


CASE REPORT

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Prominent amyloid plaque pathology and cerebral amyloid angiopathy in APP V717I (London) carrier – phenotypic variability in autosomal dominant Alzheimer’s disease

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Abstract

The discovery of mutations associated with familial forms of Alzheimer’s disease (AD), has brought imperative insights into basic mechanisms of disease pathogenesis and progression and has allowed researchers to create animal models that assist in the elucidation of the molecular pathways and development of therapeutic interventions. Position 717 in the amyloid precursor protein (APP) is a hotspot for mutations associated with autosomal dominant AD (ADAD) and the valine to isoleucine amino acid substitution (V717I) at this position was among the first ADAD mutations identified, spearheading the formulation of the amyloid cascade hypothesis of AD pathogenesis. While this mutation is well described in multiple kindreds and has served as the basis for the generation of widely used animal models of disease, neuropathologic data on patients carrying this mutation are scarce. Here we present the detailed clinical and neuropathologic characterization of an APP V717I carrier, which reveals important novel insights into the phenotypic variability of ADAD cases. While age at onset, clinical presentation and widespread parenchymal beta-amyloid (A β) deposition are in line with previous reports, our case also shows widespread and severe cerebral amyloid angiopathy (CAA). This patient also presented with TDP-43 pathology in the hippocampus and amygdala, consistent with limbic predominant age-related TDP-43 proteinopathy (LATE). The APOE ϵ 2/ ϵ 3 genotype may have been a major driver of the prominent vascular pathology seen in our case. These findings highlight the importance of neuropathologic examinations of genetically determined AD cases and demonstrate striking phenotypic variability in ADAD cases.

Keywords: Alzheimer’s disease, Amyloid precursor protein, Beta-amyloid, Cerebral amyloid angiopathy, London mutation, APOE

Introduction

Alzheimer’s disease (AD) is the most common form of dementia, currently affecting more than 5 million people in the United States [6]. Neuropathological hallmarks of AD include extracellular deposits of beta-Amyloid (A β), intracellular deposits of neurofibrillary tangles (NFT) and neuron loss [35]. The majority of cases occurs as sporadic disease (sporadic AD, SAD), modified by genetic, behavioral

and environmental risk factors, while a subset of cases is caused by autosomal-dominant mutations [14, 21, 35]. These mutations in autosomal dominant forms of AD (ADAD) are clustered in genes associated with the metabolism of A β -peptides, which are generated from Amyloid Precursor Protein (APP) in sequential cleavage events mediated by β - and γ -secretase [9]. ADAD associated mutations in APP mainly cluster around these secretase cleavage sites, while codon 717 is a mutational hotspot at the γ -secretase cleavage site [27]. To date, four different pathogenic amino acid changes for APP on codon 717 have been described: Valine to Phenylalanine (V717F, Indiana [37]), Valine to Glycine (V717G [10]), Valine to Isoleucine (V717I, London [18, 63]) and Valine to Leucine (V717L [38]). All of these

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mutations shift the ratio of $A\beta_{1-42} / A\beta_{1-40}$ towards increased production of $A\beta_{1-42}$ [27], which is more aggregation prone and can drive pathological protein accumulation. The V717I (London) mutation, was among the first mutations described to cause ADAD and this discovery has put $A\beta$ center stage in AD pathogenesis. Animal models overexpressing mutant human APP are a staple of AD research [17, 24, 46, 47, 49, 52, 54] and the APP V717I mutation was used to generate some widely used models [34, 43, 54]. Despite the numerous and detailed descriptions of pathological findings in these animal models, neuropathological characterization of patients carrying the APP V717I mutation is scarce. The brain of the original case from England was reported to show AD neuropathological changes with mild cerebral amyloid angiopathy (CAA) as well as Lewy body (LB) pathology in cortical and brainstem regions, while findings from an American family with this mutation showed AD pathology but no CAA or LB [8, 22, 36].

Case presentation

The patient was a sixty-six (66) year-old right-handed Caucasian female with a past medical history of thyroid disease. Her family history was notable for extensive AD, involving her mother (deceased from disease at age 62), two aunts (deceased from disease at ages 66 and 68), and a grandfather (also deceased from disease). Additionally, she had a brother diagnosed with AD, still living in a nursing facility.

She was first noted to develop neurologic symptoms in her mid-fifties, manifesting primarily as progressive memory loss. She presented for formal neurologic evaluation at age 60, at which time her husband described significant memory difficulty, confusion, and occasional difficulty in finishing sentences. While she had discontinued working five years prior to evaluation due to difficulty with completing occupational tasks, she maintained her ability to finish routine housework. On initial evaluation, she was oriented to person, place, and time but not year, with a Mini Mental Status Exam (MMSE) score of 17. Physical exam findings included the presence of a tremor of her head and bilateral hands, with a negative Romberg's test. These findings were assessed to be consistent with AD of moderate intensity, and she was started on donepezil and memantine therapy. Concurrent computed tomography (CT) imaging of her brain demonstrated subtle areas of low-attenuation in the periventricular white matter of the parietal lobe, suggestive of microvascular ischemic change.

Two years after initial diagnosis, she was noted to demonstrate significant clinical deterioration during a follow-up clinical visit. Her husband described a loss of her ability to maintain independent activities of daily living, becoming dependent on him for bathing and dressing on a daily basis, and that she had additionally developed urinary

incontinence. Her recent medical history was notable for a hospital admission due to dehydration and severe hypothyroidism secondary to thyroid medication non-compliance. On evaluation, she exhibited depression, anxiety, confusion, and an MMSE score of 8. These findings were assessed to be consistent with a progression to severe AD. CT imaging at this time revealed mild global brain parenchymal loss, with no evidence of focal lesions or asymmetric atrophy.

Her symptoms continued to progress, whereupon at a follow-up visit four years after initial diagnosis, her husband described the development of intermittent jerking movements by the patient, occurring a few times per week and lasting approximately 15 min in duration. At this visit, she was oriented only to person, and her MMSE score was 0, because she was unable to follow commands. A subsequent electroencephalogram revealed no focal abnormalities or epileptiform activity, noting only the presence of diffuse slowing activity, consistent with moderate encephalopathy.

By the time of her final follow-up visit approximately, six years after initial diagnosis, she had developed a wide-based gait with frequent falls, aphasia, personality changes, poor insight, and complete lack of orientation to time, place, and person. She ultimately passed away within six months of her last visit, at age 66. Her family consented to neuropathologic evaluation of her brain by the Center for Translational Research in Neurodegenerative Disease (CTRND) at the University of Florida.

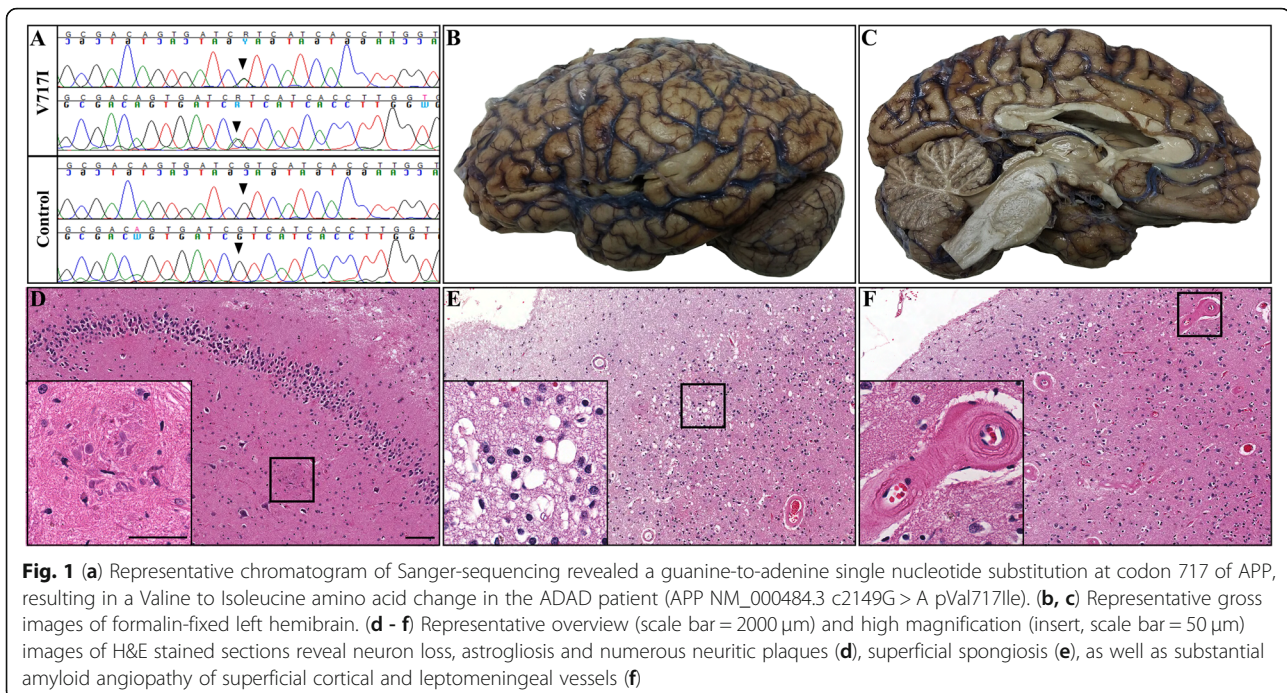
Molecular studies

A directed Sanger Sequencing screening panel for autosomal dominant mutations of *APP*, *PSEN1*, and *PSEN2* identified a guanine-to-adenine single nucleotide substitution at codon 717, resulting in a Valine to Isoleucine amino acid change (*APP* NM_000484.3 c2149G > A pVal717Ile, Fig. 1a). A PCR-based molecular assay for the *APOE* gene revealed the patient's genotype to be $\epsilon 2 / \epsilon 3$ (for details see Additional file 1).

Neuropathological evaluation

The post-mortem interval prior to brain procurement was eight hours, with a fresh brain weight of 1080 g (for details see Additional file 1). Diffuse cerebral atrophy, with relative preservation of the cerebellum (Fig. 1b, c) was noted. Minimal to no atherosclerotic changes associated with the basal vasculature were identified. Serial coronal sections of cerebral hemispheres confirmed a mild to moderate degree of atrophy, with blunting of the lateral angles of the ventricles and sulcal widening most appreciable along the Sylvian fissure. No focal lesions were otherwise observed in the remainder of the cerebrum, brain stem, or cerebellum.

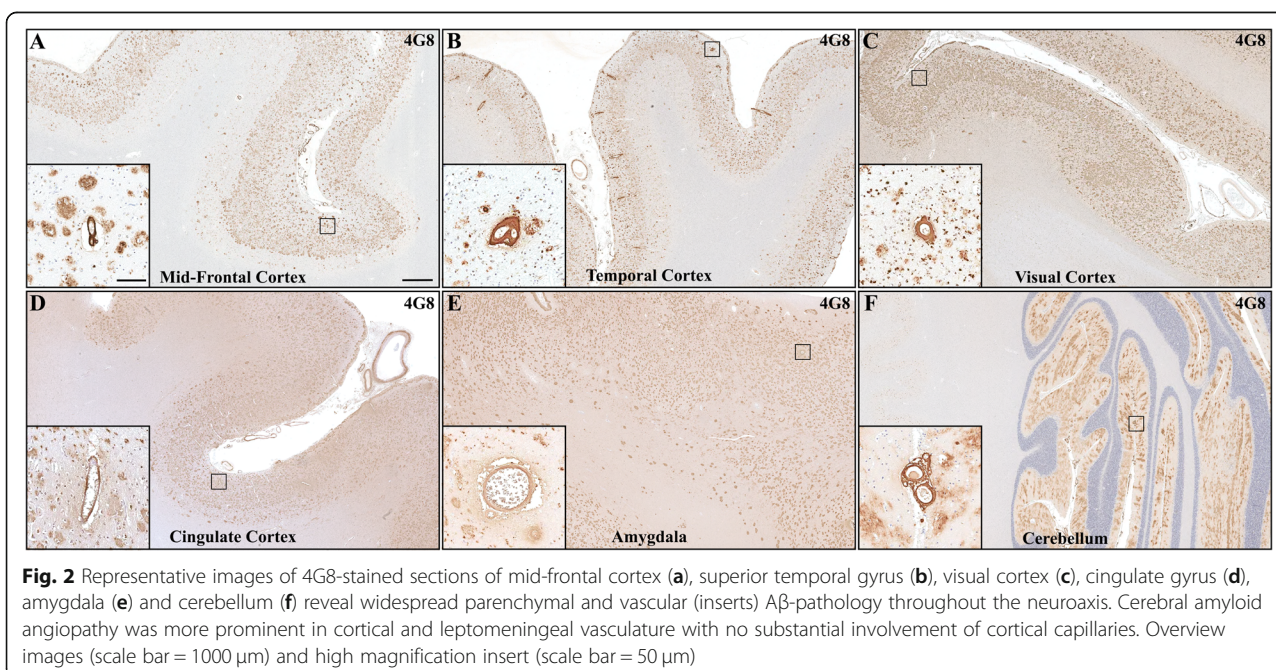
Microscopic examination demonstrated extensive neuronal loss and associated gliosis in the hippocampus and



neocortical areas, with numerous pyramidal neurons notable for flame-shaped neurofibrillary tangles. Multiple areas demonstrated prominent neuritic plaques (Fig. 1d, insert) with associated areas of neuronal loss, gliosis, and variable vacuolization and spongiosis of superficial cortical layers (Fig. 1e). In addition, extensive cerebral amyloid angiopathy (CAA) was apparent throughout parts of cerebrum and cerebellum, concentrating on superficial cortical and leptomeningeal blood vessels (Fig. 1f). In contrast, only mild

small vessel hyalinization of the basal ganglia and white matter were identified, with focal calcification of globus pallidus blood vessels. A remote microhemorrhage was identified in the primary sensory cortex. The brainstem and cerebellum demonstrated no major neuropathologic changes, with no significant neuronal loss, gliosis, or Lewy bodies identified in the substantia nigra or locus coeruleus.

Immunohistochemistry (for details see Additional files 1 and 2) with a pan-A β antibody (4G8) demonstrated a



very high A β plaque burden throughout the cerebral neocortex (Fig. 2a-d), the amygdala (Fig. 2e), basal ganglia, and tegmentum of the midbrain and pontine brainstem. A β deposition was also identified in the cerebellum, presenting as scattered fleecy diffuse plaques and neuritic plaques in the molecular layer of the cerebellar cortex (Fig. 2f). These findings translated to Thal phase 5 of A β deposition, corresponding to an “A3” plaque score according to the 2012 NIA-AA criteria [35]. The majority of A β plaques were surrounded by dystrophic neurites (Fig. 3d), with the frequency of neuritic plaques throughout the neuroaxis corresponding to a CERAD semiquantitative score of “frequent” (C3) [35].

Immunostaining for tau demonstrated a concordant pattern of severe, widespread inclusion pathology, manifesting as a heavy burden of intraneuronal neurofibrillary tangles (NFT) and dystrophic neurites associated with amyloid plaques (Fig. 3a-d). Disease topography extended from the entorhinal cortex and adjacent mesial temporal lobe cortex, deep cerebral gray matter structures, to several areas of neocortex including primary visual cortex (Fig. 3a-c). These findings correspond to an advanced Braak stage (VI), translating to a “B3” NFT score [35].

In addition, intracytoplasmic neuronal inclusions were highlighted in the hippocampal subiculum and amygdala by immunohistochemistry for TDP-43 (Fig. 3e-f), while neocortical areas were devoid of TDP-43 pathology, corresponding to stage 2 of the recently defined limbic-predominant age-related TDP-43 encephalopathy neuropathologic change (LATE-NC [41]). No α -synuclein

immunoreactive pathology was identified in the examined sections of cerebrum, brainstem, or cerebellum (data not shown).

A β pathology was additionally noted to manifest as severe, widespread cerebral amyloid angiopathy (CAA), with a predilection for the superficial cortical and leptomeningeal vasculature and relative sparing of cortical capillaries (CAA type 2, [58]). Prominent vascular A β -deposits were detected in multiple neocortical areas (Fig. 2a-c), limbic areas (Fig. 2d-e) and the cerebellum (Fig. 2f), while sections from thalamus, basal ganglia, pons and medulla did not show vascular A β -deposits. This corresponds to CAA stage 2 according to Thal et al. [57]. Focal double barreling (Fig. 2b) and disruption of vessel wall integrity was noted, corresponding to severe CAA [61] or grade 4 CAA [44]. Vascular A β deposits showed strong immunoreactivity with pan-A β antibodies (4G8, Fig. 4a), and were labelled with A β ₁₋₄₂ specific antibodies (12F4, Fig. 4b), as well as A β ₁₋₄₀ specific antibodies (13.1.1 [31], Fig. 4c). In contrast, parenchymal A β plaques were labelled strongly with pan-A β (Fig. 4a) and A β ₁₋₄₂ specific (Fig. 4b) antibodies, while A β ₁₋₄₀ specific antibodies only stained a minority of A β -plaques (Fig. 4c). We contrasted these results with staining in two cases of SAD with different APOE genotype (APOE ϵ 3/ ϵ 3 and APOE ϵ 4/ ϵ 4, for details see Additional file 3: Table S2). While CAA in both SAD cases showed a similar pattern of immunoreactivity with pan-A β antibodies (Fig. 4d, g), as well as A β ₁₋₄₂ (Fig. 4e, h) and A β ₁₋₄₀ specific antibodies (Fig. 4f, i) compared to our ADAD case (Fig. 4 A-C),

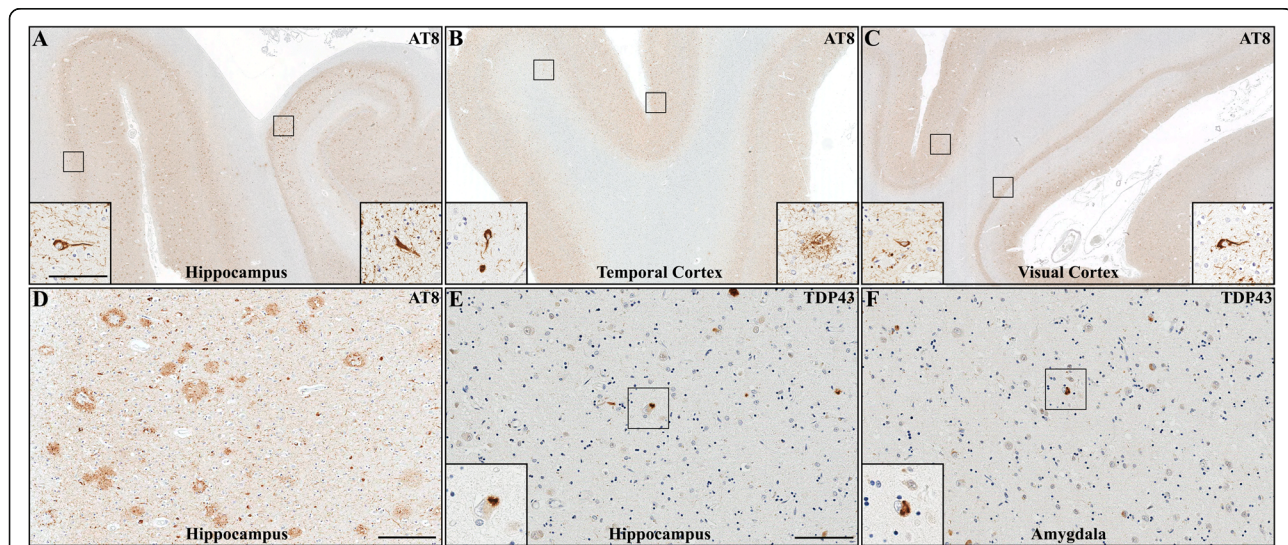
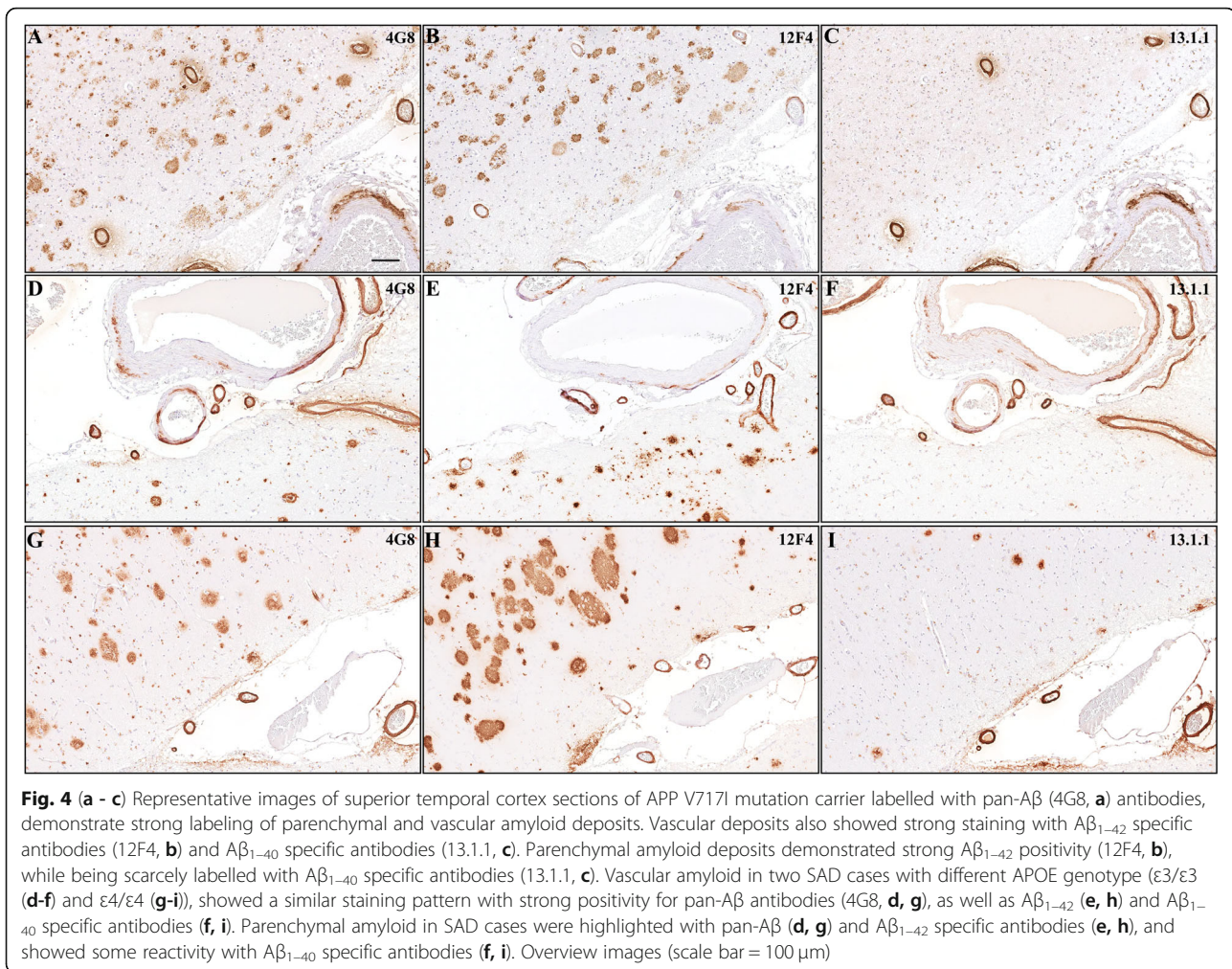


Fig. 3 Representative overview (scale bar = 2000 μ m) and high magnification (insert, scale bar = 50 μ m) images of AT8 staining in APP V717I mutation carrier for the hippocampus (a), superior temporal gyrus (b) and visual cortex (c) reveal substantial NFT pathology in all regions examined. (d) AT8 staining also reveals “frequent” neuritic plaques in the inferior temporal cortex (scale bar = 1000 μ m, insert scale bar = 50 μ m). Representative overview (scale bar = 2000 μ m) and high magnification (insert, scale bar = 50 μ m) images of TDP-43 staining demonstrate TDP-43 positive inclusions in hippocampus (e) and amygdala (f)



parenchymal deposits were highlighted to a much greater extent with Aβ₁₋₄₀ antibodies (Fig. 4F, I) than in our ADAD case (Fig. 4C).

Discussion and conclusions

The identification of missense mutations in APP underlying familial forms of AD has paved the way for the formulation of the “amyloid cascade hypothesis” [16, 22] by placing the generation of Aβ peptides as central to disease pathophysiology. To date, more than 50 mutations in APP associated with early onset AD have been described [9, 16, 29, 50, 55]; rare APP variants associated with protective properties have also been reported [28]. Several different substitutions of the intramembranous Valine residue at position 717 of APP have been described to be associated with familial forms of AD [10, 18, 37, 38]. This position is near the γ-secretase cleavage site of APP, such that amino acid substitutions at this functional locus lead to an increased ratio of Aβ₁₋₄₂/Aβ₁₋₄₀ with a trend towards increased production of Aβ₁₋₄₂ [15, 27, 49].

The patient described here carrying the APP V717I mutation presented with extensive AD neuropathological

changes, including abundant and widespread Aβ-pathology in cerebrum, subcortical nuclei, and cerebellum. Multiple different types of plaques were noted, including core-plaques, diffuse plaques and subpial band-like Aβ deposits. All of the deposits showed a uniformly strong staining pattern with Aβ₁₋₄₂ specific antibodies and relative scarcity of Aβ₁₋₄₀ positivity compared to SAD cases, in line with the reported increase in Aβ₁₋₄₂ with this mutation in cell culture studies [27]. The majority of Aβ-deposits were associated with dystrophic neurites containing phosphorylated tau species. In addition, widespread neuronal tau pathology in the form of NFT, as well as neuropil thread pathology were noted. While no concomitant α-synuclein pathology was detected, TDP-43 positive inclusions were observed in the amygdala and hippocampus. Co-occurring TDP-43 pathology in carriers of APP mutations is not as common as in sporadic (late-onset) AD but has been reported [11]. This is in line with a contribution of age to the preponderance of TDP-43 positive pathology and ties in with the recently proposed entity of limbic-predominant TDP-43 neuropathological changes (LATE-NC) [41]. In addition,

severe and widespread CAA was noted, affecting leptomeningeal and cortical blood vessels, but sparing fine capillaries. Systematic studies on CAA in ADAD cases are scarce, but a recent report from the National Alzheimer Coordinating Center (NACC) showed an increased CAA score in ADAD compared to SAD [48]. The number of APP mutation carriers in this study were limited, but phenotypic variability with respect to CAA severity was observed. Vascular amyloid in our ADAD case was strongly labelled with pan-A β , as well as A β _{1–42} and A β _{1–40} specific antibodies in a similar pattern as observed in two SAD cases with different APOE genotype. The relative abundance of A β species in parenchymal and vascular deposits has been a matter of intense debate. Initial reports suggested that the majority of vascular A β is A β _{1–40} [1, 19, 25, 26, 45], but subsequently a substantial contribution of A β _{1–42} to vascular A β -deposition was acknowledged [1, 19, 40, 51, 60], with some reports suggesting A β _{1–42} deposition driving more severe CAA [4, 20]. Mechanistic studies in murine models indicate that initial deposition of A β _{1–42} may be necessary to drive subsequent A β _{1–40} deposition in blood vessels [33, 42], but the impact of different APOE genotypes has not been analyzed systematically in this context. The relative sparing of capillary vessels by pathologic A β deposits, referred to as type 2 CAA [58] was previously reported to be associated with the presence of at least one *APOE* ϵ 2 allele [2, 32, 59]. *APOE* is currently the strongest known genetic risk factor of AD, with the ϵ 4 isoform correlating to an increased incidence of AD in people of European descent [56]. The ϵ 3 allele is associated with preservation of synaptic integrity in old human APP (hAPP) mice [7], and mediation of amyloid clearance in comparison to ϵ 4 [5], but it was also correlated to an earlier age of onset than ϵ 4 in this model [7, 30]. The ϵ 2 genotype was studied in several Italian families with the *APP* V717I mutation. It was discovered that this allele was associated with a delayed age of onset compared to individuals with the same *APP* mutation but *APOE* ϵ 3 homozygotes or ϵ 4 carriers [23, 39, 53]. Furthermore, a recent report demonstrated protective effects of the Christchurch *APOE* variant in a carrier of the Presenilin (*PSEN*) E280A mutation [3]. These disease-modifying effects of the *APOE* genotype may provide one possible explanation for the divergent phenotypes seen in the clinical and neuropathological presentation of ADAD.

The case presented herein underscores the importance of neuropathological characterization of genetically determined cases of AD. Such examinations serve to identify phenotypic diversity within the disease, clarify potential modifiers of disease progression (such as, but not limited to, APOE genotype), explore the complex interrelations between disease mechanisms, and ultimately aid in elucidating potential therapeutic targets.

Supplementary information

Supplementary information accompanies this paper at <https://doi.org/10.1186/s40478-020-0891-3>.

Additional file 1. Materials and Methods [12, 13, 31, 35, 62]

Additional file 2: Table S1. List of Antibodies used for this study

Additional file 3: Table S2. Summary of patient samples used in this study [35, 41, 61]

Abbreviations

ABC: Avidin-biotin complex; AD: Alzheimer's disease; ADAD: Autosomal dominant AD; APOE: Apolipoproteins-E; APP: Amyloid precursor protein; A β : Beta-Amyloid; CAA: Cerebral amyloid angiopathy; CT: Computed tomography; CTRND: Center for Translational Research in Neurodegenerative Disease; DAB: 3,3'-diaminobenzidine; FAD: Familial Alzheimer's disease; FBS: Fetal bovine serum; hAPP: Human amyloid precursor protein; HIER: Heat-induced epitope retrieval; LATE-NC: Limbic-predominant TDP-43 neuropathological changes; MMSE: Mini Mental Status Exam; NFT: Neurofibrillary tangles; PBS: Phosphate buffered saline; PS1: Presenilin 1; PS2: Presenilin 2; RT: Room temperature; SAD: Sporadic Alzheimer's disease; UF HBTB: University of Florida Neuromedicine Human Brain Tissue Bank

Acknowledgements

Antibodies AB5 and 13.1.1 were a generous gift from the lab of Dr. Todd Golde [31].

Authors' contributions

JTL, SP and ATY confirmed neuropathologic diagnosis. SP, ATY, GML, JTL and BG co-wrote the manuscript. JTL, GML and YX performed immunohistochemical stains, optimized protocols and prepared figures. NET, KNM and SJL performed molecular/genetic analysis. All authors read and approved the manuscript.

Funding

This study was supported by the 1Florida ADRC, funded by NIH/NIA grant P50 AG047266. NET is funded by RF1 AG051504, R01 AG061796 and U01 AG046139 which supported part of this study.

Availability of data and materials

All data generated or analyzed during this study are included in this published article.

Ethics approval and consent to participate

Staining of human tissue samples was performed with approval of the University of Florida institutional review board.

Consent for publication

Informed consent was obtained according to guidelines of the University of Florida institutional review board.

Competing interests

The authors declare that they have no competing interests.

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Received: 24 January 2020 Accepted: 30 January 2020

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