Received: 25 September 2019 | Revised: 7 September 2020 | Accepted: 12 September 2020

DOI: 10.1002/alz.12209

Alzheimer's & Dementia®
THE JOURNAL OF THE ALZHEIMER'S ASSOCIATION

FEATURED ARTICLE

Brain functional network integrity sustains cognitive function despite atrophy in presymptomatic genetic frontotemporal dementia

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Abstract

Introduction: The presymptomatic phase of neurodegenerative disease can last many years, with sustained cognitive function despite progressive atrophy. We investigate this phenomenon in familial frontotemporal dementia (FTD).

Methods: We studied 121 presymptomatic FTD mutation carriers and 134 family members without mutations, using multivariate data-driven approach to link cognitive performance with both structural and functional magnetic resonance imaging. Atrophy and brain network connectivity were compared between groups, in relation to the time from expected symptom onset.

Results: There were group differences in brain structure and function, in the absence of differences in cognitive performance. Specifically, we identified behaviorally relevant structural and functional network differences. Structure-function relationships were similar in both groups, but coupling between functional connectivity and cognition was stronger for carriers than for non-carriers, and increased with proximity to the expected onset of disease.

Discussion: Our findings suggest that the maintenance of functional network connectivity enables carriers to maintain cognitive performance.

KEYWORDS
frontotemporal dementia (FTD), functional magnetic resonance imaging (fMRI), network connectivity, presymptomatic

1 | INTRODUCTION

Across the adult healthy lifespan, the structural and functional properties of brain networks are coupled, and both are predictive of cognitive ability.[1,2] The connections between structure, function, and performance have been influential in developing current models of aging and neurodegeneration.[3–5] However, this work contrasts with the emerging evidence of neuropathological and structural changes many years before the onset of symptoms of Alzheimer's disease (AD) and frontotemporal dementia (FTD).[6–8] Genetic FTD with highly penetrant gene mutations provides the opportunity to examine the precursors of symptomatic disease. Three main genes account for 10% to 20% of FTD cases: chromosome 9 open reading frame 72 (*C9orf72*), granulin (*GRN*), and microtubule-associated protein tau

(*MAPT*). These genes vary in their phenotypic expression and in the age at onset.[9] Despite pleiotropy[10] and environmental and secondary genetic moderation[11,12] all three mutations cause significant structural brain changes in key regions over a decade before the expected age at disease onset,[7,13] confirmed by longitudinal studies.[14,15]

The divergence between early structural change and late cognitive decline provokes the question: how do presymptomatic mutation carriers stay so well in the face of progressive atrophy? We propose that the answer lies in the maintenance of network dynamics and functional organisation.[16] Across the lifespan, functional brain network connectivity predicts cognitive status,[17] and this connectivity-cognition relationship becomes stronger with age.[18–20]

Our overarching hypothesis is that for those at genetic risk of dementia, the maintenance of network connectivity prevents the manifestation of symptoms despite progressive structural changes. A challenge is that neither the anatomical and functional substrates of cognition nor the targets of neurodegenerative disease are mediated by single brain regions: They are distributed across multi-level and interactive networks. We therefore used a multivariate data-driven approach to identify differences in the multidimensional brain-behavior relationship between presymptomatic carriers and non-carriers of mutations in FTD genes. We identified key brain networks[21] from a large independent population-based age-matched data set.[22]

We tested three key hypotheses: (1) presymptomatic carriers differ from non-carriers in brain structure and brain function, but not in cognitive function, (2) brain structure and function correlate with performance in both groups, but functional network indices are stronger predictors of cognition in carriers, and (3) the dependence on network integrity for maintaining cognitive functioning increases as carriers approach the onset of symptoms.

RESEARCH IN CONTEXT

1. Systematic review: The authors reviewed systematically the literature using Web of Science, preprint repositories (eg, BioRxiv) and research citing key articles. The connections between structure, function, and performance have been influential in developing current models of aging and neurodegeneration. We discuss these citations in light of emerging evidence of contrasting views that neuropathological changes occur many years before the onset of symptoms of Alzheimer's disease and frontotemporal dementia.
2. Interpretation: Our results suggest that the maintenance of brain functional network integrity enables presymptomatic carriers of frontotemporal dementia mutations to remain cognitively well despite progressive brain atrophy.
3. Future directions: The novel methods and results will inform the design of pre-symptomatic disease-modifying therapy trials and guide strategies to maintain cognitive function with age and age-related neurodegenerative diseases.

2 | METHODS

2.1 | Participants

Thirteen research sites across Europe and Canada recruited participants as part of an international multicenter partnership, the Genetic Frontotemporal Initiative (GENFI). A total of 313 participants had usable structural and resting state functional magnetic resonance imaging (fMRI) data.[7,13] The study was approved by the institutional review boards for each site, and participants providing written informed consent. Inclusion criteria included anyone over the age of 18 who is symptomatic or an asymptomatic first-degree relative. Five participants were excluded due to excessive head motion (see below), resulting in 308 data sets for further analysis.

Participants were genotyped based on whether they carried a pathogenic mutation in *MAPT*, *GRN*, and *C9orf72*. Mutation carriers were classified as either symptomatic or presymptomatic based on clinician evaluation. Participants were only classified as symptomatic if the clinician judged that symptoms were present, consistent with a diagnosis of a degenerative disorder, and progressive in nature. An additional group of controls, termed non-carriers, comprised mutation-negative family members. In this study, we focus on non-carriers (NC, N = 134) and presymptomatic carriers (PSC, N = 121). Participants and site investigators were blinded to the research genotyping, although a minority of participants had undergone predictive testing outwith the GENFI study. See Table 1 for demographic information and Table 2 for behavioral, cognitive, and neuropsychological information of both groups. In keeping with other GENFI reports, the years to expected onset (EYO) were calculated as the difference between age at assessment and mean age at onset within the family.[7]

2.2 | Neurocognitive assessment

Each participant completed a standard clinical assessment consisting of medical history, family history, functional status, and physical examination, in complement with collateral history from a family member or a close friend. In the current study, 13 behavioral measures of cognitive function were correlated with neuroimaging measures. These included the Uniform Data Set[23]: the Logical Memory subtest of the Wechsler Memory Scale-Revised with Immediate and Delayed Recall scores, Digit Span forwards and backwards from the Wechsler Memory Scale-Revised, a Digit Symbol Task, Parts A and B of the Trail Making Test, the short version of the Boston Naming Test, and Category Fluency (animals). Additional tests included Letter Fluency,

TABLE 1 Demographics of participants included in the analysis, grouped by genetic status as non-carriers (NCs) and presymptomatic carriers (PSCs)

	Gene status group		Statistical tests[a]	
	NC	PSC	X2 or F-test	*P*-value
N	134	121		
Mutated gene, n (%)			0.86	0.649
MAPT	17 (12.7)	19 (15.7)		
GRN	77 (57.5)	63 (52.1)		
C9Orf72	40 (29.9)	39 (32.2)		
Gender, n (%)			0.01	0.908
Male	53 (39.6)	47 (38.8)		
Handedness, n (%)			0.06	0.806
Right-handed	122 (91)	107 (88.4)		
Age (y)			2.68	0.103
Mean/SD	49/14	46/11		
Range [Min/Max]	19/86	20/70		
Expected years to onset			0.23	0.631
Mean/SD	−10/12	−11/11		
Range [Min/Max]	−25/10	−25/10		
Education (y)			0.05	0.826
Mean/SD	14/3	14/3		
Range [Min/Max]	5/24	5/22		

[a]Statistical test to indicate whether demographics vary between NC and PSC groups.

TABLE 2 Behavioral, cognitive, and neuropsychological estimates in presymptomatic carriers and non-carriers

	Gene status group		Statistical tests[a]	
	NC	PSC	X^2	*P*-value
Behavioral				
Cambridge Behavioral Inventory—Revised (/180)	3.5 (5.4)	4.7 (10)	0.03	.864
Cognitive				
Mini-Mental State Examination	29.3 (1.1)	29.2 (1.3)	<0.01	.963
Neuropsychological				
Logical Memory—Immediate Recall	15.2 (5.6)	15.7 (5.6)	0.47	.495
Logical Memory—Delayed Recall	14.1 (4.7)	14 (5)	0.97	.356
Digit Span—Forwards	6.4 (1.2)	6.3 (1.3)	0.52	.470
Digit Span—Backwards	4.9 (1.2)	4.8 (1.2)	1.62	.203
Digit Symbol Task	32 (14.1)	35 (14)	0.35	.556
Trail Making Test Part A	28.9 (17.2)	28.9 (11.5)	0.97	.325
Trail Making Test Part B	72.5 (43.7)	72.3 (45.5)	0.02	.895
Verbal Fluency—Letter	42 (12.2)	40.7 (15.1)	0.95	.330
Verbal Fluency—Animal	23.3 (6)	23.7 (5.8)	0.58	.445
Boston Naming Test	28.1 (2.1)	27.6 (2.7)	0.58	.446
Block Design	41.8 (16.1)	42.5 (17.1)	0.17	.683

[a]Statistical test to indicate whether scores vary between NC and PSC groups.

Wechsler Abbreviated Scale of Intelligence Block Design task, and the Mini-Mental State Examination. Latency measures for the Trail Making Test were inverted so that higher values across all tests reflect better performance.

2.3 | Neuroimaging assessment

Figure 1 provides a schematic representation of imaging data processing pipeline and the analysis strategy for linking brain-behavior data. MRI data were acquired using 3T scanners and 1.5T where no 3T scanning was available from various vendors, with optimized scanning protocols to maximize synchronization across scanners andsites.[7,13] A three-dimensional (3D) structural MRI was acquired for each participant using T1-weighted magnetic prepared rapid gradient echo (MPRAGE) sequence over at least 283 s (283 to 462 s) and had a median isotropic resolution of 1.1 mm (1 to 1.3 mm), repetition time of 2000 ms (6.6 to 2400), echo time of 2.9 ms (2.6 to 3.5 ms), inversion time of 8 ms (8 to 9 ms), and field of view 256 × 256 × 208 mm (192 to 256 × 192 to 256 × 192 to 208 mm). The co-registered T1 images were segmented to extract probabilistic maps of six tissue classes: grey matter (GM), white matter (WM), cerebrospinal fluid (CSF), bone, soft tissue, and residual noise. The native-space GM and WM images were submitted to diffeomorphic registration to create equally represented gene-group template images (DARTEL[24]). The templates for all tissue types were normalized to the Montreal Neurological Institute (MNI) template using a 12-parameter affine transformation. The normalized images were smoothed using an 8-mm Gaussian kernel.

For resting state fMRI measurements, echo-planar imaging (EPI) data were acquired with at least 6 minutes of scanning. Analogous imaging sequences were developed by the GENFI Imaging Core team, and used at each GENFI study site to accommodate different scanner models and field strengths. EPI data were acquired over at least 300 s (interquartile range [IQR] 309 to 440) and had a median repetition time of 2200 ms (2200 to 3000 ms), echo time of 30 ms, in-plane resolution of 2.75 × 2.75 mm (2.75 to 3.31 × 2.75 to 3.31), and slice thickness of 3.3 mm (3.0 to 3.3).

The imaging data were analyzed using Automatic Analysis [AA 4.0[25]] pipelines and modules, which called relevant functions from Statistical Parametric Mapping (SPM12).[26] To quantify the total motion for each participant, the root mean square volume-to-volume displacement was computed using the approach of Jenkinson et al.[27] Participants with 3.5 or more standard deviations (SD) above the group mean motion displacement were excluded from further analysis (N = 5). To further ensure that potential group bias in head motion did not affect later analysis of connectivity, we took three further steps:

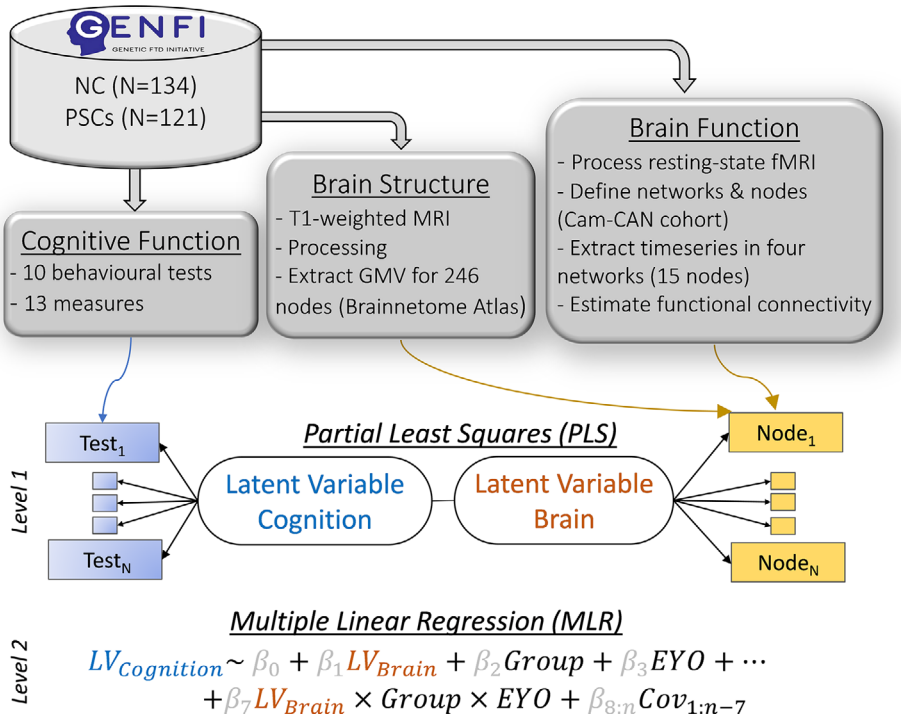


FIGURE 1 Schematic representation of data processing and analysis pipeline to test for brain-behavior differences between presymptomatic carriers (PSCs) and non-carriers (NCs) as a function of expected years to onset (EYO) of symptoms, while controlling for covariates of no interest (Covs). Brain structural measures were based on the mean gray matter volume (GMV) in 246 nodes, as defined in the Brainnetome atlas.[35] Brain functional measures were based on the functional connectivity between 15 nodes as part of four large-scale networks, which were defined in an independent cohort of 298 age-matched individuals part of the Cam-CAN data set

(1) fMRI data were further postprocessed using whole-brain independent component analysis (ICA) of single subject time-series denoising, with noise components selected and removed automatically using a priori heuristics and the ICA-based algorithm,[28] (2) postprocessing of network node time-series (see below), and (3) a subject-specific estimate of head movement for each participant[27] included as a covariate in group-level analysis.[29]

2.4 | Network definition

The location of the key cortical regions in each network was identified by spatial-ICA in an independent data set of 298 age-matched healthy individuals from a large population-based cohort.[22] Full details about preprocessing and node definition have been described previously.[30] Four networks commonly affected by neurodegenerative diseases including FTD[21] were identified by spatially matching to pre-existing templates.[31] The default mode network (DMN) contained five nodes: the ventral anterior cingulate cortex (vACC), dorsal and ventral posterior cingulate cortex (vPCC and dPCC), and right and left inferior parietal lobes (rIPL and lIPL). The salience network (SN) was defined using right and left anterior insular (rAI and lAI) and dorsal anterior cingulate cortex (dACC). The frontoparietal network (FPN) was defined using right and left anterior superior frontal gyrus (raSFG and laSFG) and right and left angular gyrus (rAG and lAG). The dorsal attention network (DAN) was defined using right and left intraparietal sulcus (rIPS and lIPS). The node time-series were defined as the first principal component resulting from the singular value decomposition of voxels in an 8-mm radius sphere, which was centered on the peak voxel for each node.[18] Visual representation of the spatial distribution of the nodes is shown in Figure 2.

We aimed to further reduce the effects of noise confounds on functional connectivity effects of node time-series using the general linear model (GLM).[29] This model included linear trends, expansions of realignment parameters, as well as average signal in WM and CSF, including their derivative and quadratic regressors from the time-courses of each node. The WM and CSF signals were created by using the average signal across all voxels with corresponding tissue probability >0.7 in associated tissue probability maps available in SPM12. A band-pass filter (0.0078 to 0.1 Hz) was implemented by including a discrete cosine transform set in the GLM. Finally, the functional connectivity (FC) between each pair of nodes was computed using Pearson correlation on postprocessed time-series.

2.5 | Statistical analysis

2.5.1 | Group differences in brain structure, function, and cognition

To assess the group differences in neuroimaging and behavioral data set we used multiple linear regression with a well-conditioned shrink-

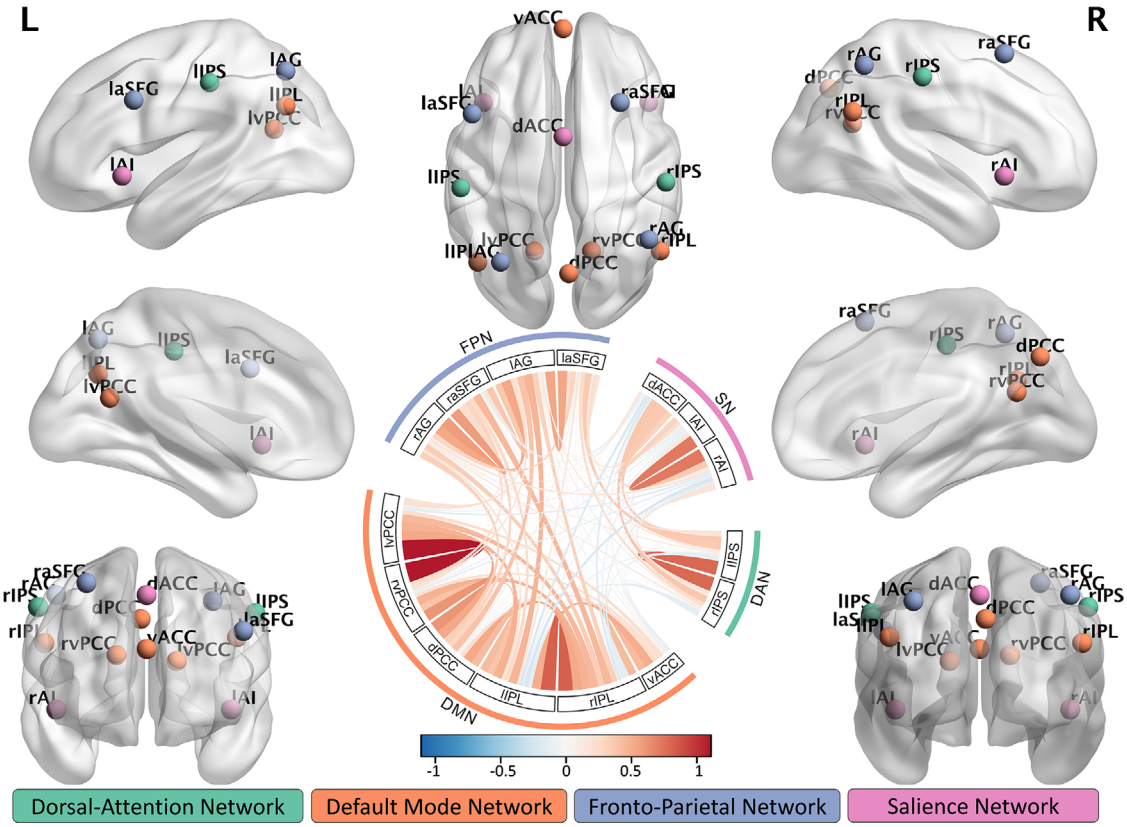


FIGURE 2 Visualization of spatial localization of the nodes part of the four large-scale networks and their mean functional connectivity (circular plot) across all participants in this study. Nodes and networks were defined in an independent cohort of 298 age-matched individuals part of the Cam-CAN data set.[30] The default mode network (DMN) contained five nodes: the ventral anterior cingulate cortex (vACC), dorsal and ventral posterior cingulate cortex (vPCC and dPCC), and right and left inferior parietal lobes (rIPL and lIPL). The salience network (SN) was defined using right and left anterior insular (rAI and lAI) and dorsal anterior cingulate cortex (dACC). The frontoparietal network (FPN) was defined using right and left anterior superior frontal gyrus (raSFG and laSFG) and right and left angular gyrus (rAG and lAG). The dorsal attention network (DAN) was defined using right and left intraparietal sulcus (rIPS and lIPS)

age regularization[32,33] and 10-fold cross-validation.[34] In the analysis of brain structure we used as independent variables the mean GM volume (GMV) of the 246 brain nodes in the Brainnetome atlas.[35] The Brainnetome atlas was developed to link functional and structural characteristics of the human brain[35] and provides a fine-grained whole-brain parcellation with a superior representation of age-related differences in brain structure compared to other cortical parcellation schemes.[36,37] In the analysis of brain function, we used the functional connectivity between 15 nodes, which were part of the four large-scale functional networks described earlier. In the analysis of cognitive function, the independent variables comprised the performance measures on the 13 neuropsychological tests performed outside of the scanner. In all three analyses the dependent variable was the genetic status (PSC vs NC) including age as a covariate of no interest. GENFI's large-sampled cohort was created using harmonized multi-site neuroimaging data. Although, scanning protocols were optimized to maximize comparability across scanners and sites,[7,13] different scanning platforms can introduce systematic differences that might confound true effects of interest.[38] Therefore, in the analysis of neuroimaging data we included scanner site and head motion as additional covariates of no interest.

2.5.2 | Brain-behavior relationships

For the brain-behavior analysis, we adopted a two-level procedure. In the first-level analysis, we assessed the multidimensional brain-behavior relationships using partial least squares.[39] This analysis described the linear relationships between the two multivariate data sets, namely neuroimaging (either GMV or FC) and behavioral performance, by providing pairs of latent variables (Brain-LVs and Cognition-LVs) as linear combinations of the original variables that are optimized to maximize their covariance. Namely, data set 1 consisted of a brain feature set, which could be either GMV (GMV data set) or functional connectivity strength between pairs of regions for each individual (FC data set). Data set 2 included the performance measures on the 13 tests (ie, Cognition data set), as considered in the multiple linear regression analysis of group differences in cognition. Covariates of no interest included head motion, scanner site, gender, and handedness. In addition, we also included average GMV across all 15 nodes as a covariate of no interest in the FC-behavior analysis to ensure that the observed effects are over and above differences in the level of atrophy.

Next, we tested whether the identified behaviorally relevant LVs of brain structure and function were differentially expressed by NC and

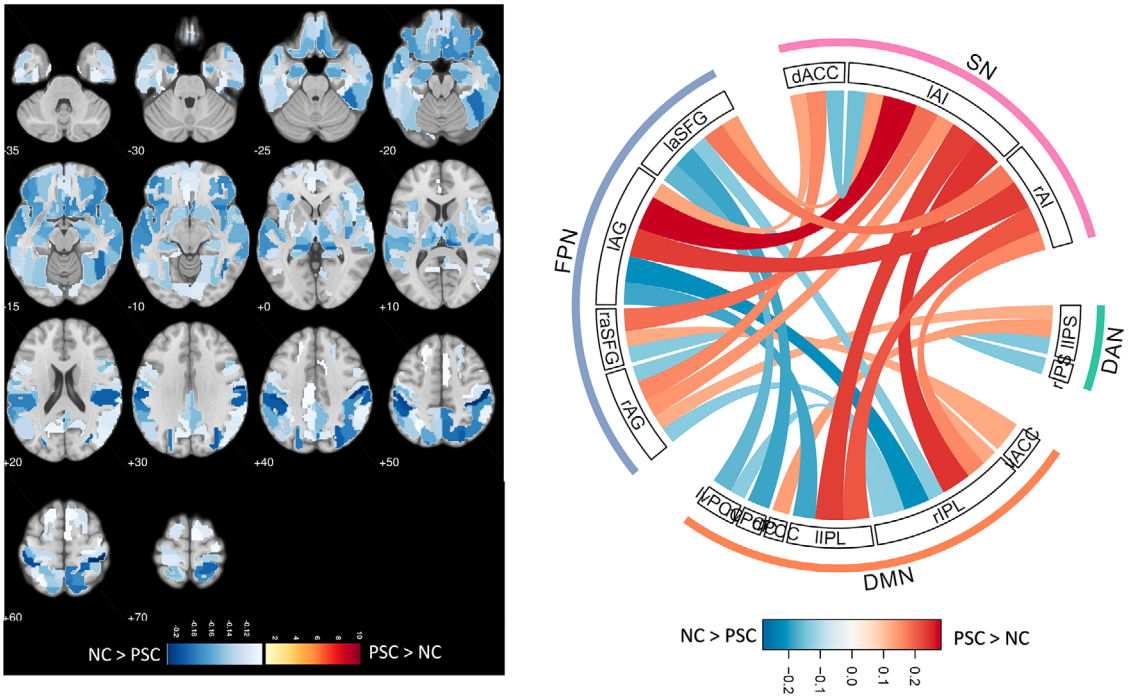


FIGURE 3 Group differences between PSC and NC in gray matter volume (left panel) and functional connectivity between nodes within four large scale networks (right panel). Hot color scheme indicates the strength of effect size of PSC showing higher GMV and FC than NC, while cold color scheme indicates the opposite effect (ie, NC > PSC)

PSC as a function of expected years to onset. To this end, we performed a second-level analysis using multiple linear regression with robust fitting algorithm as implemented in MATLAB's function "fitlm.m." Independent variables included subjects' brain scores from first level PLS (either Structure-LV or Function-LV subject scores), group information, expected years to onset and their interaction terms (eg, brain scores x group, brain scores x years to expected onset, and so on). The dependent variable was subjects' cognitive scores from the first level analysis in the corresponding PLS (Cognition-LV). Given that the interaction effects were derived from continuous variables, we tested and interpreted interactions based on simple slope analysis and slope difference tests.[40–42] Covariates of no interest included gender, handedness, head movement, and education (Figure 1). In addition, we included average GMV across all 15 nodes as a covariate in the FC-behavior analysis to ensure that the observed effects are over and above differences in the level of atrophy.

3 | RESULTS

3.1 | Group differences in neuroimaging and cognitive data

3.1.1 | Brain structure

The multiple linear regression model testing for overall group differences in GMV between PSC and NC was significant (r = .14, *P* = .025), reflecting expected presymptomatic differences in brain-wide atrophy. The frontal, parietal, and subcortical regions had most atrophy in PSC (Figure 3). As expected, the group difference in GMV of these regions increased as EYO decreased (see Supplementary Materials).

3.1.2 | Brain function

The multiple linear regression model testing for overall group differences in functional connectivity between PSC and NC was marginally significant (r = .12, *P* = .049). The pattern of connectivity indicated mainly increased connectivity between SN-DMN and SN-FPN in presymptomatic carriers, coupled with decreased connectivity within the networks and DMN-FPN connectivity (Figure 3).

3.1.3 | Cognitive function

We did not identify group differences in cognition and behavior (r = .002, *P* = .807), confirming the impression of "healthy" status among presymptomatic carriers. However, in the next section, we consider the relationships between structure, function, and cognition that underlie this maintenance of cognitive function.

3.2 | Brain-behavior relationships

3.2.1 | Structure-cognition

Partial least squares analysis of GMV and cognition identified one significant pair of latent variables (r = .40, *P* = .019). This volumetric latent variable expressed negative loadings in frontal (superior frontal

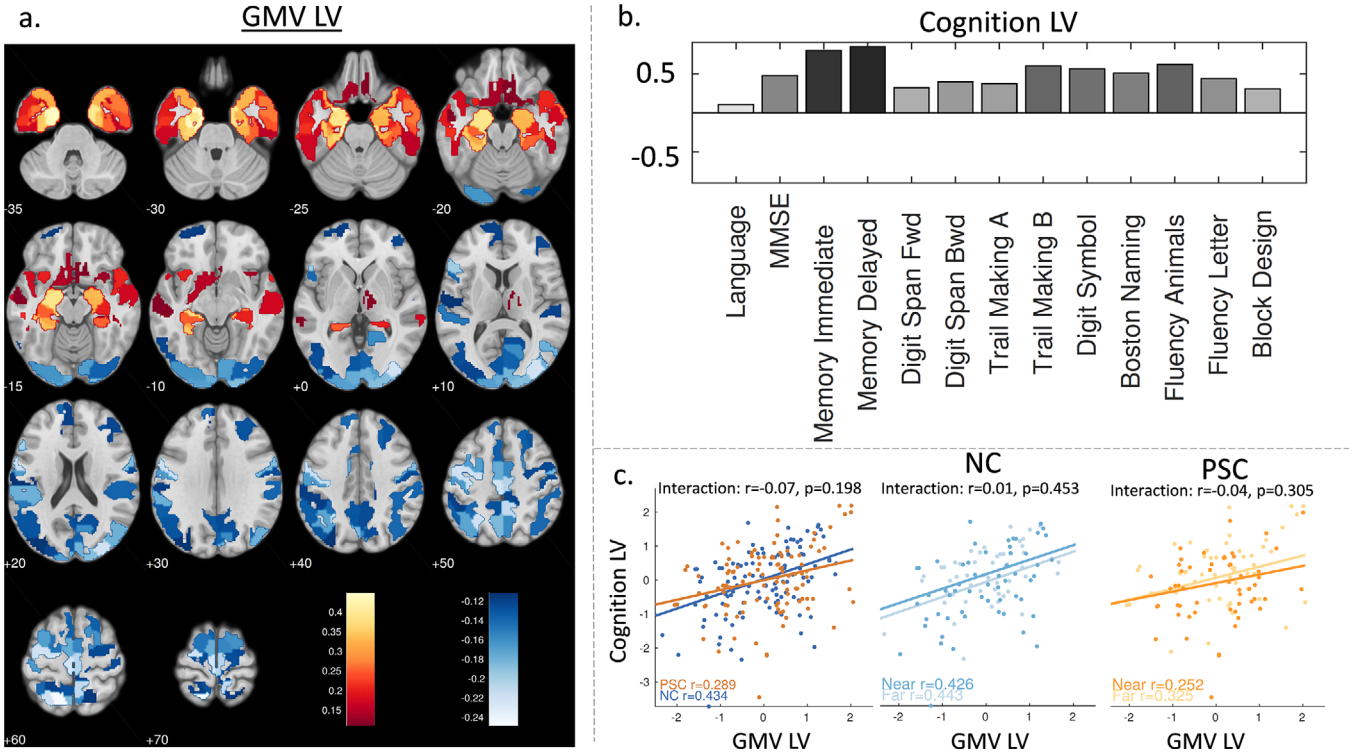


FIGURE 4 PLS analysis of gray matter volume (GMV) and cognition indicating the spatial distribution of GMV loading values (A), where hot and cold color schemes are used for the strength of positive and negative correlations with the profile of Cognitive-LV (B). (C) The scatter plot on the left represents the relationship between subjects scores of GMV-LV and Cognition-LV for presymptomatic carriers (PSCs) and non-carriers (NCs). The scatter plots in the middle and right hand-side represent GMV-Cognition LV relationship as a function of expected years to onset (EYO, split in two groups, near and far, see text) in each genetic status group separately

gyrus, precentral gyrus, paracentral lobule), parietal (postcentral gyrus, precuneus, superior and inferior parietal lobule), and occipital (lateral and medial occipital cortex) regions and positive loadings in parahippocampal and hippocampal regions in addition to inferior temporal and insular cortex (Figure 4). The Cognition-LV profile expressed positively a large array of cognitive tests, with strongest values on delayed memory, Trail Making, Digit Symbol, Boston Naming, and Fluency tests. The positive correlation between volumetric and cognitive LV's confirms the expected relationship across the cohort as a whole, between cortical GMV and executive, language, and mnemonic function (Figure 4).

To understand the structure-cognition relationship in each group and in relation to the expected years of onset, we performed a second-level interaction analysis using a regression model: We entered Cognition-LV subject scores as dependent variable, and GMV LV subject scores, genetic status (ie, mutation carrier or non-carrier), expected years to onset, and their interactions as independent variables in addition to covariates of no interest. The results indicated that the relationship between GMV and cognition could not be explained by genetic status, expected years to onset, or their interactions with GMV LV subject scores. There was no evidence for genetic status- and onset-dependent differences (over and above aging and other covariates) in the associations between GMV and cognition in this analysis (Figure 4).

3.2.2 | Connectivity-cognition

PLS analysis of functional connectivity and cognition also identified one significant pair of LVs (Function-LV and Cognition-LV, r = .32, P = .020; see Figure 5). This Function-LV reflected weak between-network connectivity, coupled with strong within-network connectivity. This pattern indicates the segregation or modularity of large-scale brain networks. The Cognition-LV expressed all tests, with positive loading values indicating that higher performance on a wide range of cognitive tests is associated with stronger functional network segregation. Cognitive deficits were associated with loss of segregation, with increased between-network connectivity and decreased within-network connectivity.

To further test whether the observed behaviorally relevant pattern of connectivity is differentially expressed between genetic status groups and expected years of onset, we constructed a second-level regression model with robust error estimates by including Function-LV subject scores, genetic status, expected years of onset, and their interaction terms as independent variables and Cognition-LV as dependent variable in addition to covariates of no interest (Figure 5).

We found evidence for significant interaction between expected years of onset and Function-LV (r = .21, P < .001) and between group and Function-LV (r = .16, P = .002) explaining unique vari-

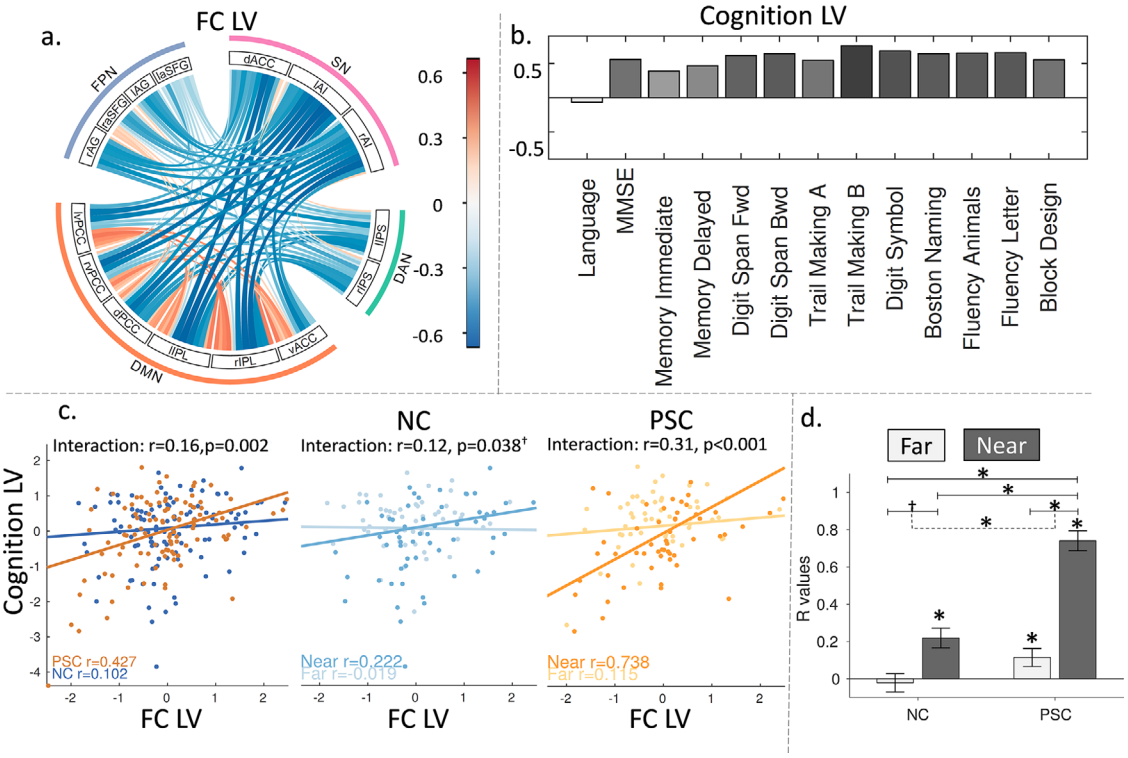


FIGURE 5 PLS analysis of functional connectivity and cognition indicating the connectivity pattern of loading values (A), where hot and cold color schemes are used for the strength of positive and negative correlations with the profile of cognitive-LV (B). (C) The scatter plot on the left represents the relationship between subjects scores of function LV and cognition LV for presymptomatic carriers (PSCs) and non-carriers (NCs). The scatter plots in the middle and right hand-side represents function-cognition LV relationship as a function of expected years to onset (EYO split in two groups, near and far, see text) in each genetic status group separately. This is also represented using a bar chart in (D), where continuous and dashed lines indicate significance of effect differences and difference in differences, respectively. † and * denote significant tests at *P*-value < .05 (one- and two-sided, respectively)

ance in Cognition-LV. We used simple slope analysis and slope difference tests[40–42] to test formally for differences in the relationship between Function-LV and Cognition-LV for PSC and NC. The relationship between Function-LV and Cognition-LV was stronger for PSC relative to NC (r = .16, *P* = .002), indicating the increasing importance of functional connectivity between the large-scale networks for PSC participants to maintain performance (Figure 5).

For ease of interpretation and illustration, we also computed the correlation between Cognition-LV and Function-LV for high and low levels of expected years to onset (or EYO) within each group separately, where the levels were taken to be 1 SD above and below the mean values of EYO following the simple slopes approach.[40–42] The two EYO subgroups were labeled "near" and "far," with "near" for EYO values close to zero (ie, participant's age is "near" the age at which disease symptoms were demonstrated in the family), and "far" for EYO being a largely negative value (ie, participant's age is "far" from the age at which disease symptoms were demonstrated in the family). The analysis indicated that as the EYO decreases (ie, participant's age is reaching the years of onset of symptoms) the relationship between functional connectivity and performance becomes stronger. This effect was highly significant in presymptomatic carriers (r = .31, *P* < .001) and tended towards significance in non-carriers (r = .12, *P* = .038, one-sided). The differences in effects between presymptomatic carriers and non-carriers was qualified by a significant interaction term (t = 2.27, *P* = .024, ie, the effect in presymptomatic mutation carriers was statistically stronger than the effect detected in non-carriers). These findings indicate that the relationship between FC and cognition is stronger in PSC relative to NC, and that this relationship increases as a function of EYO.

4 | DISCUSSION

In the present study, we confirmed previous findings of group differences in brain structure and function, in the absence of differences in cognitive performance between non-carriers and presymptomatic carriers of FTD-related genetic mutations. But, although the relationship between structure and cognition was similar in both groups, the coupling between function and cognition was stronger for presymptomatic carriers, and increased as they approached the expected onset of disease.

These results suggest that people can maintain good cognitive abilities and successful day-to-day functioning despite significant neuronal loss and atrophy. This disjunction between structure and function is a

feature of healthy aging, but we have shown that it also characterizes presymptomatic FTD, over and above the age effects in their other family members, despite widespread progressive atrophy. The multivariate approach reveals two key findings: (1) stronger within-network and weaker between-network functional connectivity is associated with better cognition, more strongly in presymptomatic carriers than in age-matched non-carriers, and (2) as carriers approach their estimated age of symptom onset, and atrophy becomes evident, the maintenance of good cognition is increasingly associated with sustaining balance of within- and between-network integration.

This balance of within- and between-network connectivity is characteristic of segregated and specialized network organization of brain systems. Such functional segregation varies with physiological aging,[17,18,43] with cognitive function,[18] and in individuals at risk for AD.[44] Graph-theoretic quantification of network organization confirms the relevance of modularity and efficiency to function in FTD.[16] Conversely, the loss of neural systems' modularity mirrors the loss of functional specialization with age[45] and dementia.[44] Here, we show the significance of the maintenance of this functional network organization, with a progressively stronger correlation with cognitive performance as seemingly healthy adults approach the age of expected onset of FTD.

The uncoupling of brain function from brain structure indicates that there may be independent and synergistic effects of multiple factors leading to cognitive preservation. This is consistent with a previous work in healthy aging where brain activity and connectivity provide independent and synergistic predictions of performance across the lifespan.[19] Therefore, future studies need to consider the independent and synergistic effects of many possible biomarkers, based on MRI, computed tomography, positron emission tomography, CSF, blood, and brain histopathology. For example, functional network impairment may be related to tau expression and tau pathology, amyloid load, or neurotransmitter deficits in neurodegenerative diseases, independent of atrophy.[30,46–48] It is important to note that studies need to recognize the rich multivariate nature of cognition and of neuroimaging in order to improve stratification procedures, for example, based on integrative approaches that explain individual differences in cognitive impairment.[30,49] On a clinical level, this may facilitate future studies to establish whether presymptomatic carriers who maintain such connectivity profiles and thereby neuropsychological function in the presence of atrophy may have a lower risk of progression and better prognosis—information that will be important for future triallists, patients, and carers.

We also recognize the difficulty in determining a unique contribution of each factor (eg, brain structure and brain function), given the increasing interaction between factors in advanced stages of disease.[50] This is further complicated by these alterations becoming irreversible with progression of neurodegeneration.[51] This suggests that the critical interplay between multiple factors (including brain structure and function) may be better studied in the asymptomatic and preclinical stages as well as across the healthy lifespan, which could still be modifiable and their influences are likely to be more separable.

Our findings agree with the model of compensation in the presymptomatic and early phases of Huntington disease, where network coupling predicted better cognitive performance.[52] In a recent longitudinal study, a non-linear concave-down pattern of both brain activity and behavior was present, despite a linear decline in brain volume over time.[53] Similar effects have been observed also in healthy aging and amnestic mild cognitive impairment, where greater connectivity with the default-mode network and weaker connectivity between default-mode network and dorsal-attention network was associated with higher cognitive status in both groups.[54] Network integrity may also play a role in compensatory mechanisms in non-cognitive symptoms, such as motor impairment in Parkinson disease.[55] Accordingly, increased network efficiency and connectivity have been shown in prodromal phases, followed by decreased local connectivity in symptomatic phases, suggesting the emergence and dissipation of neural compensation.[56]

The current study has several limitations. First, despite the large size of the overall GENFI cohort, we did not analyze each genetic group separately. The subdivision of each clinical group (PSC, NC) by three genes would have led to small and unbalanced subgroups, lowering statistical power and robustness. Moreover, genetic FTD is also characterized by multiple mutations within *MAPT* and *GRN*, and pleiotropy of clinical phenotypes from the same mutation.[10] Pleiotropy of clinical phenotype is avoided by the study of presymptomatic carriers, but we cannot rule out pleiotropy of intermediate phenotypes expressed as say neural network diversity. In FTD as in other dementias, clinical heterogeneity is modified by environmental factors such as education (which may be a surrogate of cognitive reserve[12,57]). In addition, our analysis included the estimated age at onset in some models, but we recognize that the precision of the estimated years at onset (based on family history of onset) varies across mutations and families,[7,58] being highest for *MAPT* and low for *C9orF72* expansion. Genetic modifiers such as *TMEM106B*[59] and *APOE*[60] have also been identified. Further work with larger cohorts is required to test for gene-specific effects, and the role of environmental and genetic moderators on the relationships between brain structure, functional networks, and cognition. The harmonization of sequences and data acquisition protocols in this multi-site neuroimaging study aimed to reduce the susceptibility to systematic differences across scanning platforms, but residual site variance cannot be ruled out.[38,61] The inclusion of study site as a covariate of no interest[61] and the nature of our multivariate approach to identify shared signals between brain and behavioral data reduce residual effects of scanner variance.[38,62] Future studies may use alternative brain measures that reflect differences in cortical surface and thickness estimates,[63,64] or which infer neural connectivity directly from neurophysiology or from the separation of neurovascular from neuronal contributors to blood oxygen level–dependent (BOLD) fMRI variance,[18,65] given the confounding effects of age, drug, or disease on neurovascular signals.[66,67]

The current study is cross-sectional. Therefore, we cannot infer longitudinal progression within subjects as the unambiguous cause of the effects we observe in relation to expected years of onset. Accumulating evidence suggests that network integrity serves to maintain performance with either physiological ageing or pathological conditions.

However, longitudinal mediation studies and pharmacological or electroceutical interventions would be needed to prove its causal role in cognitive preservation. Finally, our findings are limited to autosomal dominant FTD, which represents a minority of FTD: Generalization to sporadic forms of disease would be speculative.

In conclusion, we used a multivariate data-driven approach to demonstrate that brain functional integrity may facilitate presymptomatic carriers to maintain cognitive performance in the presence of progressive brain atrophy for years before the onset of symptoms. The multivariate approach to cognition and brain function is well-suited to address the effects of multiple interacting risk factors on biomarkers of the progression of neurodegeneration, ahead of clinical conversion to dementia. The approach and our findings have implications for the design of presymptomatic disease-modifying therapy trials, which are likely to rely initially on surrogate markers of brain health rather than clinical end points.

ACKNOWLEDGMENTS

K.A.T. is supported by the British Academy Postdoctoral Fellowship (PF160048) and the Guarantors of Brain (101149). J.B.R. is supported by the Wellcome Trust (103838), the Medical Research Council (SUAG/051 G101400), and the Cambridge NIHR Biomedical Research Centre. R. S.-V. is supported by the Instituto de Salud Carlos III and the JPND network PreFrontAIs (01ED1512/AC14/0013) and the Fundació Marató de TV3 (20143810). M.M and E.F are supported by the UK Medical Research Council, the Italian Ministry of Health, and the Canadian Institutes of Health Research as part of a Centres of Excellence in Neurodegeneration grant, and also a Canadian Institutes of Health Research operating grant (MOP 327387) and funding from the Weston Brain Institute. J.D.R., D.C., and K.M.M. are supported by the NIHR Queen Square Dementia Biomedical Research Unit, the NIHR UCL/H Biomedical Research Centre, and the Leonard Wolfson Experimental Neurology Centre (LWENC) Clinical Research Facility. J.D.R. is supported by an MRC Clinician Scientist Fellowship (MR/M008525/1) and has received funding from the NIHR Rare Disease Translational Research Collaboration (BRC149/NS/MH), the MRC UK GENFI grant (MR/ M023664/1), and The Bluefield Project. F.T. is supported by the Italian Ministry of Health (Grant NET-2011-02346784). L.C.J. and J.V.S. are supported by the Association for Frontotemporal Dementias Research Grant 2009, ZonMw Memorabel project number 733050103 and 733050813, and the Bluefield project. R.G. is supported by Italian Ministry of Health, Ricerca Corrente. J.L. was funded by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation) under Germany's Excellence Strategy within the framework of the Munich Cluster for Systems Neurology (EXC 2145; SyNergy - ID 390857198). The Swedish contributors C.G., L.O., and C.A. were supported by grants from JPND Prefrontals Swedish Research Council (VR) 529-2014-7504, JPND GENFI-PROX Swedish Research Council (VR) 2019-02248, Swedish Research Council (VR) 2015- 02926, Swedish Research Council (VR) 2018-02754, Swedish FTD Initiative-Schorling Foundation, Swedish Brain Foundation, Swedish Alzheimer Foundation, Stockholm County Council ALF, Karolinska Institutet Doctoral Funding, and StratNeuro, Swedish Demensfonden, during the conduct of the study.

CONFLICT OF INTEREST

There were no financial or other conflicts of interest requiring declaration.

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How to cite this article: Tsvetanov KA, Gazzina S, Jones PS, et al. Brain functional network integrity sustains cognitive function despite atrophy in presymptomatic genetic frontotemporal dementia. *Alzheimer's Dement*. 2021;17:500–514. https://doi.org/10.1002/alz.12209

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