other thalamus cholinergic marker genes showed high expression in limbic samples and low expression in cortical samples within both networks, \( NPPA, SOSTDC1, \) and \( TYRP1 \) showed opposite expression patterns with low expression in limbic samples, including the thalamus, and high expression in cortical samples (Figure S4).
3.3 Cingulate networks are enriched for genes associated with disorders relevant to PD

Dysregulation of functional networks may result in a broader spectrum of disorders than PD. Therefore, we assessed which disease-associated genes from DisGeNET were overrepresented among the differentially upregulated genes in Network C as well as Network D. Since both networks shared many upregulated genes, similar disease associations were also found. We found that...
genes upregulated in both networks were significantly associated with epileptic and nonepileptic seizures, many mental disorders (bipolar, panic, autistic, [age-related] memory, mood, major depressive, and anxiety disorder), pain, and schizophrenia (Figure 6). Network C, the posterior cingulate network, was more related to memory and pain-related disorders, while Network D, the anterior cingulate network, was more related to mental and neuropsychiatric disorders. Furthermore, we found that differentially expressed genes were associated with disorders related to alcohol and drug abuse. These included withdrawal symptoms, drug withdrawal symptoms, alcohol withdrawal syndrome, cocaine dependence, cocaine abuse, and cocaine-related disorders. In summary, we found associations with disorders that relate to defects in brain functions that are relevant to PD.

4 | DISCUSSION

We examined transcriptomic signatures of the healthy brain in brain regions defined by SCNs that were identified in an earlier imaging analysis study (Hafkemeijer et al., 2014). In particular, we focused on molecular mechanism underlying two SCNs that were previously associated with decreased gray matter in PD patients (de Schipper et al., 2017) and were named the posterior cingulate network (Network C) and anterior cingulate network (Network D) as they mostly covered these anatomical areas. Pathway analysis revealed genes related to GPCR signaling, transcriptional regulation by MECP2, and neurotransmitter receptors and postsynaptic signal transmission. We found that genes that were upregulated in the posterior cingulate gyrus and anterior cingulate gyrus were also enriched for thalamus
and thalamus in PD patients may contribute to the transition from PD to PD with dementia (Ballinger et al., 2016). We found that glutamatergic and GABAergic marker genes were also highly expressed within the posterior and anterior cingulate networks, although statistical significance could not be assessed due to the small number of marker genes for these cell-types. Interestingly, acetylcholine release by cholinergic neurons affects glutamatergic and GABAergic signaling by altering the synaptic excitability (Buendia et al., 2019; Granger et al., 2015). Moreover, it is thought that dysfunction of cholinergic circuits contributes to cognitive decline associated with neurodegenerative diseases (Ballinger et al., 2016).

Cholinergic marker genes NPPA, SOSTDC1, and TYRP1 were highly expressed in the posterior cingulate network and anterior cingulate network of the healthy brain compared to the other seven SCNs. While the functions of these genes likely involve cholinergic signaling, several studies suggest that they also function as extracellular regulators of multiple other signaling pathways, including cAMP,

### Table 2: Differentially upregulated cell-type marker genes in Network C (posterior cingulate network) and Network D (anterior cingulate network)

<table>
<thead>
<tr>
<th>Gene</th>
<th>Marker</th>
<th>Network C</th>
<th>Network D</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>FC</td>
<td>BH Estimate</td>
<td>BH</td>
</tr>
<tr>
<td>LHX2</td>
<td>Astrocyte</td>
<td>2.21</td>
<td>3.92E-03</td>
</tr>
<tr>
<td>IGFBP2</td>
<td>Astrocyte</td>
<td>0.69</td>
<td>5.80E-02</td>
</tr>
<tr>
<td>RORB</td>
<td>Astrocyte</td>
<td>0.82</td>
<td>3.09E-02</td>
</tr>
<tr>
<td>WIF1</td>
<td>Bergmann</td>
<td>1.02</td>
<td>8.74E-03</td>
</tr>
<tr>
<td>VIP</td>
<td>GabaVIPReln</td>
<td>1.67</td>
<td>4.23E-03</td>
</tr>
<tr>
<td>PCSK1</td>
<td>Hypocretinergic</td>
<td>1.15</td>
<td>1.25E-02</td>
</tr>
<tr>
<td>NEUROD6</td>
<td>Pyramidal</td>
<td>1.90</td>
<td>4.78E-03</td>
</tr>
<tr>
<td>NPPA</td>
<td>ThalamusCholin</td>
<td>1.64</td>
<td>6.98E-03</td>
</tr>
<tr>
<td>TYRP1</td>
<td>ThalamusCholin</td>
<td>0.81</td>
<td>2.41E-02</td>
</tr>
<tr>
<td>SOSTDC1</td>
<td>ThalamusCholin</td>
<td>0.83</td>
<td>1.21E-02</td>
</tr>
</tbody>
</table>

Note: Fold-change (FC) and Benjamin–Hochberg (BH) corrected p-value are shown for cell-type marker genes that were differentially expressed in the two networks compared to the remaining networks. FC >1 and BH <0.05 are highlighted in bold text.

**Figure 4** Expression of differentially upregulated cell-type marker genes in Network C (posterior cingulate network) and Network D (anterior cingulate network). Heatmaps of differentially expressed marker genes (rows) are shown for one of the six donors in the Allen Human Brain Atlas (donor 10,021). Samples from different anatomical substructures within the networks are color annotated (columns). Expression was averaged across samples from an anatomical substructure with the same acronym ignoring left and right hemisphere annotations. See Figure S3 for heatmaps of all six donors from the AHBA and Table S9 for full names of the region-specific acronyms.
Wnt, and β-catenin signaling (Bansho et al., 2017; Brenner et al., 1990; De Vito, 2014; Hirobe, 2011; Kutchko & Siltberg-Liberles, 2013; Millan et al., 2019).

*NPPA* (natriuretic peptide precursor A) and other natriuretic peptides are thought to be involved in a wide range of functions, including neurovascular functions, blood-brain barrier, brain homeostasis, neuroprotection, and synaptic transmission by regulating the release and re-uptake of neurotransmitters such as noradrenalin, dopamine, and glycine (Mahinrad et al., 2016). Impaired function of natriuretic peptides in brains of AD patients could accelerate neurodegeneration and may impair structural integrity of the brain leading to a higher risk of cognitive decline (Mahinrad et al., 2018). Our results suggest that *NPPA* might similarly be involved in PD pathogenesis given its high expression within the anterior and posterior cingulate networks.

*SOSTDC1* (sclerostin domain-containing 1) is known as a negative regulator of bone morphogenetic protein (BMP) and Wnt-signaling, but recent studies also show that *SOSTDC1* regulates natural killer cell maturation and cytotoxicity (Millan et al., 2019). An increased number of natural killer cells have been found in PD, but the actual relevance with PD risk is still unclear (Jiang et al., 2017). The BMP signaling pathway promotes the development of midbrain dopaminergic neurons (Jovanovic et al., 2018), in which *SOSTDC1* may play a role. Furthermore, *SOSTDC1* was upregulated in the striatum of Parkinsonian rats that were treated by subthalamic nucleus high-frequency stimulation and is therefore suggested to have neuroprotective effects (Lortet et al., 2013).

*TYRPI* (tyrosinase-related protein 1) produces melanocytes-specific proteins involved in the biosynthesis of melanin in brain, skin, and eyes (Lu et al., 2011; Wang & Hebert, 2006). Melanoma and PD share genes involved in the synthesis of melanin and dopamine, including *SNCA* which encodes the α-synuclein protein found in Lewy bodies (Pan et al., 2012). Furthermore, neuromelanin is produced almost exclusively in human catecholaminergic neurons and is responsible for the pigmentation of dopaminergic neurons of the substantia nigra and noradrenergic neurons of the locus cereleus (Pavan & Dalpiaz, 2017). It is considered to be protective due to its ability to chelate metals, especially iron for which levels increases with age (Pavan & Dalpiaz, 2017).
The posterior and anterior cingulate networks shared similar highly expressed genes and were likewise associated with similar diseases. Based on our analysis of transcriptomic signatures in the healthy brain, we found that the posterior cingulate network showed stronger associations with memory and pain-related disorders compared to the anterior cingulate networks which showed stronger associations with mental and neuropsychiatric disorders. As part of the default mode network, both the posterior and anterior cingulate cortex have been shown to be dysregulated in neuropsychiatric disorders (Broyd et al., 2009; Öngür et al., 2010). We also found that both networks were associated with alcohol and drug withdrawal symptoms and more specifically cocaine-related disorders. Cocaine abuse has been ambiguously related to PD, for example, cocaine binds to dopamine transport proteins, and cocaine users show excess iron accumulation in the brain. However, there has been no direct association between cocaine usage and an increasing risk to develop PD (Ball et al., 2019). Furthermore, alcohol use disorder has been associated with neurodegenerative diseases, including Alzheimer’s disease and PD, as chronic alcohol intake can induce oxidative stress and trigger the neuroimmune response and excitotoxicity (Kamal et al., 2020).

Although we are interested in brain regions that are vulnerable to PD, our study is limited to transcriptomic data from the healthy brain. In this study, the regions of interest are defined by brain networks based on SCNs and one such a network can comprise of multiple distant and disconnected regions. Therefore, a region of interest in this study cannot be compared with the typical anatomical structures that have been analyzed in previous PD transcriptomic studies. In addition, validation with PD brains is challenging due to the scarcity of spatial transcriptomic data of PD brains. There are few studies that analyzed multiple brain regions in PD, but they only cover few brain regions of interest. To map transcriptomic samples to brain regions defined by SCNs, a high spatial resolution is needed for the transcriptomic data, which is currently not available for PD. Therefore, it will be interesting for future studies to profile the transcriptomes of PD brain regions at a higher spatial resolution.

In transcriptional maps, such as the AHBA, samples are strongly spatially autocorrelated meaning that nearby brain regions share more similar expression patterns than distant brain regions (Fulcher et al., 2020). This may cause a bias in enrichment analyses towards gene sets that are higher co-expressed in the brain and thus describe more general brain-related functions. While there are interesting methods to correct for this spatial bias, they are still being developed. In addition, we believe that our results are not affected by spatial autocorrelation, as our regions of interests, two SCNs, consist of separate distant brain regions that span parts of multiple anatomical brain regions.

In summary, our results highlight molecular mechanisms that underlie two specific SCNs in the healthy brain: the posterior cingulate network and anterior cingulate network. Both SCNs represent anatomical networks that function normally.

**FIGURE 6** Disease associations of Network C (posterior cingulate network) and Network D (anterior cingulate network). Differentially upregulated genes in each network were assessed for the enrichment of disease-associated genes from DisGeNET (hypergeometric test, BH-corrected \( p < .05 \)). Top plot shows odds ratios (ORs) for the number of overlapping genes, and bottom plot shows the significance of overlap indicated with \(-\log_{10}p\)-values (y-axis). Disorders (columns) are sorted based on highest ORs in either one of the networks.
in healthy brains, but their activity is reduced in aging and PD (Hafkemeijer et al., 2014; de Schipper et al., 2017). Our findings suggest that genes involved in multiple signaling pathways, such as serotonin, GPCR, GABA, glutamate, and RAS, contribute to healthy functions of the posterior and anterior cingulate networks. While these observations apply to the healthy brain, they provide insight into the structures that are vulnerable in PD. Further research will be needed to better understand the transcriptomics of brain networks and how they are involved in PD.

ACKNOWLEDGEMENTS

We thank Dr. L. E. Jonkman for her critical insight on the manuscript. This research received funding from The Netherlands Technology Foundation (STW), as part of the STW Project 12721 (Genes in Space). Dr. O. Dzyubachyk received funding from The Dutch Research Council (NWO) project 17126 (3DOMics). Dr. W.D.J. van de Berg received funding from Alzheimer Netherlands and LECMA (ISAO #14536-LECMA #14797) to study transcriptome datasets in the context of Parkinson’s and Alzheimer’s disease and was financially supported by grants from Amsterdam Neuroscience, Dutch Research council (ZonMW), Stichting Parkinson Fonds, Alzheimer association, and the MJ Fox foundation and Rotary Aalsmeer-Uithoorn. Dr. Wilma van de Berg performed contract research and consultancy for Hoffmann-La Roche, Lysosomal Therapeutics, CHDR, and Cross beta Sciences and received research consumables from Hoffmann-La Roche and Prothera. Prof. J.J. van Hilten received grants from Alkemade-Keuls Foundation, Stichting Parkinson Fonds (Optimist Study), The Netherlands Organisation for Health Research and Development (#40-46000-98-101), The Netherlands Organisation for Scientific Research (#628.004.001), Hersenstichting, AbbVie, Hoffmann-La-Roche, Lundbeck, and Centre of Human Drug Research outside the submitted work. This work was partially supported by an NWO Gravitation project: BRAINSCAPES (024.004.012).

CONFLICT OF INTEREST

The authors declare no competing interests.

AUTHOR CONTRIBUTIONS

AK, JJH, MR, and AM designed the study. Imaging data were provided by JG and AH and processed by OD. AK performed the data analysis. AK, WDJB, JJH, MR, and AM interpreted the data and wrote the manuscript with input from all authors. AM and MR supervised the overall project. The final manuscript was read and approved by all authors.

PEER REVIEW

The peer review history for this article is available at https://publons.com/publon/10.1111/ejn.15216.

DATA AVAILABILITY STATEMENT

Transcriptomic data from the AHBAs are publicly available online (http://human.brain-map.org/). Imaging data are available upon request. Scripts to run all analyses can be found online at https://github.com/arlinkeo/pd_scn and were run in R version 4.

ORCID

Arlin Keo https://orcid.org/0000-0002-7501-1033
Oleh Dzyubachyk https://orcid.org/0000-0003-1344-7189
Jeroen van der Gronde https://orcid.org/0000-0002-0185-3158
Anne Hafkemeijer https://orcid.org/0000-0002-2940-4768
Wilma D.J. van de Berg https://orcid.org/0000-0002-6175-5357
Jacobus J. van Hilten https://orcid.org/0000-0002-7030-0362
Marcel J.T. Reinders https://orcid.org/0000-0002-1148-1562
Ahmed Mahfouz https://orcid.org/0000-0001-8601-2149

REFERENCES


SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.