#### **RESEARCH ARTICLE**

Alzheimer's & Dementia®

# **Biomarker pathway heterogeneity of amyloid-positive individuals**

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# **Abstract**

**INTRODUCTION:** In amyloid-positive individuals, disease-related biomarker heterogeneity is understudied.

**METHODS:** We used Subtype and Stage Inference (SuStaIn) to identify data-driven subtypes among cerebrospinal fluid (CSF) amyloid beta (1-42)–positive individuals from the Alzheimer's Disease Neuroimaging Initiative (ADNIGO/2 [*n* = 376]). Variables included: CSF phosphorylated tau (p-tau181), hippocampal and whole-brain volume, logical memory (LM), composite Trail Making Test score, and white matter hyperintensity (WMH) volumes. CSF amyloid-negative, apolipoprotein E *ε*4 non-carrier cognitively unimpaired controls (*n* = 86) were used to calculate *z* scores.

**RESULTS:** One subtype (*n* = 145) had early LM changes, with later p-tau and WMH changes. A second subtype (*n* = 88) had early WMH changes, were older, and more hypertensive. A third subtype (*n* = 100) had early p-tau changes, and reflected typical Alzheimer's disease. Some amyloid positive (*n* = 43) individuals were similar to the amyloid-negative group.

**DISCUSSION:** This work identified heterogeneity in individuals who are conventionally considered homogeneous, which is likely driven by co-pathologies including cerebrovascular disease.

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#### **KEYWORDS**

Alzheimer's disease, amyloid positive, heterogeneity, mixed dementia, subtype and stage inference, vascular pathology

#### **Highlights**

- ∙ Data-driven modeling identified marker heterogeneity in amyloid-positive individuals.
- ∙ Heterogeneity reflected Alzheimer's disease-like, vascular-like, and mixed pathology presentations.
- ∙ Some amyloid-positive individuals were more similar to amyloid-negative controls.
- ∙ Vascular pathology plays a key role in understanding heterogeneity in those on the amyloid pathway.

# **1 INTRODUCTION**

The National Institute on Aging–Alzheimer's Association research framework suggests that the detection of amyloid beta (A*β*) 1-42 (amyloid) is sufficient as a biological definition of the Alzheimer's disease  $(AD)$  continuum,<sup>[1](#page-10-0)</sup> with amyloid abnormality (measured either by cerebrospinal fluid [CSF] or positron emission tomography [PET]) preceding other AD manifestations.<sup>[2](#page-10-0)</sup>

Following the amyloid cascade hypothesis, $3$  hypothetical models have proposed a temporal ordering of biomarkers prior to symptom development.<sup>[1](#page-10-0)</sup> In these, first amyloid deposition occurs, followed by accumulation of intracellular tangles comprised of tau protein, then brain atrophy, and finally worsening memory and daily functioning. While this provides some understanding of the expected biomarker ordering pathway, there is likely some heterogeneity in the ordering among groups of individuals. One study exploring the temporal ordering of biomarkers in a combined group of cognitively unimpaired individuals, those with mild cognitive impairment (MCI), and those with AD, derived heterogeneous subtypes displaying a typical AD pathway, alongside others displaying a more vascular or mixed pathology tempo-ral ordering.<sup>[4](#page-10-0)</sup> Heterogeneity was further explored by Habes et al.,<sup>[5](#page-10-0)</sup> and identified atrophy pattern differences (hippocampal sparing, medial temporal lobe dominant, parietal dominant, limbic predominant) in an AD-like cohort.

Other factors like those mentioned above contribute to the heterogeneity of disease, meaning homogeneity of those already on the amyloid pathway is unlikely. As potential therapies target removal of amyloid deposition, $6$  having a clear understanding of the possible progression pathways that individuals may follow would allow better prediction of potential trajectories in studies and assessments.

Known examples of heterogeneity in amyloid-positive individuals include a subtype in which there is minimal atrophy in the hippocam-pus while general cerebral atrophy is present.<sup>[7](#page-10-0)</sup> Meanwhile there is evidence that although individuals may be amyloid positive, they do not necessarily further progress clinically. $8$  Heterogeneity may also be driven by the presence of vascular pathology, with white matter

hyperintensities (WMH) being a key marker related to future clinical progression.<sup>[9](#page-10-0)</sup> WMH pathology seems to have an additive relationship with A*β*, [10](#page-10-0) accelerating the progression of AD.

As AD processes likely occur over decades, long-term follow-up of individuals would be ideal to identify different groupings of disease trajectories. However, such studies are expensive and prone to substantial drop-out. Recent data-driven methods allowed identification of heterogeneity in biomarker ordering using cross-sectional data. One such data-driven method, Subtype and Stage Inference (SuStaIn) can be used to simultaneously subtype and stage individuals using cross-sectional data, $11$  and has been applied in multiple diseases and is validated longitudinally. $12-14$ 

This study applied SuStaIn to amyloid-positive individuals, to discover data-driven subtypes of those on the amyloid pathway. Here we look at typical markers associated with AD (cognitive impairment, tau, and brain volumes), along with a marker of presumed cerebrovascular disease (WMH). It was hypothesized that one subtype would follow the typically identified pattern (tau, then atrophy, then cognitive scores), whereas another subtype might show early presumed cerebrovascular disease. It is also hypothesized that, despite these individuals having evidence of amyloid deposition, a group like cognitively unimpaired controls would be identified.

## **2 METHODS**

## **2.1 Cohort**

Data used in the preparation of this article were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database (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), PET, other biological markers, and clinical and neuropsychological assessments can be combined to measure the progression of MCI and early AD. For up-to-date information, see [www.](http://www.adni-info.org) [adni-info.org.](http://www.adni-info.org)

#### **RESEARCH IN CONTEXT (120/150)**

- 1. **Systematic review**: Authors reviewed literature using traditional (e.g., PubMed) sources. We assessed articles that examined Alzheimer's disease (AD)–related and vascular marker heterogeneity in amyloid-positive individuals. This included associations between markers, and potential temporal orderings of marker abnormalities.
- 2. **Interpretation**: We found that three heterogenous subtypes were present in a cohort of amyloid-positive individuals. This included a group of individuals with a typical AD-like pathway, a more mixed pathology group, and a more vascular-dominant group. We add to the continued literature that emphasizes the likely important role of vascular pathologies in AD.
- 3. **Future directions**: As the role of vascular pathologies becomes more present in AD, understanding how this further reflects temporal and continued heterogeneity in AD-assumed cohorts is necessary.

Newly enrolled ADNI2 and ADNIGO individuals were used in the current study. This included (1) a CSF amyloid-negative, cognitively normal (CN) diagnostically stable group (amyloid-negative controls) and (2) a group of amyloid-positive cases.

The amyloid-negative controls were used to produce normalized *z* scores of the amyloid-positive cases. To be included in this group, controls had to be CSF amyloid negative (above cut-point 262 pg/mL), apolipoprotein E (*APOE*) *ε*4 non-carriers, and have remained diagnostically CN throughout their follow-up in ADNI.

The amyloid-positive cases were those used to create data-driven SuStaIn subtypes. This group was defined as CSF amyloid positive (below cut-point 262 pg/mL). Individuals could have any diagnosis at baseline or follow-up.

CN individuals were defined by having a Mini-Mental State Examination (MMSE) score between 24 and 30 (inclusive) at baseline and a Clinical Dementia Rating (CDR) score of 0. CN individuals were normally functioning as measured by education-adjusted scores on delayed recall of one paragraph from Wechsler Memory Scale Logical Memory II. CN individuals who reported subjective memory concerns were labelled SMC. Individuals with MCI were required to have an MMSE score between 24 and 30 (inclusive) at baseline, objective memory loss by education-adjusted scores on Wechsler Memory Scale Logical Memory II, a global CDR equal to 0.5, and report subjective memory concern. Individuals with AD were defined by having an MMSE score between 20 and 26 (inclusive), a CDR of 0.5 or 1.0, subjective memory concern, and National Institute of Neurological and Communicative Disorders and Stroke–Alzheimer's Disease and Related Dementias Association criteria for probable AD.

Individuals were given a diagnosis at baseline, month 6, month 12, and then yearly. At follow-up, those with evidence of clinical progression were given a converting diagnosis by a physician on site, whereas those with improvements may receive a reverting diagnosis.

To be included in this study, individuals had to have a complete set of observations of CSF A*β*1-42 and phosphorylated tau (p-tau181) at their baseline visit; suitable MRI scans that produced quality measures ofWMH, whole-brain, hippocampal, and total intracranial volume (TIV) measurements; and neuropsychology test scores for Trail Making Test (TMT) A, TMT B, and logical memory (LM).

# **2.2 CSF measurements**

Baseline CSF A*β*1-42 and p-tau181 measurements (raw) from the ADNI biomarker core (University of Pennsylvania) using the microbead-based multiplex immunoassay, the INNO-BIA AlzBio3 RUO test (Fujirebio, Ghent, Belgium), on the Luminex platform (LuminesCorp, Austin, TX, USA) were obtained (UPENN-CSF-Biomarker-Data-Master [ADNI1, GO, 2], Version: 2016-07-05).

A Gaussian mixture model (GMM) established the value of CSF amyloid used to identify amyloid-negative and amyloid-positive individuals, using available baseline CSF amyloid raw values for all ADNI2/GO individuals. In this, a histogram was plotted for the data and two datadriven bimodal Gaussians were identified. A cut-point was used to separate the two Gaussians at 99th percentile.

### **2.3 Cerebrovascular measurements**

WMH of presumed vascular origin were previously calculated using cross-sectional Bayesian model selection (BaMoS) applied to T2 fluidattenuated inversion recovery (FLAIR) and T1-weighted images,  $15$  with all outputs visually assessed by experienced raters.<sup>[16](#page-10-0)</sup> Numbers of probable and definite microbleeds were previously identified and counted using the Microbleed Anatomical Rating Scale (MARS).<sup>[17](#page-10-0)</sup>

The number of lacunes of presumed vascular origin were obtained from measures in previous work by our group. $4$  Lacunes were identified on T2-FLAIR, using co-registered T1-weighted imaging as an anatomical reference. Lacunes were only included in regions of white matter in the territory of perforating arterioles and of size between 3 and 15 mm. All lacunes were checked by a neuroradiologist.

#### **2.4 Brain volume measurements**

Whole-brain, hippocampal, and total intracranial volume (TIV) were previously extracted from T1-weighted scans. Whole-brain volumes were calculated using the automated Multi-Atlas Propagation and Segmentation (MAPS) tool, $18$  with quality control and manual edits made using MIDAS.<sup>[19](#page-11-0)</sup> Hippocampal volumes were obtained using a similar approach, using Similarity and Truth Estimation for Propagated Segmentations (STEPS),<sup>20</sup> and TIVs were calculated from T1-weighted images using geodesic information flows (GIF). $21$ 

# **2.5 Neuropsychology**

LM and TMT A and TMT B were acquired as part of ADNI neuropsychology battery. LM scoring was based on total number of story units recalled. Both TMT A and TMT B are scored as time to complete. For TMT B, a ceiling is present for individuals that took longer than 300 seconds to complete the task. A composite TMT score was produced, as scores are correlated, and TMT A and B are argued to be a less specific measure of executive functioning alone. A more specific measure of executive functioning was derived using TMT B minus TMT  $A^{22}$ , as it is suggested to minimize visuoperceptual and working memory demands.

#### **2.6 Neurofilament light**

Neurofilament light (NfL) quantification was performed by Blennow labs and downloaded from ADNI. Plasma NfL was analyzed using the single molecule array (Simoa) technique. The assay used a combina-tion of monoclonal antibodies and purified bovine NfL as a calibrator.<sup>[23](#page-11-0)</sup> Samples were measured in singlicate, with a technical lower limit 6.7 pg/mL.

# **2.7 Demographics,** *APOE***, and medical history**

Diagnostic and demographic data (age, sex, *APOE ε*4 carrier status, medical history [hypertension and stroke]), and follow-up time were downloaded from the ADNI database (adni.loni.usc.edu/).

### **2.8 Statistical analysis**

# 2.8.1 | Data transformation

WMH were log transformed ( $log<sub>2</sub>$ ). As SuStaIn regards increasing numbers as a poorer score, negative direction scores (LM, hippocampal volume, whole-brain volume) were inverted.

Using the amyloid-negative controls, *z* scores were produced for LM, TMT composite, and p-tau. For WMH, whole-brain volume, and hippocampal volume, covariate-corrected *z* scores were produced to account for TIV.<sup>[24](#page-11-0)</sup>

# 2.8.2 | SuStaIn

A *z* score SuStaIn approach was followed, and is explained in previous wor[k11](#page-10-0) Briefly, *z* score SuStaIn is a generalization of the original event-based model.<sup>[25,26](#page-11-0)</sup> The event-based model describes disease progression as a series of events, with each event corresponding to biomarker progression from normal to abnormal. The *z* score model of SuStaIn follows from this approach with each event representing the linear accumulation of biomarkers from one *z* score (1 standard deviation difference from amyloid-negative control group mean) to

another. This results in variable patterns of *z* score events, producing heterogeneous groups (subtypes).

To be included in the SuStaIn model, *z* scores from continues markers were needed. Here we look at typical markers associated with AD (cognitive impairment, tau, and brain volumes), along with a marker of presumed cerebrovascular disease (WMH) as cerebrovascular disease and dysfunction has been shown to be a core feature of AD.[27,28](#page-11-0) The markers of interest included in the current model assess features anticipated to become abnormal in those progressing along the amyloid pathway according to the hypothetical model of AD. This includes cognition (LM, composite TMT); tau (CSF p-tau181); neurodegeneration (whole-brain volume and hippocampal volumes), along with a measure of presumed cerebrovascular disease (WMH volume). As lacunes and cerebral microbleeds (CMBs) were binary measures, they were not included in the SuStaIn model, but were included in demographics.

This implementation of SuStaIn used *z* scores 1 through 3, and had a maximum number of *z* scores of 5. Histograms of the *z* scores were produced to visualize that three *z* scores was appropriate to represent the data, with three *z* scores representing  $\approx$  75% of the data (Figure [S1](#page-12-0) in supporting information).

The log likelihood across Markov chain Monte Carlo (MCMC) samples were initially used, across each subtype. Separation of MCMC trace suggests distinctly different subtypes. Ten-fold cross-validation was performed to further investigate the optimal number of subtypes within the data. The cross-validation information criterion (CVIC) is an information criterion that balances model complexity with model accuracy, with a lower CVIC indicating a better balance between the two. Models with the lowest CVIC would be the better fit; however, small improvements  $(< \approx 6)$  in CVIC with a more complex model would suggest use of a less complex (fewer subtyped) model. A maximum of four subtypes were tested, with the best balance from MCMC and CVIC found using three subtypes (see Figures [S2, S3](#page-12-0) in supporting information). Sample sizes were also plotted as a histogram in Figure [S4](#page-12-0) in supporting information, with smaller sample sizes in later stages suggesting higher stage uncertainty. Probabilities over SuStaIn stages were plotted in Figure [S5](#page-12-0) in supporting information, to ensure no crossover events are present in each stage.

## 2.8.3 | Evaluation of cohort

We provided demographic details of the entire cohort by their baseline diagnosis, prior to subtyping using SuStaIn. This included markers used in the SuStaIn model, and other markers of interest.

# 2.8.4 Evaluation of identified subtypes

Tables and figures were produced to better explain the data-driven subtypes, and differences between groups are described. This included reporting demographics, genetics, imaging markers, and medical history, with linear regression and Fisher exact test. We also present mean and standard deviations for SuStaIn markers after subtypes were

#### **TABLE 1** SuStaIn cohort basic demographic data.



*Note*: Basic demographics for both the controls and cases used in SuStaIn. Mean values and SD are reported, unless otherwise stated.

Abbreviations: AD, Alzheimer's disease; CMB, cerebral microbleed; CN, cognitively normal/healthy control; CSF, cerebrospinal fluid; IQR, interquartile range; LM, logical memory; MCI, mild cognitive impairment; MMSE, Mini-Mental State Examination;*N*#, number; p-tau, phosphorylated tau; SD, standard deviation; SuStaIn, subtype and stage inference; TIV, total intracranial volume; TMT, Trail Making Test; WMH, white matter hyperintensities.

\*Probable AD.

\*\*Volumes report in the table are unadjusted.

derived. Later diagnostic progression of individuals (from diagnostic CN, or MCI) within their subtype, is also reported with Fisher exact test used to evaluate proportional difference between subtypes.

# 2.8.5 Visualization of results

Subtypes are plotted in a positional variance diagram to interpret subtype progression. This includes the staging of the event by *z* score distance away from the normalized amyloid-negative controls (one *z* score [red], two *z* scores [magenta], three *z* scores [blue]). We refer to this as a *change* or *event* throughout this work. Colors between these three *z* scores represent uncertainty in the event staging. In later stages with smaller sample sizes Figure [S4\)](#page-12-0), we include a dashed line in each positional variance diagram, $^{13}$  starting from instances with two consecutive stages of two subjects or fewer.

To accompany mean values of SuStaIn markers in each subtype, we also presented individual marker values per SuStaIn stage within each subtype, and report pairwise correlation coefficients to examine relationships of marker difference between event stage within subtype. We report semi-partial correlations for composite TMT (adjusted for a ceiling effect of TMT B), and for WMH, whole-brain, and hippocampal volumes (TIV adjusted). We further produced pie charts for each subtype based on their baseline diagnosis, and later diagnostic progression (with Fisher exact test to formally examine these proportions).

#### **3 RESULTS**

Of an initial sample of 649, 187 were excluded as they did not meet criteria for the amyloid-negative controls (CSF amyloid-negative, *APOE ε*4 non-carrier, stable CN) or amyloid-positive cases (CSF amyloidpositive). A further 24 were excluded due to missing marker data (TMT B). This is visualized in Figure [S6](#page-12-0) in supporting information.

The remaining 462 individuals (amyloid-negative controls  $n = 86$ , amyloid-positive cases  $n = 376$ ) were included in the study.

Table 1 details the demographics of the amyloid-negative controls and amyloid-positive cases. Descriptively, the amyloid-negative controls were on average younger, had higher cognitive scores (composite TMT, LM), lower p-tau, lower WMH, lower proportions of CMB, and higher whole-brain and hippocampal volume than the amyloidpositive cases. Within the amyloid-positive cases, cognitive scores were lower, hippocampal volume was lower, and p-tau levels were higher, with diagnostic progression. WMH burden was highest in AD, while CMB proportions were similar between diagnostic subgroups of the amyloid-positive cases.

From *z* score SuStaIn, three distinct subtypes were derived (see Figure [1](#page-5-0) for subtype proportional variance diagrams). A portion of individuals were not subtyped as they did not have different measures to the stable CN group ( $n = 43$ ). We refer to this group as unsubtyped. For subtype one ( $n = 145$ ), named Memory led, SuStaIn determined LM change to be the initial event, followed by p-tau, hippocampal

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**FIGURE 1** SuStaIn subtyping depicting biomarker event staging by ordering of standardized scores (one *z* score [red], two *z* scores [magenta], three *z* scores [blue]), with colors between these scales highlighting uncertainty in event staging. WMH used log<sub>2</sub>. A dashed line for each subtype is included to represent higher uncertainty in the diagrams, in which number of subjects is ≤ 2 for two consecutive stages. pTau, phosphorylated tau; SuStaIn, subtype and stage inference; WMH, white matter hyperintensities.

volume, and whole-brain volume. For subtype two  $(n = 88)$ , named WMH led, SuStaIn determined WMH change as an initial event, followed by LM, whole-brain volume, and composite TMT. For subtype three (*n* = 100), named p-tau Led, SuStaIn determined p-tau change as an initial event, followed by LM, hippocampal volume, and composite TMT. Event uncertainty is seen in all subtypes, notably in stages  $\geq 10$ , and is characterized by color spread toward later stages.

SuStaIn-determined subtype demographics are reported in Table [2.](#page-6-0) The unsubtyped group ( $n = 43$ ) were younger ( $P < 0.001$ ), with a high proportion of CN individuals (53%; two tailed *P <* 0.001). This group also has, on average, more years in education (*p <* 0.001) and the highest MMSE score (*p <* 0.001). They descriptively have a higher proportion of *APOE ε*4 carriers compared to the WMH led subtype, but lower than the Memory and p-tau led subtypes. The Memory led

subtype (*n* = 145) has a higher proportion of MCI and AD individuals (MCI = 64%, AD = 31%; two tailed *p <* 0.001), and is more male  $(P = 0.003)$ . The WMH led subtype  $(n = 88)$  is older than other subtypes (*p <* 0.001), and has the highest proportion of individuals with hypertension (two-tailed  $P = 0.03$ ), and lacunes present ( $P = 0.02$ ).

Mean values for markers used in SuStaIn subtyping are reported in Table [3,](#page-6-0) with marker level per SuStaIn stage reported in Figure [2](#page-7-0) (and Table [1\)](#page-12-0).

The unsubtyped group were on average less cognitively impaired (LM, composite TMT), had lower CSF p-tau, reduced WMH volume, and larger whole-brain and hippocampal volumes.

The Memory led subtype had the lowest LM score and smallest hippocampal volumes on average. Considering marker difference over SuStaIn stage, there was evidence to suggest significantly lower

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#### **TABLE 2** SuStaIn-determined subtype demographics, genetics, imaging markers, and medical history.



*Note*: Demographics of SuStaIn-derived subtypes, and the unsubtyped cohort. *p* values representing linear regression or Fisher exact test (diagnosis, sex, CMB, lacunes, APOE *ε*4 carrier, hypertension, stroke) between unsubtyped and subtyped groups,<sup>a</sup> and between subtypes.<sup>b</sup> Mean values and SD are reported unless otherwise stated.

Abbreviations: AD, Alzheimer's disease; *APOE*, apolipoprotein E; CMB, cerebral microbleed; CN, cognitively normal/healthy control; MCI, mild cognitive impairment; MMSE, Mini-Mental State Examination; N#, number; NfL, neurofilament light; SD, standard deviation; SuStaIn, subtype and stage inference; TIV, total intracranial volume; WMH, white matter hyperintensities.

**TABLE 3** Values of markers included in SuStaIn per subtype.



*Note*: Neuropsychological test scores and CSF/imaging biomarker values per subtype. Mean values and SD are reported unless otherwise stated.

Abbreviations: CSF, cerebrospinal fluid; IQR, interquartile range; LM, logical memory; *N*#, number; p-tau, phosphorylated tau; SD, standard deviation; TMT, Trail Making Test; WMH, white matter hyperintensities.

\*Volumes report in the table are unadjusted.

LM, whole-brain volume, hippocampal volume, and increased TMT composite, p-tau, and WMH (*p <* 0.001; all tests).

The WMH led subtype had  $\approx$  5 mL more WMH volume, lower whole-brain volumes, and had greatest impairment in composite TMT. Considering marker difference over SuStaIn stage, there was evidence to suggest significantly lower LM, composite TMT, whole-brain and hippocampal volume (*p <* 0.001; all tests), and a weaker increased p-tau (pairwise correlation coefficient 0.2, *P <* 0.03). There was no evidence of a difference in WMH volume over event stage.

The p-tau led subtype had the highest p-tau values, by *>* 20 pg/mL. Individuals in this subtype are more likely to be female (*p <* 0.003) and had a higher proportion of *APOE ε*4 carriers (*P <* 0.001) compared to the other subtypes. Considering marker difference over SuStaIn stage, there was evidence to suggest significantly lower LM, whole-brain volume, hippocampal volume, and increased TMT composite, p-tau, and WMH (*p <* 0.001; all tests).

Results for subsequent diagnostic progression (within 24 months) are displayed in Figure [3.](#page-8-0) There was no statistical evidence of a difference in progression between the unsubtyped and subtyped groups, or between subtypes. Missing diagnostic data for each subtype is further reported in Table [S2](#page-12-0) in supporting information.

<span id="page-7-0"></span>

FIGURE 2 Biomarkers by SuStaIn stage, across subtype. Individual volumes for subtypes for each stage across subtype are plotted, with a line of best fit. Pairwise correlation coefficient across subtype stage is reported in Table S1 in supporting information. pTau, phosphorylated tau; SuStaIn, subtype and stage inference; WMH, white matter hyperintensities.

# **4 DISCUSSION**

In this study *z* score SuStaIn was used to investigate biomarker ordering heterogeneity in a cohort of amyloid-positive individuals. SuStaIn identified three distinct subtypes, and an unsubtyped group.

## **4.1 Memory led subtype**

In this subtype (*n* = 145), SuStaIn determined an initial LM event, followed by p-tau, hippocampal volume, whole-brain volume, WMH, and composite TMT. Early LM events were likely as most MCI and AD in this cohort were amnestic, with deficits found in  $MCI<sup>29</sup>$  $MCI<sup>29</sup>$  $MCI<sup>29</sup>$  and AD.<sup>[30](#page-11-0)</sup> The subsequent events of p-tau, hippocampal, and whole-brain volume are expected according to the amyloid cascade hypothesis. $1$ 

CSF p-tau181 would be expected of those following a conventional AD-like pathway, although early staging uncertainty may suggest a non-typical AD pathway.

Earlier hippocampal volume events prior to cognitive domain tasks are typical in those with AD, as associative memory tasks are related to hippocampal activity.<sup>[29](#page-11-0)</sup> Amyloid deposition increases vulnerability of the hippocampus, $29$  which is a sensitive structure often affected prior

to global brain atrophy. $30$  This is supported by outcomes in previous work,<sup>[9](#page-10-0)</sup> with hippocampal volume a predictor of diagnostic progression. Whole-brain volume can be considered a general measure of neurodegeneration, and is expected to follow the more specific hippocampal atrophy in those with AD. Like whole-brain volume, WMH has later stage uncertainty, suggesting vascular pathology may not be as present in this subtype. Composite TMT events were later in this subtype, despite early LM events. This is likely because LM assesses general memory, $31$  while composite TMT assesses executive functioning.<sup>[22](#page-11-0)</sup>

Overall, this subtype seems to represent a mixed AD-like trajectory, with more cognitive impairment. This is reflective of many AD cases,[32](#page-11-0) particularly after initial diagnosis and at *post mortem*. [33,34](#page-11-0) Although early LM, p-tau, and hippocampal events suggest an AD-like group, marker stage uncertainty with p-tau could suggest other copathologies are present. As pathogenic features in vascular dementia (VaD) and  $AD^{35}$  $AD^{35}$  $AD^{35}$  overlap, vascular features are anticipated to influence this group's mixed presentation although lower WMH volume and hypertension risk suggest other underlying co-pathologies besides cerebrovascular disease may be present. Many with probable AD often show co-pathologies like TAR DNA-binding protein 43, *α*-synuclein pathology, Lewy bodies, or hippocampal sclerosis at *post mortem*, [36](#page-11-0) and future *post mortem* work must evaluate this.

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Diagnostically stable; Progression by month 24, Diagnostic regressor, Missing data Fisher's exact test for CN, between the unsubtyped group and those subtypes ( $p = 0.8$ ), and within subtypes ( $p = 0.6$ ) Fisher's exact test for baseline MCI individuals, between the unsubtyped group and those subtypes ( $p = 0.8$ ), and within subtypes ( $p = 0.6$ )

**FIGURE 3** Pie charts for diagnostic progression by 24 months within baseline diagnostic group (CN or MCI), by subtype group. CN, cognitively normal; MCI, mild cognitive impairment; pTau, phosphorylated tau; WMH, white matter hyperintensities.

## **4.2 WMH led**

In this subtype  $(n = 88)$ , SuStaIn determined an initial WMH event, followed by LM, whole-brain, and then hippocampal volume and composite TMT events. This subtype was on average older with higher hypertension risk. Both higher age and hypertension risk are associated with WMH, and may relate to the increased median WMH for the group.<sup>[37](#page-11-0)</sup> Elevated NfL is likely a non-specific marker of aging and white matter integrity,<sup>[38](#page-11-0)</sup> further supporting higher WMH volumes.

Early WMH events (two *z* score) are elevated and remain at similar levels over staging. This group may comprise individuals on a mixed vascular and AD pathway with increased early vascular burden. Given the older age of this cohort, the probability of mixed co-morbidities is higher than other subtypes.<sup>[35](#page-11-0)</sup> Similarly to WMH staging, whole-brain staging has an initial event and then a gap (between stages 6 and 10), which may suggest some variability in neurodegeneration in this group. The later and more uncertain hippocampal volume event staging may suggest minimal hippocampal atrophy. Some literature has suggested that hippocampal volume is reduced in AD populations over  $VaD<sub>1</sub><sup>39</sup>$  $VaD<sub>1</sub><sup>39</sup>$  $VaD<sub>1</sub><sup>39</sup>$ although WMH does still predict hippocampal volume reduction in those with abnormal amyloid.<sup>[40](#page-11-0)</sup>

The late event of p-tau, lower mean p-tau, and lower p-tau across stages is consistent with literature showing VaD is less affected by p-tau abnormality. $41,42$  CSF amyloid-positive individuals with small vessel disease (SVD) have lower cognitive scores and more rapid pro-gression to AD.<sup>[43](#page-11-0)</sup> Both amyloid abnormality<sup>44</sup> and increased WMH<sup>45</sup> are related to cognitive impairment, and seem to be additive.<sup>[10](#page-10-0)</sup> This

may explain why subtype two individuals have earlier cognitive impairment (TMT).

Overall, this subtype seems to represent a population with more SVD burden. They have increased vascular pathology (WMH) and risk factors (hypertension), as well as other indications that separate them from pure AD (low p-tau, less hippocampal involvement, poorer executive functioning). It is impossible to suggest that this is a diagnostically VaD-like population, but the similarities to previous literature (reduced hippocampal and p-tau influence), does suggest that vascular pathologies may be prevalent in this group.

# **4.3 p-tau led subtype**

In this subtype (*n* = 100), SuStaIn determined an initial p-tau event, followed by LM, hippocampal volume, TMT, and then whole-brain and WMH volume. This mirrors a typical presentation of those on an AD pathway.[46](#page-11-0) Unlike the other subtypes, there are clear changes (*z* score = 3) for both p-tau and LM before any changes to other markers included in the model (Figure [2\)](#page-7-0).

The initial and clear event staging of p-tau would be the expected next stage in the amyloid cascade hypothesis,<sup>[46](#page-11-0)</sup> and is well correlated with amyloid deposition. $47$  If this is a subtype with extensive tau deposition in the brain, this may influence changes to the hippocampus, which has an event close to that of p-tau in this subtype. Like the Memory led subtype, earlier lower hippocampal volume events compared to whole-brain volume is likely due to the hippocampus

being specifically affected in  $AD<sup>30</sup>$  $AD<sup>30</sup>$  $AD<sup>30</sup>$  It is one of the first structures to have degenerative change in  $AD<sub>1</sub><sup>48</sup>$  $AD<sub>1</sub><sup>48</sup>$  $AD<sub>1</sub><sup>48</sup>$  and reduced volumes are also present in younger (71 years) individuals with AD compared to healthy counterparts.<sup>[49](#page-11-0)</sup>

The p-tau led subtype is the youngest subtype. WMH do increase with age,  $50$  which may suggest why this subtype has on average lower WMH compared to the WMH led subtype. This group has a lower proportion of hypertension risk (51%), suggesting lower risk of vascular pathology.[51,52](#page-11-0)

The early p-tau events and positive association with stages may suggest this subtype is greatly affected by tau abnormality. This subtype is less affected by vascular risk and disease (WMH, hypertension) and may be a more AD-like group that follows the pathway outlined in the hypothetical model of AD biomarkers.<sup>[46](#page-11-0)</sup>

#### **4.4 Unsubtyped**

A proportion (11%) of amyloid-positive individuals show more similarities to the amyloid-negative control cases. This may suggest a pre-symptomatic cohort before clinical decline,<sup>[53](#page-11-0)</sup> further characterized by the high proportion of CN in this group (53%) although future diagnostic progression within 24 months is not seen (Figure [3\)](#page-8-0). These individuals do have CSF amyloid levels closer to the cut-point (Figure [S7](#page-12-0) in supporting information). As CSF amyloid seems to be a more sensitive marker of early change compared to amyloid PET, $54$  these individuals may be at very early stages of a disease pathway that will later accumulate amyloid. This group has a similar proportion of *APOE ε*4 carriers compared to the subtyped groups. This is consistent with previous work that showed increased amyloid positivity in CN *APOE ε*4 carriers,[54](#page-11-0) and a general link between *APOE ε*4 carrier status and amyloid positivity. [8,54,55](#page-10-0)

### **4.5 Clinical implications**

Identifying a mixed-pathology group less affected by both p-tau and other variables or pathologies that may affect decline should be considered. Recognizing alternative trajectories might improve differential diagnosis, better understand future prognosis, and provide better identification of suitable treatment pathways.

Presence of a WMH led subtype in an ADNI cohort that excludes those with increased vascular burden at screening (Hachinski score *>* 4), suggests cerebrovascular disease impact may be increased in community-based populations. Markers like WMH provide important information about individuals' disease pathways and must be considered.

## **4.6 Limitations**

This version of SuStaIn provides temporal ordering, but not relative timings between events. A more recent development of SuStaIn has included this feature $56$  and should be explored.

This work assumes amyloid abnormality occurs prior to other biomarkers. Some early events in subtypes may occur prior to amyloid abnormality, like WMH volumes in the WMH led subtype.

*Z* score SuStaIn assumes a linear pattern, meaning individuals would be expected to follow their subtype longitudinally. This cannot currently be considered, although previous work has validated SuStaIn longitudinally.[12–14](#page-10-0)

Sample sizes in subtypes beyond event stages ten are small (Figure [S4\)](#page-12-0) and this makes later stage interpretation more difficult.

The use of a different *z* score normalization group would influence subtype identification. CSF amyloid-negative, *APOE ε*4 non-carrier, diagnostically stable CN individuals were used to produce *z* scores so as to have more confidence this group represented healthy aging.

The existence of a Memory led group is unsurprising as the normalization group is cognitively unimpaired. Post hoc exploration of SuStaIn without LM (Figures [S8, S9, S10](#page-12-0) in supporting information) did not overly alter derived subtypes.

# **5 CONCLUSION**

Four amyloid-positive subtypes were derived using data-driven *z* score SuStaIn. Two of these subtypes (Memory led and p-tau led), were likely subtly different populations than those on the AD pathway: one being more indicative of an AD-typical pathway (p-tau led), and the other with both AD and some potential co-pathology (Memory led). Interestingly, an additional subtype of individuals with much higher presumed vascular pathology (WMH led) was also present. An unsubtyped group was amyloid positive and may represent a very early AD group with amyloid abnormality. This work has shown the heterogeneity in a cohort of individuals that may be assumed homogeneous. Our results show the importance of using data-driven techniques that find heterogeneity in disease and has stressed the influence of presumed cerebrovascular pathology and other co-pathologies in those who are amyloid positive.

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#### **ADNI Collaborators**

Data used in preparation of this article were obtained from the Alzheimer's Disease Neuroimaging Initiative (ADNI) database [\(adni.loni.usc.edu\)](http://adni.loni.usc.edu). As such, the investigators within the ADNI contributed to the design and implementation of ADNI and/or provided data but did not participate in analysis or writing of this report. A complete listing of ADNI investigators can be found at: [http://adni.loni.usc.edu/wp-content/uploads/how\\_to\\_apply/ADNI\\_](http://adni.loni.usc.edu/wp-content/uploads/how_to_apply/ADNI_Acknowledgement_List.pdf) [Acknowledgement\\_List.pdf.](http://adni.loni.usc.edu/wp-content/uploads/how_to_apply/ADNI_Acknowledgement_List.pdf)

#### **CONFLICT OF INTEREST STATEMENT**

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## **CONSENT STATEMENT**

For ADNI, protocol and informed consent forms were approved by the institutional review board at each participating site.

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# <span id="page-12-0"></span>**SUPPORTING INFORMATION**

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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