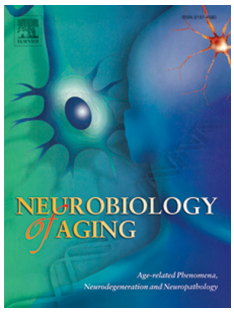

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Single-subject grey matter networks predict future cortical atrophy in preclinical Alzheimer's disease

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Author contributions

E.D. processed all image data, performed the statistical analyses, interpreted data and drafted the manuscript. W.M.v.d.F., F.B. and P.S. interpreted data. B.M.T. was responsible for the study design and concept, contributed to the analyses and interpreted data. All co-authors have read and critically revised the manuscript.

Abstract

The development of preventive strategies in early-stage Alzheimer's disease (AD) requires measures that can predict future brain atrophy. Grey matter network measures have such potential as they are sensitive to detect very early brain structural alterations that are related to amyloid burden in cognitively normal older individuals, and predict clinical progression in preclinical AD. Here, we show that within individuals with preclinical AD, grey matter network measures predict hippocampal atrophy rates, whereas other AD biomarkers (total grey matter volume, CSF total tau and MMSE) do not. Furthermore, in brain areas where amyloid is known to start aggregating (i.e., anterior cingulate and precuneus) disrupted network measures predict faster subsequent atrophy in other distant areas, mostly involving temporal regions, which are associated with AD. When repeating analyses in a sample of age-matched, cognitively unimpaired individuals with normal levels of amyloid and total tau in CSF, we did not find any associations between network measures and hippocampal atrophy, indicating that the associations seem specific for individuals with preclinical AD. Our findings suggest that disrupted grey matter networks may indicate a treatment opportunity in individuals with preclinical AD but before the onset of irreversible overt atrophy and cognitive impairment.

Keywords: Alzheimer's disease; amyloid; atrophy; preclinical; single-subject grey matter networks

1. Introduction

Alzheimer's disease (AD) is a neurodegenerative disorder that is the most common cause of dementia (Lobo et al., 2000; Plassman et al., 2007). Among the earliest pathological changes in AD is aggregation of amyloid beta into plaques (Bateman et al., 2012; Jansen et al., 2015), starting in the anterior cingulate cortex and the precuneus (Palmqvist et al., 2017; Villain et al., 2012; Villeneuve et al., 2015). Once amyloid has aggregated, it may take up to 10 years before atrophy starts (Bateman et al., 2012), which most prominently affects more distant brain areas in the medial temporal lobes (Chetelat et al., 2012; Dickerson et al., 2009; Whitwell et al., 2007) and is more closely related to cognitive decline (van Rossum et al., 2012). How amyloid aggregation in one brain area eventually leads to neurodegeneration in more distant brain areas remains largely unclear. For development of preventive strategies it is important to predict future brain atrophy, as this may aid in identifying which individuals with abnormal amyloid but still normal cognition (i.e., preclinical AD; Sperling et al., 2011) will show disease progression but before the onset of irreversible atrophy.

Amyloid aggregation disrupts local synaptic functioning (Koffie et al., 2009; Shankar et al., 2008; Walsh et al., 2002), potentially leading to disruptions of large-scale brain connectivity networks (Buckner et al., 2005; Kuchibhotla et al., 2008; Kurudenkandy et al., 2014; Palmqvist et al., 2017; Palop et al., 2007; Sperling et al., 2009). One approach to measure brain networks is based on intracortical similarity on structural MRI (i.e., grey matter connectivity; Mechelli et al., 2005; Tijms et al., 2012). Intracortical similarity has been associated with coordinated growth patterns (Alexander-Bloch et al., 2013b), functional co-activation (Alexander-Bloch et al., 2013a) and axonal connectivity (Gong et al., 2012). We and others have shown that grey matter networks are disrupted in AD (He et al., 2008; Pereira et al., 2016; Tijms et al., 2013a; Tijms et al., 2013b; Yao et al., 2010), associated with

cognitive impairment (Tijms et al., 2013a; Tijms et al., 2014) and related to faster disease progression and cognitive decline in the predementia stage of AD (Dicks et al., 2018; Tijms et al., 2018; Verfaillie et al., 2018). Furthermore, disrupted grey matter network organization has been associated with aggregating amyloid in cognitively normal individuals (ten Kate et al., 2018; Tijms et al., 2016) and before overt atrophy is evident (Voevodskaya et al., 2018). Taken together, these findings suggest that grey matter network measures might have use to identify those individuals who will progress to AD dementia in the earliest, preclinical stages of AD *and before* the onset of irreversible atrophy. In a cross-sectional study, Seeley and colleagues previously showed that atrophy patterns in AD dementia patients reflect brain regions that show both strong functional co-activation as well as covariation in grey matter volume across a group of cognitively normal individuals, suggesting that regions that are highly interconnected share vulnerability for neurodegeneration (Seeley et al., 2009). It could be hypothesized that grey matter network disruptions due to amyloid aggregation in one region of the brain may capture the earliest neurodegenerative changes in preclinical AD and predict future atrophy in more distant regions. However, as previous findings were based on cross-sectional studies and/or used only one network per group of individuals, it is still unclear whether grey matter network disruptions can predict the rate and location of future atrophy *within* individuals.

In this study, we used a subject-specific approach to construct grey matter networks in individuals with preclinical AD and investigated whether altered grey matter network measures at baseline could predict the rate and location of future atrophy. We first compared the predictive performance for future hippocampal atrophy between whole-brain grey matter network measures and other Alzheimer's disease markers that have been previously associated with reduced grey matter volume (i.e., total grey matter volume, CSF total tau levels and MMSE scores). We then investigated whether grey matter network measures

specifically in regions, where amyloid has previously been shown to start aggregating (i.e., anterior cingulate and precuneus; Palmqvist et al., 2017; Villeneuve et al., 2015), could predict the rate of subsequent atrophy in other brain areas within single individuals with preclinical AD. We also performed analyses in cognitively unimpaired, age-matched individuals without evidence of amyloid or tau pathology to study whether results were specific for preclinical AD, and additionally investigated the effects of clinical progression, tau pathology and sex on network disruptions and their associations with future hippocampal atrophy.

2. Methods

2.1. Participants

Data used in the preparation of this article were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database (http://adni.loni.usc.edu). The ADNI was launched in 2003 as a public-private partnership, led by Principal Investigator Michael W. Weiner, MD. The primary goal of ADNI has been to test whether serial magnetic resonance imaging (MRI), positron emission tomography (PET), other biological markers, and clinical and neuropsychological assessment can be combined to measure the progression of mild cognitive impairment and early Alzheimer's disease. ADNI was approved by the institutional review board of all participating institutions and written informed consent was obtained from all participants at each site.

We selected all participants with preclinical AD from ADNI as defined by normal cognition and abnormal amyloid CSF markers at baseline who had at least 1 year of MRI-follow-up with a minimum of two structural MRI scans available. Additionally, we included cognitively unimpaired, age-matched individuals without amyloid or tau pathology as a control group (control; n=71), in order to determine whether results were specific for individuals with preclinical AD. Details of clinical diagnostic criteria have been previously described (Aisen et al., 2015; Petersen et al., 2010). Briefly, cognitively normal individuals had to have a CDR score of 0, an MMSE score between 24 and 30, and no impaired memory as based on education-adjusted cut-offs on the delayed recall subtest of the Logical Memory II subscale of the Wechsler Memory Scale-Revised (Aisen et al., 2015; Petersen et al., 2010). In total, 110 preclinical AD individuals were included with a median of 5 (min-max: 2-10) repeated MRI scans over a median follow-up time of 2.2 (min-max: 1-9) years, during which time 25% of individuals progressed to mild cognitive impairment or dementia due to AD. Diagnoses of

mild cognitive impairment or dementia were based on cognitive impairment on the CDR, MMSE or logical memory delayed recall (for cut-off scores, see Aisen et al., 2015; Petersen et al., 2010). Additionally, dementia patients had to have a clinical diagnosis of probable AD according to the NINCDS-ADRDA criteria (McKhann et al., 1984).

We used CSF measures for amyloid beta 1-42 to determine amyloid abnormality and additionally CSF total tau to determine tau abnormality in control individuals. Amyloid beta 1-42 and total tau were measured with the multiplex xMAP Luminex platform (Luminex Corp, Austin, TX) and Innogenetics (INNO-BIA AlzBio3; Ghent, Belgium) immunoassay kit-based reagents (Shaw et al., 2009). Abnormal amyloid was indicated by levels <192 pg/ml, and abnormal tau was indicated by levels of >95 pg/ml (Shaw et al., 2009).

2.2. MRI acquisition & preprocessing

Image acquisition details and initial preprocessing have been previously described (http://adni.loni.usc.edu/methods/mri-analysis/; Jack et al., 2008). We downloaded all 3D T1-weighted structural scans that were preprocessed with gradient-nonlinearity correction, B1 inhomogeneity and/or N3 correction and of sufficient quality from the ADNI LONI Image & Data Archive (IDA) [date of last access: 29.03.2017; n=534]. Scans that were acquired using different field strengths within subjects were excluded.

First, all images were reoriented with FSL (v5.0.6). Next, to reduce bias in longitudinal registration (Reuter et al., 2012), we created a subject-specific median template image with Freesurfer (v5.3.0) to which all longitudinal scans were co-registered. We then segmented images into grey matter, white matter and cerebrospinal fluid with the Markov Random Fields parameter set to 2 and default settings for all other parameters. Co-registration and

segmentation was performed with SPM12 running under Matlab (v.7.12.0.635). Finally, using the subject specific inversed normalization parameters, the automated anatomical labeling atlas (AAL; Tzourio-Mazoyer et al., 2002) was warped from standard space to subject space and we calculated regional grey matter volumes for each of the 90 cortical and subcortical AAL areas. Total intracranial volume was computed as the sum of grey matter, white matter and cerebrospinal fluid volumes in cm^3 and grey matter volume was normalized to baseline total intracranial volume. All grey matter segmentations and subject-specific atlases were visually checked for quality.

2.3. Single-subject grey matter network measures

Single-subject grey matter networks were reconstructed from subject space grey matter segmentations of baseline MRI scans using an automated method (https://github.com/bettytijms/Single_Subject_Grey_Matter_Networks), which has been described previously (Tijms et al., 2012). Briefly, nodes were defined as small regions of interest of 3×3×3 voxel cubes and connected when they showed similar gray matter structure as defined by a significant correlation between voxels of two nodes. By defining nodes as cubes, both spatial information (i.e., the folding structure of the cortex) and local grey matter values were used to assess the correlation between nodes. Because the cortex is a curved object, regions of interest could be located at an angle to each other, thus possibly decreasing correlations. Therefore, for each pairwise comparison, the seed cube was rotated by an angle with multiples of 45° to identify the maximum correlation coefficient. Next we binarized the networks using subject-specific thresholds based on empirical null model distributions (Noble, 2009) that ensured that all individuals showed a similar chance of 5% false-positive connections within the network. A detailed description of the single-subject network

extraction technique can be found in (Tijms et al., 2012). For each single-subject grey matter network we computed the network size, degree, connectivity density, clustering coefficient and path length. The network size is the number of nodes (i.e., cubes) in the network. The degree corresponds to the number of connections per node. The connectivity density is the ratio of present connections divided by the number of possible connections in the network. The clustering coefficient indicates the interconnectedness of neighboring nodes and the path length corresponds to the average shortest paths between all nodes in the network (Rubinov and Sporns, 2010). To obtain network measures for the precuneus and anterior cingulate we averaged measures across nodes that were labeled according to the AAL atlas. Global network measures were obtained by averaging measures across all nodes of the network. We additionally computed the global normalized clustering coefficient, normalized path length (gamma, lambda) and small-world coefficient for the whole brain in order to estimate how these network measures deviated from randomly organized networks as follows: Gamma and lambda were computed by normalizing clustering coefficient and path length values with the respective mean values of five randomized reference networks, which kept the degree distribution intact (Maslov and Sneppen, 2002). The small-world coefficient is defined as the ratio of gamma to lambda (Humphries and Gurney, 2008). All network measures were calculated using functions from the Brain Connectivity Toolbox (https://sites.google.com/site/bctnet/; Rubinov and Sporns, 2010) adjusted for large-sized networks.

2.4. Statistical analysis

Cortical atrophy was determined by fitting linear mixed models for each AAL area with longitudinal grey matter volume as outcome and time from baseline as predictor. We fitted

random slopes for time and intercepts for individuals, and assumed an unstructured covariance structure using the R package 'lme4' (Bates et al., 2015). We first assessed whether global network measures could predict future hippocampal atrophy, as a prominent region for AD associated atrophy. Repeated hippocampal volume over time was used as the outcome (i.e., hippocampal volume at baseline, hippocampal volume at visit 1, hippocampal volume at visit 2 etc.) and baseline network measures (NM), time and their interaction as the predictors.

$$Hippocampal\ volume = \beta_{Intercept} + \beta_{NM}NM + \beta_{Time}Time + \beta_{NM\times Time}NM \times Time + (1 + Time|Subject)$$

We repeated these analyses including clinical progression as a main term and interaction effect (i.e., network measure × time × clinical progression) to investigate whether the observed effects were stronger for those individuals who progressed during follow-up. Similarly, we also investigated the effects of tau and sex on baseline network disruptions and associations with future hippocampal atrophy by including tau abnormality or sex as additional interaction term in the analyses. We qualitatively compared the predictive performance between global network measures and other markers that are associated with reduced grey matter volume (i.e., CSF total tau, MMSE scores, total grey matter volume). For visualization purposes and to aid in comparison of the predictive performances we additionally performed linear regression analyses with subject-specific hippocampal atrophy slopes as outcome and baseline whole-brain grey matter network measures or Alzheimer's disease markers as predictor.

$$\Delta\ Hippocampal\ volume = \beta_{Intercept} + \beta_{NM}NM$$

In order to investigate whether altered network measures in early amyloid accumulating regions (i.e., anterior cingulate and precuneus) could predict the rate and location of future

atrophy we repeated analyses as for hippocampal volume but with longitudinal local grey matter volumes for each AAL region as the outcome and local network measures of the anterior cingulate or precuneus, time and their interaction as the predictors. All local grey matter volumes and network measures were standardized across regions according to the mean baseline values of individuals who remained cognitively stable to aid interpretation of the results. We also performed analyses for hippocampal and whole-brain atrophy in control individuals, who were age-matched to the original sample using the R package 'Matching' (Sekhon, 2008) to study specificity of results for preclinical AD. All analyses were adjusted for age, gender, field strength and total grey matter volume. Statistical analyses were performed in R (version 3.4.4, 2018-03-15) and Surf Ice (version 2017-08-08) was used to visualize regional results.

3. Results

3.1. Characteristics of the study sample

In this study we selected all individuals from the ADNI cohort who had normal cognition and abnormal CSF levels of amyloid beta 1-42 at baseline and at least 1 year of MRI follow-up available (n=110). Table 1 shows the baseline characteristics of the included sample and by clinical progression. Individuals were on average 75±6 years old and 57 % were female. During follow-up (median (IQR) 2.2 (2-4) years), 28 participants (25%) showed clinical progression (n=21 to prodromal AD and n=7 to AD dementia). Progressing participants were on average older, had more MRI scans over a longer follow-up period available and had higher total intracranial volume (p<0.05). Additionally, progressing participants had higher network size and degree (due to higher grey matter volume; p<0.065) and lower gamma and small-world coefficient values at baseline (p<0.05) and showed a tendency for lower lambda values compared to those who remained stable (p<0.065). Over time, the total sample showed cortical atrophy with fastest rates observed in the hippocampus (β±SE; left hippocampus: -0.15±0.01, right hippocampus: -0.14±0.01; all p<0.001) (Fig. 1 and Fig. 2A). Individuals who progressed during follow-up showed faster hippocampal atrophy rates compared to those who remained stable ($p_{interaction}$<0.001; Fig.2A; see also Supplementary Fig. 1 and Supplementary Table 1). Additional analyses performed in a subset of individuals who had amyloid PET available showed highest uptake in the precuneus as compared to controls with normal CSF amyloid levels (see Supplementary Fig. 2).

3.2. Prediction of hippocampal atrophy rates

We first investigated whether baseline global network measures and other AD-markers that have been related to cognitive decline (MMSE scores, CSF total tau, total grey matter volume) could predict hippocampal atrophy rates. Baseline MMSE scores, CSF total tau and whole-brain grey matter volume did not show associations with subject-specific hippocampal atrophy rates (all $p>0.05$; Table 2) (see also Figure 2B-D). Lower connectivity density and lower clustering at baseline predicted faster subsequent hippocampal atrophy (β±SE; both 0.04±0.01; $p<0.005$; Table 2) (see also Fig. 2E-F). Analyses including disease progression as an additional interaction term did not show significant interaction effects (all $p>0.05$; see Supplementary Table 1), suggesting that the association of baseline network measures and subsequent atrophy was similar for individuals who remained stable and those who showed clinical progression during follow-up.

3.3. Prediction of whole-brain atrophy patterns

We further investigated whether network measures in the anterior cingulate and precuneus could predict the spatiotemporal pattern of atrophy. Both local clustering and path length values showed associations with subsequent grey matter atrophy, for specific parts of the brain (Fig. 3, see Supplementary Fig. 3 for cross-sectional relationships): Lower clustering values in the anterior cingulate and precuneus of both hemispheres were associated with faster atrophy in mostly temporal regions, including the right superior, middle temporal pole, hippocampus and left parahippocampal gyrus (all $p<0.05$; Fig. 3A-D). Higher path length values in the right anterior cingulate and bilateral precunei were associated with faster atrophy in mostly frontal regions, including the right superior, middle frontal gyrus and left middle cingulate (all $p<0.05$; Fig. 3E-H). Grey matter volumes of the anterior cingulate or precuneus

did not predict future hippocampal atrophy rates (all $p>0.05$; see Supplementary Table 2), indicating that network measures contain information that relate to the rate of hippocampal atrophy beyond volumetric measures.

3.4. Prediction of atrophy rates in control individuals

We then performed analyses in cognitively unimpaired, amyloid/tau normal, age-matched individuals (control) to investigate whether the observed effects were specific for preclinical AD individuals. At baseline, controls had more years of education ($p<0.05$) and slightly higher grey matter volume ($p<0.065$) compared to preclinical AD (see Supplementary Table 3). We observed slightly higher path length values ($p<0.065$) and higher gamma, lambda and small-world coefficient values (all $p<0.05$) for control as compared to preclinical AD, suggesting that networks were more random in preclinical AD individuals. Over time, controls also showed cortical atrophy with the steepest rate in the left hippocampus (β±SE; -0.1±0.01; $p<0.001$; see Supplementary Figure 4), albeit at a much slower rate than preclinical AD. We found no effects of baseline whole-brain grey matter network measures or other AD markers (i.e., CSF total tau, MMSE, total grey matter volume) on the rate of future hippocampal atrophy in control individuals (see Supplementary Table 4). On a regional level, higher baseline clustering and path length values of the anterior cingulate and precuneus were associated with faster atrophy rates in mostly frontal and temporal regions, but not the hippocampus (see Supplementary Fig. 5; see Supplementary Fig. 6 for cross-sectional relationships).

3.5. Effect of tau and sex on network disruptions and associations with hippocampal atrophy rates

Finally, we investigated the potential influences of tau abnormality and sex on our analyses. Individuals with abnormal levels of total tau (n=30) were on average older, had lower levels of CSF amyloid beta 1-42 and had lower connectivity density and clustering values at baseline compared to those with normal levels of tau (n=80) (p<0.05; see Supplementary Table 5). There was no effect of tau abnormality on hippocampal atrophy rates over time (see Supplementary Table 6). When including tau abnormality as additional interaction term with the predictors for hippocampal atrophy we observed no significant effects, suggesting that individuals with abnormal and normal tau levels show similar associations between AD markers or grey matter network measures and hippocampal atrophy rates (all $p_{interaction}$ >0.05; Supplementary Table 6).

Comparing female to male individuals with preclinical AD, male individuals were on average older, more highly educated, had higher total intracranial volume and grey matter volume, while they showed lower normalized grey matter volume compared to female preclinical AD individuals (p<0.05; Supplementary Table 7). Male individuals further showed higher network size and degree and lower lambda values at baseline. Both sexes had similar hippocampal atrophy rates over time ($p_{interaction}$>0.05; Supplementary Table 8). Repeating analyses for hippocampal atrophy including sex as an additional interaction term showed stronger associations between connectivity density and clustering values with future hippocampal atrophy rates in female preclinical AD individuals as compared to males (interaction β±SE; both -0.05±0.02, p<0.05; Supplementary Table 8).

4. Discussion

The main result of our study is that individuals with preclinical AD who had low clustering and high path length values in early amyloid accumulating regions (i.e., anterior cingulate and precuneus) showed faster rates of subsequent atrophy in distant temporal and frontal regions. These results suggest that grey matter network measures may have use for identifying those individuals with preclinical AD who will show disease progression, but before overt atrophy.

Individuals with preclinical Alzheimer's disease are at increased risk for cognitive decline (Donohue et al., 2017; Parnetti et al., 2019; Vos et al., 2013). In our sample 25% of individuals with preclinical Alzheimer's disease progressed to mild cognitive impairment or dementia during follow-up, which is in line with previous estimates (Donohue et al., 2017; Parnetti et al., 2019; Vos et al., 2013). Furthermore, we observed that individuals with preclinical Alzheimer's disease who later showed clinical progression had lower gamma values at baseline than those who remained stable, replicating our previous observations in another clinical cohort (Tijms et al., 2018). We further found that lower grey matter network measures at baseline predicted future hippocampal atrophy rates, whereas MMSE scores, CSF total tau or total grey matter volume were not associated with individual rates of hippocampal atrophy, suggesting that network measures might capture more subtle neurodegenerative changes in very early preclinical stages. We did not find associations between network measures and future hippocampal atrophy rates in cognitively-unimpaired age-matched individuals without amyloid or tau pathology, suggesting that these effects were specific for individuals with preclinical AD. A practical implication of our findings is that disrupted grey matter network measures may have use to identify those individuals with preclinical AD who will show disease progression but *before* the onset of irreversible atrophy and cognitive impairment. These results warrant further study in multiple independent datasets to

investigate to what extent single-subject grey matter network measures can be used for e.g. patient identification in clinical trials.

One unresolved question in AD is the seeming spatiotemporal disconnect between the brain areas that are prone to aggregate amyloid early in the disease, and medial temporal lobe atrophy in later disease stages. One hypothesis is that this might be driven by network (dis)connections: disruption of local synaptic functioning or connectivity due to amyloid (Koffie et al., 2009; Shankar et al., 2008; Walsh et al., 2002) and subsequent early neuronal cell death might lead to the loss of neurotrophic factors and/or absence of stimulation, and thus atrophy of connected, but still more distant regions (Salehi et al., 2006; Seeley et al., 2009). A previous study showed that group-based structural covariance networks were indeed predictive for the locations of dementia type specific atrophy patterns (Seeley et al., 2009). Our results further extent on that work by showing with our single-subject approach in preclinical AD that grey matter network measures in early amyloid accumulating regions can predict the rate of future atrophy and the anatomical location in *individual* persons. It should be noted, however, that grey matter networks reflect similarity in grey matter morphology, or atrophy patterns, which could exist in the absence of direct anatomical connections. Future studies should further investigate the neurobiological basis of these findings in combination with functional measures, such as functional MRI or EEG/MEG, or anatomical measures such as DTI to further investigate in what way these distant regions are connected.

We also found that clustering coefficient and path length values were both related to subsequent atrophy in other distant and different regions of the brain, respectively in temporal and more frontal regions. This suggests that clustering and path length may reflect different aspects of neuronal degeneration as captured with grey matter covariance networks. Clustering values indicate the interconnectedness of neighboring nodes, while path length measures the average shortest connections between all nodes in the entire network (Rubinov

and Sporns, 2010). Possibly, lower clustering values (i.e., higher dissimilarity between neighboring nodes) reflect asynchronous atrophy of brain areas that were initially more similar to each other, while higher path length values (i.e., higher dissimilarity network-wide) potentially reflect asynchronous atrophy over the entire brain. Higher path length values were associated with faster future atrophy rates in predominantly frontal, but still widespread areas of the brain. These regions are affected relatively late in the disease by tau pathology (Braak & Braak, 1991). It would be of interest for future studies to investigate how network alterations are associated with tau PET patterns. Our analyses in age-matched individuals without amyloid or tau pathology, higher clustering and path length values were most consistently associated with faster atrophy rates in frontal and temporal regions, which are more associated with 'normal' aging processes (Fjell et al., 2014; Fjell et al., 2009). Our finding that *higher* clustering values were associated with faster atrophy rates in these individuals suggests that neighboring regions show uniform neurodegenerative changes, presumably due to causes other than amyloid aggregation. Taken together, our findings suggest that lower clustering values might indicate AD specific atrophy, while higher path length values may indicate brain alterations that might reflect 'normal' aging.

Our finding that preclinical AD showed globally lower path length values than controls, but similar local associations of higher path length values with faster atrophy rates seems conflicting. Additional post hoc comparisons for local path length values showed that for preclinical AD, path length values were lower in mostly temporal regions compared to controls (Supplementary Figure 7), which explains the differences in global path length values. Importantly, local path length values did not differ between the groups for our a priori defined target regions (i.e., anterior cingulate and precuneus). These results and our findings of similar local associations of higher path length values with faster atrophy rates further

support that local path length values of the anterior cingulate and precuneus may reflect normal aging processes.

We found no associations between baseline MMSE scores, CSF total tau or total grey matter volume with future hippocampal atrophy. Individuals with preclinical AD are still cognitively normal, and all had very high MMSE scores, and so the limited variability may explain the lack of predictive power for hippocampal atrophy. Furthermore, while changes in CSF total tau levels might occur relatively early in the disease process around the same time as atrophy in the hippocampus starts (Bateman et al., 2012), previous studies in individuals with preclinical AD also did not find direct associations between levels of CSF total tau and hippocampal (Wang et al., 2015) or entorhinal cortex atrophy (Desikan et al., 2011), which is in line with our findings. Additionally, the observed associations between network measures and hippocampal atrophy did not depend on tau abnormality, and there were no differences between individuals with abnormal and normal levels of total tau in grey matter network disruptions (when accounting for age differences). Possibly, this indicates that CSF total tau levels and grey matter network disruptions may reflect different aspects of neurodegeneration. In line with this explanation, we previously also found that when predicting clinical progression in predementia AD grey matter network measures contained predictive information in addition to CSF total tau levels (Tijms et al., 2018). Another previous study reported higher clustering values for individuals with abnormal levels of phosphorylated tau in CSF (Cantero et al., 2018). Possibly, the discrepancy with our results is that those individuals had normal amyloid levels, which has also been called ‘suspected non-Alzheimer disease pathophysiology’ or ‘SNAP’ (Jack et al., 2016) which reflects other disease causes than AD. Possibly, grey matter networks changes differently depending on the underlying pathology, and future research should further investigate grey matter network alterations in SNAP populations. Additionally, baseline total grey matter volume, precuneus and anterior

cingulate volumes were not associated with future hippocampal atrophy, suggesting measurable, gross atrophy had not manifested yet in these individuals. These findings are in line with the notion that whole-brain grey matter network measures contain more information than more simple volumetric measures and suggest that network measures can predict hippocampal atrophy before irreversible overt atrophy and cognitive impairment manifest.

Finally, we observed that the associations of connectivity density and clustering values on hippocampal atrophy were stronger for female as compared to male individuals, while there were no significant differences between female and male individuals in baseline network measures or hippocampal atrophy rates over time. While to date no study has investigated the effect of sex specifically on grey matter disruptions in AD, this result seems to be in line with other studies showing that female individuals who have higher levels of amyloid show relatively faster hippocampal atrophy or cognitive decline as compared to male individuals, and as such hint at potentially higher susceptibility for AD pathology in women (Buckley et al., 2018; Koran et al., 2017). Future studies should further investigate potential implications of sex differences for individual patient-based measures on their e.g. grey matter network measure profile.

A potential limitation of our study is that although this is the largest longitudinal dataset on preclinical AD available, with individuals followed up to nine years, the median follow-up duration was of 2.2 years. Therefore, we cannot exclude the possibility that more individuals would have shown disease progression if they would have been followed for a longer period of time. Still, even within this relatively short median follow-up duration we were able to observe a relationship between baseline grey matter network measures and subsequent atrophy. Another potential limitation of this study is that, while we ensured that scans of the same field strength were included within subjects, field strengths differed between individuals. To account for this we included field strength as covariate in our analyses, and

although we cannot exclude that this might have influenced our results, previous studies in ADNI have shown similar atrophy rate estimates for 1.5 Tesla and 3 Tesla scans (Dicks et al., 2019; Ho et al., 2010). A strength of this study is the use of our method to construct individual participant level grey matter networks, whereas previous approaches only allowed to construct one network across a group of individuals. This method enabled us to investigate associations of grey matter network measures and atrophy rates within individuals. Furthermore, grey matter networks were reconstructed from structural MRI, which is routinely acquired in patient care and therefore has high potential to translate to daily practice.

5. Conclusion

In conclusion, we showed that lower grey matter network measures in early amyloid accumulating regions predict the rate and anatomical pattern of future atrophy in cognitively normal individuals with abnormal amyloid markers. These results suggest that grey matter network measures are a sensitive measure to detect future grey matter atrophy, and so may be useful as a tool to select individuals for potential prevention opportunities in the earliest stages of AD.

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Disclosure Statement

E. Dicks has nothing to disclose.

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Tables and Figures

Table 1. Baseline characteristics of the total sample and by clinical progression.

	Total	Stable	Progression
N	110	82 (75%)	28 (25%)
Female	63 (57%)	51 (62%)	12 (43%)
Age in years	74.871 (6.084)	74.05 (6.357)	77.275 (4.487)*
MMSE	29 (29-30)	29 (29-30)	29 (28-30)
Education in years	16 (14-18)	16 (14-18)	16 (14-18)
CSF Aβ 1-42 in pg/ml	149.166 (25.393)	150.138 (25.626)	146.321 (24.934)
CSF total tau in pg/ml	73.845 (38.418)	71.063 (39.216)	81.989 (35.391)
Abnormal total tau >93 pg/ml	30 (27%)	20 (24%)	10 (36%)
Total intracranial volume in cm^3	1439.591 (144.808)	1417.037 (145.665)	1505.643 (122.185)**
Grey matter volume in cm^3	0.601 (0.067)	0.597 (0.069)	0.614 (0.064)
[a]Normalized grey matter volume in cm^3	0.419 (0.04)	0.423 (0.038)	0.409 (0.043)
Number of repeated MRI	5 (4-6)	5 (4-5.8)	6 (3.8-7.2)*
Follow-up time in years	2.2 (2-4)	2.1 (2-4)	4 (2.2-6)**
Size	6753.082 (606.983)	6658.341 (616.29)	7030.536 (490.741)**
Degree	1204.765 (132.373)	1191.003 (129.279)	1245.069 (135.429)†
Connectivity density	17.845 (1.14)	17.896 (1.092)	17.697 (1.279)
Clustering	0.49 (0.022)	0.491 (0.021)	0.485 (0.023)
Path length	1.998 (0.021)	2 (0.021)	1.993 (0.022)
Gamma	1.688 (0.079)	1.698 (0.076)	1.661 (0.084)*
Lambda	1.097 (0.012)	1.098 (0.012)	1.093 (0.012)†
Small-world coefficient	1.539 (0.058)	1.545 (0.055)	1.519 (0.064)*

Data are presented as N (%), mean (SD) or median (IQR) where appropriate.

[a]Grey matter volume was normalized to total intracranial volume.

†$p<0.065$; *$p<0.05$; **$p<0.01$

Figure 1. Surface plots of regional atrophy rates over time. The color bar indicates standardized betas of regional atrophy rates and were obtained with linear mixed models. Analyses were adjusted for age, sex, education, field strength and total intracranial volume. Subcortical structures are plotted in ventricular areas as approximation. L, left hemisphere; R, right hemisphere.

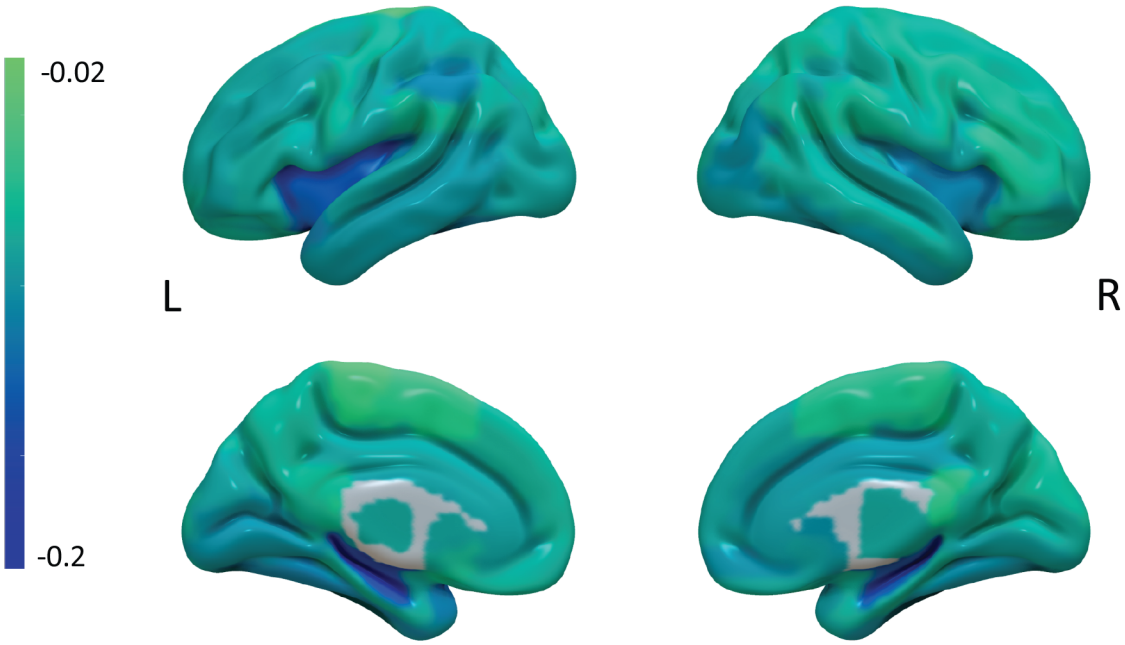
Table 2. Effects of baseline AD markers and grey matter network measures on cross-sectional and longitudinal hippocampal volume.

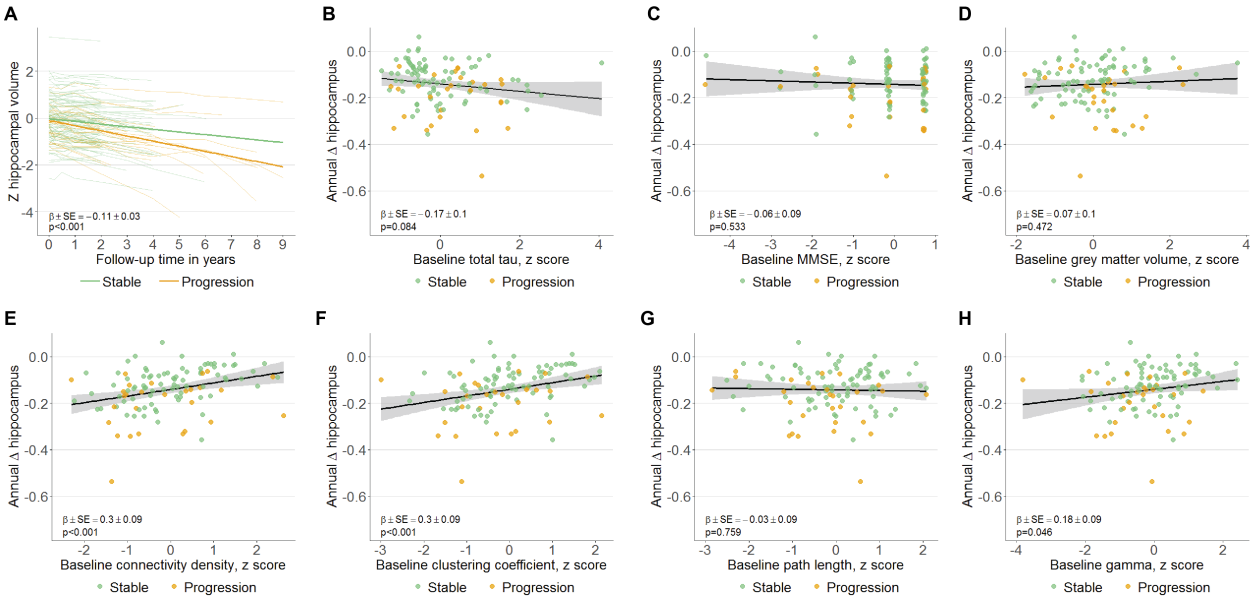
	Cross-sectional effects	Longitudinal effects
MMSE	0.11±0.07	-0.01±0.01
CSF total tau	0±0.08	-0.02±0.01
Grey matter volume	0.63±0.07***	0±0.01
Grey matter network measures		
Size	0.04±0.1	-0.02±0.01
Degree	-0.11±0.1	0.01±0.01
Connectivity density	-0.06±0.06	0.04±0.01**
Clustering	-0.04±0.07	0.04±0.01**
Path length	0.1±0.05	-0.01±0.01
Gamma	0.07±0.07	0.02±0.01
Lambda	0.09±0.06	0.02±0.01
Sigma	0.06±0.08	0.02±0.01

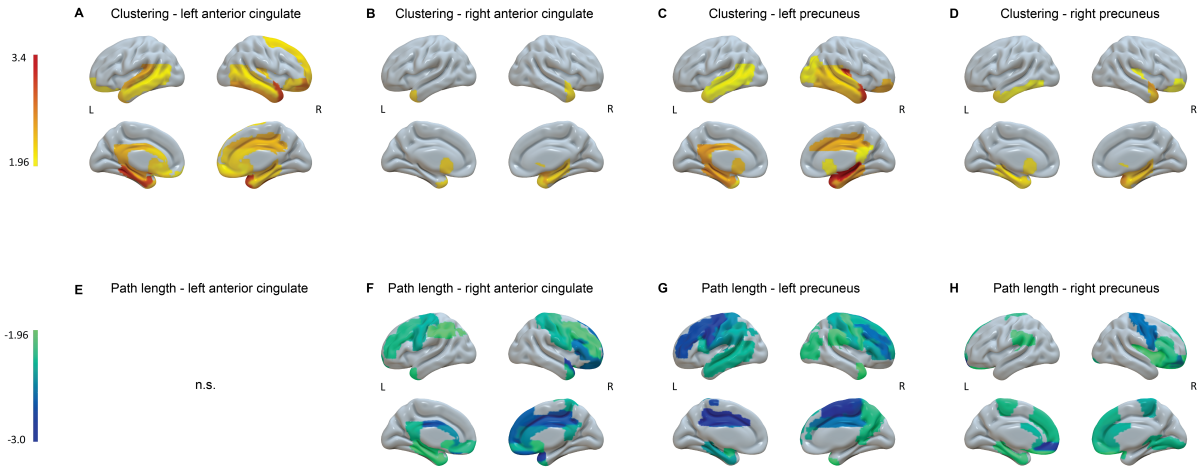
Data are presented as β±SE. Linear mixed models included the terms for the baseline values of the respective predictor (e.g. baseline MMSE), follow-up time in years and their interaction (e.g. baseline MMSE × time). Cross-sectional effects represent the association between AD markers or grey matter network measures and hippocampal volume when time is held constant and are given by the main term for the respective predictor. Longitudinal effects describe the association between baseline AD markers or grey matter network measures on the rate of change in hippocampal volume over time and are given by the interaction term for the respective AD marker or network measure × time. All analyses were corrected for age and gender, and additionally adjusted for field strength for grey matter volume, and field strength and baseline grey matter volume for grey matter network measures. **p<0.01; ***p<0.001. P-values are adjusted with the false-discovery rate.

Figure 2. Association of baseline AD markers and whole-brain grey matter network measures with hippocampal atrophy rates. Predicted decline in hippocampal volume over time (a) and associations of baseline AD markers (b-d) and whole-brain grey matter network measures (e-h) with subject-specific annual hippocampal atrophy rates. Longitudinal decline in hippocampal volume over time was estimated with linear mixed models adjusted for age, sex, field strength and total grey matter volume. To aid in comparison of predictive performances we report standardized β±SE for (b-h) as estimated with linear regression analyses. Linear regression analyses included the terms for subject-specific annual hippocampal atrophy rates as outcome and baseline values of AD markers (b-d) or grey matter network measures (e-h) as the respective predictor. Note that standardized betas for (b-h) estimated with linear regression analyses do not correspond to the betas in Table 2, which were estimated with linear mixed models.

Figure 3. Longitudinal effects of baseline precuneal and anterior cingulate network measures on regional atrophy over time. The color bar indicates the effect strength as t ratios, which were obtained with linear mixed model analyses with longitudinal regional grey matter volume as outcome and time, baseline network measure (e.g. clustering in the left anterior cingulate for panel a) and their interaction (time × network measure) as predictors. Analyses were adjusted for age, sex, field strength and total grey matter volume. Subcortical structures are plotted in ventricular areas as approximation. L, left hemisphere; R, right hemisphere n.s., not significant.







Single-subject grey matter networks predict future cortical atrophy in preclinical Alzheimer's disease

Ellen Dicks[a], Wiesje M. van der Flier[a,b], Philip Scheltens[a], Frederik Barkhof[c], Betty M. Tijms[a], for the Alzheimer's Disease Neuroimaging Initiative*

Highlights

- Study if grey matter network measures can predict future atrophy in preclinical AD
- Network measures, but not other AD biomarkers, predict hippocampal atrophy rates
- Network measures in early-Aβ accumulating regions predict the rate and location of atrophy
- Grey matter networks detect AD-related pathological changes before overt atrophy

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Author contributions

E.D. processed all image data, performed the statistical analyses, interpreted data and drafted the manuscript. W.M.v.d.F., F.B. and P.S. interpreted data. B.M.T. was responsible for the study design and concept, contributed to the analyses and interpreted data. All co-authors have read and critically revised the manuscript.

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Verification

We confirm that the data contained in the manuscript being submitted have not been previously published, have not been submitted elsewhere and will not be submitted elsewhere while under consideration at *Neurobiology of Aging*.

All authors have reviewed the contents of the manuscript being submitted and approve of its contents.

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