

“New Old Pathologies”: AD, PART, and Cerebral Age-Related TDP-43 With Sclerosis (CARTS)

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Abstract

The pathology-based classification of Alzheimer’s disease (AD) and other neurodegenerative diseases is a work in progress that is important for both clinicians and basic scientists. Analyses of large autopsy series, biomarker studies, and genomics analyses have provided important insights about AD and shed light on previously unrecognized conditions, enabling a deeper understanding of neurodegenerative diseases in general. After demonstrating the importance of correct disease classification for AD and primary age-related tauopathy, we emphasize the public health impact of an underappreciated AD “mimic,” which has been termed “hippocampal sclerosis of aging” or “hippocampal sclerosis dementia.” This pathology affects >20% of individuals older than 85 years and is strongly associated with cognitive impairment. In this review, we provide an overview of current hypotheses about how genetic risk factors (*GRN*, *TMEM106B*, *ABCC9*, and *KCNMB2*), and other pathogenetic influences contribute to TDP-43 pathology and hippocampal sclerosis. Because hippocampal sclerosis of aging affects the “oldest-old” with arteriosclerosis and TDP-43 pathologies that extend well beyond the hippocampus, more appropriate terminology

for this disease is required. We recommend “cerebral age-related TDP-43 and sclerosis” (CARTS). A detailed case report is presented, which includes neuroimaging and longitudinal neurocognitive data. Finally, we suggest a neuropathology-based diagnostic rubric for CARTS.

Key Words: Arteriosclerosis, Cerebrovascular disease, Frontotemporal lobar degeneration, Genome-wide association study, Neurofibrillary tangles, Plaques, VCID.

INTRODUCTION

Prospects for diagnosing and treating neurodegenerative diseases are enhanced when disease classifications reflect the underlying biologic complexity of these conditions. For most neurodegenerative diseases, neuropathologic observations constitute the “gold standard” used in diagnosis and nosology. Yet the pathology-based classifications of neurodegenerative diseases are also dynamic and have evolved recently to capture an increased proportion of the changes in the aged brain that are associated with cognitive impairment (1). These advances have come about with the help of larger and more diverse autopsy cohorts, increasingly robust and quantitative pathological parameters, and greater collaboration among neuropathologists, clinician-scientists, and basic researchers. Here we discuss both recent advances and some areas that merit revision in the study of dementia-related neurodegenerative diseases (Table 1). These studies are directly relevant to the most well-known dementia-inducing disorder, Alzheimer disease (AD).

Focusing on AD

AD has an enormous impact on public health and recent studies have substantially revised the classic literature on AD clinicopathologic correlations. For example, we have learned that much of the morbidity attributed to AD as recently as 20 years ago is more accurately associated with non-AD diseases. A basic assumption is that AD is defined by 2 pathologic hallmarks: A β amyloid plaques and tau neurofibrillary tangles (NFTs) (2). The complex but coherent association between AD pathologies and cognitive status was previously addressed

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TABLE 1. Topics and Organization of the Current Review

Disease condition	Impact of recent progress and revised pathology-based classification
Alzheimer disease (AD)	Increased appreciation of importance of autopsy data and non-AD pathologies
Primary age-related tauopathy (PART)	Revised classification is useful for study of non-AD brain disease
Hippocampal sclerosis of aging (HS-Aging)/ Cerebral age-related TDP-43 and sclerosis	A common age-related brain disease, lacking an accurate classification

(3, 4). Here, we focus on 3 basic factors that must be taken into account in disease classifications: autopsy data, non-AD pathologies, and chronological age.

Autopsy-based neuropathological diagnoses are central to AD research. The salience of neuropathologic data and, by extension, pathology-based classification schemes, is illustrated by many prior studies that arrived at correct conclusions only when using the pathological criteria for AD diagnosis rather than using purely clinical criteria for AD diagnosis. One example selected from among many is in testing the association between AD and type 2 diabetes mellitus (T2D), the latter of which affects over a quarter of individuals >65 years of age (5). Studies analyzing clinical data have reported that T2D is a risk factor for AD (6–8). By contrast, studies that incorporated autopsy results have consistently arrived at the opposite conclusion, i.e. that T2D is not a risk factor for AD pathology. Instead, T2D appears to exert its impact through a different disorder, that is cerebrovascular disease (9–14). The inclusion of the single study design element of autopsy data is critical to guide all other related work.

The reason for the discrepancy between clinical and pathology-based AD diagnoses relates to the prevalence of non-AD brain diseases, including α -synucleinopathies, non-AD tauopathies, hippocampal sclerosis ([HS] as discussed below), and many subtypes of cerebrovascular disease, all of which can mimic AD clinically (4, 15–17). In Table 2 we provide data from the University of Kentucky autopsy series (18, 19) listing the frequency of non-AD pathologies by Braak NFT stage (20). Note that >95% of brains in this cohort have

at least 1 brain pathology and most participants had more than 1 pathologic diagnosis. These results are consistent with prior autopsy series (4, 19, 21–35).

Biomarker studies confirm the prevalence of *in vivo* “suspected non-Alzheimer pathology” (SNAP) (36, 37), which refers to neurodegeneration without A β amyloidosis according to biomarkers. Approximately 25% of “mild cognitive impairment” (MCI) cases show the SNAP biomarker signature (36).

This does not indicate that only approximately 25% of MCI subjects show substantial non-AD pathology, but instead, approximately 25% of MCI subjects show impairment that is almost *exclusively* related to non-AD pathology.

The clinical and biomarker data on patients with cognitive impairments must be guided by pathologic classification to appreciate the heterogeneous diseases underlying these impairments. A first-line biomarker used for diagnosing the cause of cognitive impairment in the elderly is brain MRI (38). Although MRI-detected hippocampal shrinkage is a relatively strong predictor of subsequent cognitive deterioration (39–41), this finding has low specificity because multiple separate brain pathologies are associated with hippocampal atrophy. For example, HS of aging (HS-Aging) is a common condition that causes even more severe hippocampal atrophy than AD (42–44). Distinguishing between causes of hippocampal atrophy is critical because therapies that might impact one condition (eg AD) may not have any effect in another disease (eg HS-Aging). Thus, optimal AD biomarkers would indicate the severity of AD neuropathology rather than cognitive impairment *per se*, which is not specific to AD (27, 29, 45).

TABLE 2. Even in an Autopsy Cohort That Includes Many Subjects Free of Dementia, Most Individuals Manifest More Than 1 Subtype of Brain Pathology

	Braak NFT Stages						
	0	I	II	III	IV	V	VI
Cases (n)	20	57	97	58	57	101	188
Cases with B-ASC: moderate or severe	0%	12.3%	21.6%	12.1%	21.1%	19.8%	14.4%
Cases with CAA: moderate or severe	20.0%	10.5%	20.6%	19.0%	24.6%	37.6%	50.5%
Cases with Lacunar and/or microinfarcts	35.0%	36.8%	43.3%	37.9%	49.1%	46.5%	38.3%
Cases with Neocortical Lewy bodies	5.0%	14.0%	9.3%	10.3%	7.0%	10.9%	19.7%
Cases with HS-Aging	15.0%	10.5%	6.2%	17.2%	8.8%	18.8%	15.4%
Cases with >1 non-AD pathology ^a	20.0%	21.1%	27.0%	24.1%	33.3%	43.6%	40.1%
Cases with PART	n/a	71.9%	56.7%	37.9%	17.5%	n/a	n/a

Shown are pathologies among subjects at the University of Kentucky Alzheimer’s Disease Center autopsy cohort who died after age 75 years (total n = 578, of whom 161 subjects had final MMSE score of 28/30 or better) without frontotemporal dementia, stratified by Braak NFT stages. Data are presented as percentages.

B-ASC: brain arteriolosclerosis; CAA: cerebral amyloid angiopathy; HS-Aging: hippocampal sclerosis of aging; PART: primary age-related tauopathy.

^aFor this purpose, PART is not considered “non-AD” pathology.

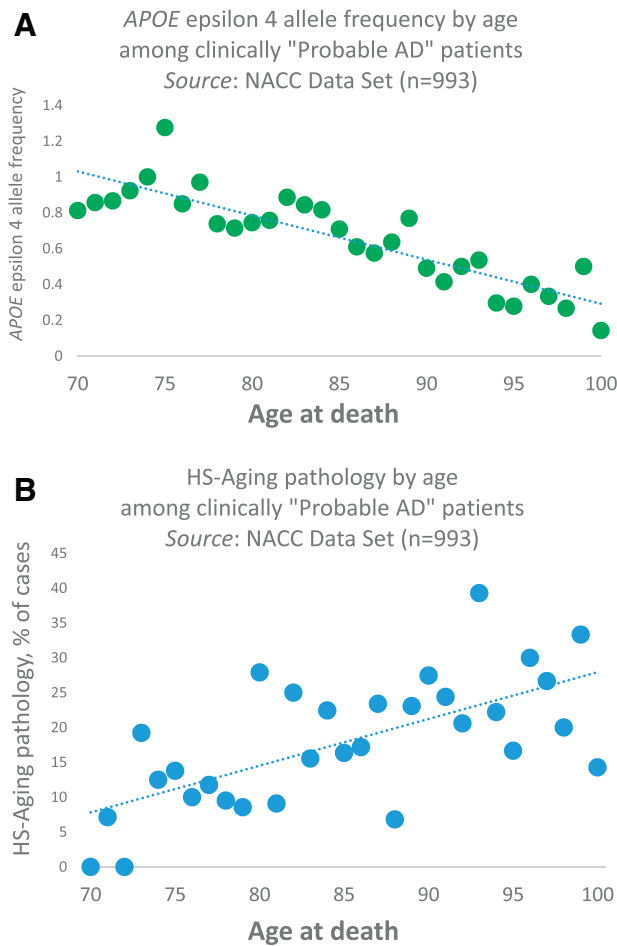


FIGURE 1. Dementia is associated with risk factors and pathologies that vary across the human aging spectrum. **(A, B)** Among the “oldest-old” with the clinical diagnosis of “Probable AD,” *APOE* $\epsilon 4$ alleles are decreasingly common after age 75 years **(A)**, whereas HS-Aging pathology is more prevalent with increasing age ($p < 0.001$ for both) in the NACC Data Set ($n = 993$ of subjects who died between 2005 and 2013) **(57)** **(B)**. Methodology for data analyses was as described previously **(58)**. These data demonstrate the contribution to dementia of non-*APOE* genetic risk factors, and common non-AD pathologies in advanced old age.

Recent autopsy studies have also shed new light on the interaction between aging and brain disease. The classic AD clinical-pathologic correlation studies of Tomlinson and colleagues were performed on cohorts with average age of death in their early 70s **(46–49)**. However, the fastest growing population group is persons older than 85 years of age **(10)**. It is increasingly clear that this “oldest-old” population is affected by conditions that differ from younger cohorts **(10, 50–52)**. “Pure” AD cases tend to be younger and to have particular gene variants **(10, 29, 31, 53–55)**, whereas the prevalence of AD pathology levels off or decreases in advanced old age **(10, 15, 31, 56)** **(Figs. 1 and 2)**. By contrast, some non-AD brain pathologies increase in the “oldest-old” **(10, 24, 59)**. Thus, the statement

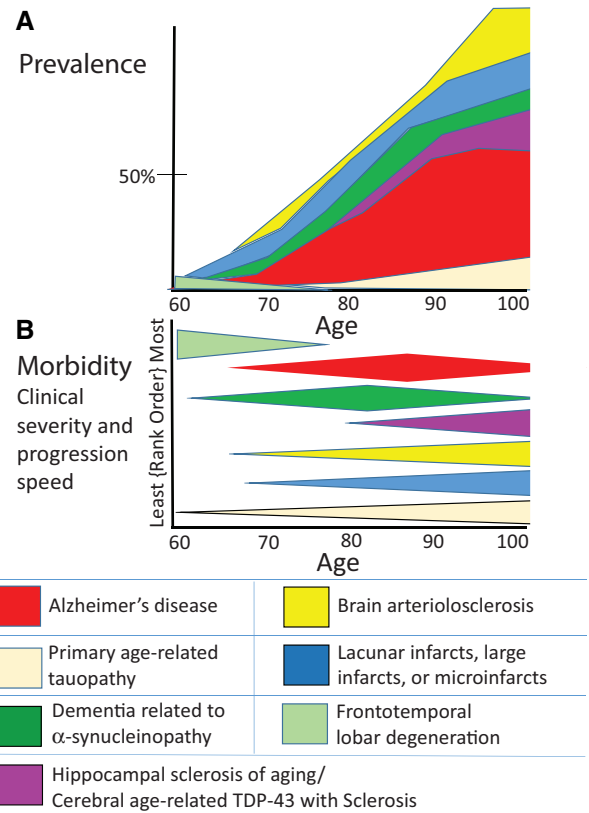


FIGURE 2. Depiction of prevalence and morbidity of specific pathologies that contribute to dementia. These charts represent the subjective synthesis of the results of multiple published studies **(19, 29, 33, 52, 59, 60, 61, 62, 63, 58, 64, 65–86)**. **(A)** The prevalence of multiple different specific CNS disease pathologies is depicted (50% prevalence is shown for reference). Note that in large autopsy series the prevalence of advanced AD pathology levels off or decreases in advanced old age whereas other pathologies (HS-Aging, cerebrovascular diseases) increase in that group. Panel **(B)** shows the same conditions ranked according to the morbidity (neurologic impact and rate of disease progression). Prevalence, morbidity, and age range vary significantly. For example, FTL is a rare but devastating illness whereas PART is relatively common but lower morbidity, and each mostly afflicts people at separate parts of the human aging spectrum.

that age is the greatest risk factor for AD should not be taken literally **(24, 87)**; a more accurate statement is that age is a risk factor for dementia due to multiple diseases that usually include AD.

Although new insights into AD-related brain pathologies have been achieved, many more questions remain. These questions illustrate that there are controversies about disease classifications: What, other than *APOE* $\epsilon 4$, leads to the development of plaques and tangles? Do some cognitively intact individuals tolerate a high burden of plaques and tangles for long periods? Are there environmental and genetic influences that confer protection against the disease? And why do many individuals in advanced old age lack amyloid plaques but still develop hippocampal NFTs?

A Common Pathology With a New Classification: Primary Age-Related Tauopathy (PART)

We consider PART to represent a distinct non-AD pathology (59, 88), as indicated in the most recent consensus-based guidelines for the neuropathologic assessment of AD (2) (Fig. 3). However, since tau, α -synuclein, A β , and TDP-43 are all pathologically aggregated in multiple diseases (1, 4, 92–98), there are debates about the pathology-based criteria applied to define each disease, including PART (99, 100). What is agreed upon is that NFTs are virtually always seen with advanced age, whereas A β amyloid plaques are absent in a substantial proportion of elderly brains (24, 59, 87–91, 101–103). The NFT+/A β - pathologic combination (PART) is common, occurring in approximately 20% of all individuals (Table 2).

The update of pathology classification to include PART (59) provides a universal terminology with both theoretical and clinical implications. To summarize multiple prior studies, human autopsy data indicate the existence of at least 2 common but distinct biologic processes producing NFTs in the hippocampus of elderly persons (23, 60, 104–106). One process (AD) includes A β plaques as well as tau NFTs and tends to evolve into dementia. The other (PART) lacks the A β plaques and is associated with lesser degree of cognitive impairment and/or other morbidities. Notably, *APOE* ϵ 4 genotype does not appear to be a risk factor for PART, whereas the *MAPT* “H1” haplotype confers an increased risk for PART (59, 105, 107) and for less common non-AD tauopathies (108, 109).

PART differs from AD in terms of overall morbidity and the age range of maximum vulnerability (59) (Fig. 2). The higher stage PART cases (Braak NFT stages III/IV) tend to show evidence of cognitive impairment (59). Prior biomarker studies identified neurodegeneration biomarkers in the absence of brain or cerebrospinal fluid A β amyloidosis (37, 110–112). We also found evidence that PART is a pathologic substrate for individuals who die with subjective memory complaints (113), which is a very common clinical phenomenon among elderly individuals (114, 115).

Whether PART pathology inevitably progresses to AD is controversial (99, 107). Approximately 20% of individuals have PART pathology by their ninth decade (87). The overall proportion of AD and PART cases seems to be stable in centenarians, supporting the hypothesis that PART pathology is not necessarily destined to progress to AD (24, 87). A separate issue that remains to be addressed relates to the presence of PART in individuals who satisfy criteria for AD (i.e. moderate or frequent neuritic plaques). Using current diagnostic classification (Fig. 3), those cases are not classifiable as PART. However, with the identification of PART, clinicians, pathologists, and basic scientists worldwide can better discriminate amongst various tauopathic diseases, aiding both clinical and basic research. Such studies will set the stage for future preventive or therapeutic strategies.

At the Frontier of Disease Classification: HS-Aging

Despite the recent progress in the field, there are still common and high-morbidity age-related brain diseases that

Alzheimer’s disease neuropathologic changes

Thal A β Stage (0-5)	CERAD neuritic amyloid plaque stage (0-3)	Braak NFT Stage (0-VI)			
		0	I or II	III or IV	V or VI
0	0	Not	Not	Not	Not
1 or 2	0 or 1	Low	Low	Low	Low
1 or 2	2 or 3	Low	Low	Intermediate	Intermediate
3	Any	Low	Low	Intermediate	Intermediate
4 or 5	0 or 1	Low	Low	Intermediate	Intermediate
4 or 5	2 or 3	Low	Low	Intermediate	High

Definite PART	
Possible PART	

FIGURE 3. Both Alzheimer disease (AD) and primary age-related tauopathy (PART) are diagnosed based on a grid that incorporates pathologic staging information related to amyloid plaques and neurofibrillary tangles (NFTs). Shown is the grid for determining the level of AD neuropathologic changes at autopsy (2), based on Thal A β stages (89), CERAD neuritic amyloid plaque stages (90), and Braak NFT stages (91). Superimposed on the AD classification scheme are criteria for “Definite PART” (red) and “Possible PART” (yellow) (59) based on the same information.

lack a consensus-based classification. Here, we focus on a specific brain disease, with clinical manifestations that overlap with AD, and which has been classified using the term “HS” based on pathologic observations (116–126). HS in aged individuals is diagnosed at autopsy (according to consensus-based guidelines) when neuron loss and astrogliosis are observed in the hippocampal formation, “out of proportion to AD neuropathologic change in the same structures” (2).

Unfortunately, the current terminology is suboptimal. There is no formal operationalization of what “out of proportion” exactly means. Moreover, the word “sclerosis” (Gr., *sklēros*is, “hardness”) lacks a specific connotation in terms of molecular pathogenesis. Pathologists observe what they describe as HS in widely differing conditions including epilepsy, hypoxia and hypoglycemia, frontotemporal lobar degeneration (FTLD), chronic traumatic encephalopathy, and some tauopathies (125, 127–133). Recently, a group of experts discussed HS pathologic classification terminology (134); however, the research subjects in that study were relatively young (most <80 years at death) in comparison to many HS-Aging cases (53, 116, 135, 136).

The term “HS-Aging” was previously applied to separate this disease from other conditions referred to as HS (15, 56, 116, 137–139). HS-Aging is distinguished by the advanced age of the affected individuals, by the usual lack of either seizure disorder or frontotemporal dementia symptoms clinically, and by the presence of hippocampal TDP-43 pathology (116, 117, 140–143). Other terms that have been applied include “HpScl” (124, 125, 144) and “HS dementia” (125, 145, 146), with “combined” and “pure” subtypes recognized according to the presence or absence of comorbid pathologies (128). We note that fewer than 2% of citations returned after a current PubMed search using the words

“hippocampal sclerosis” are related to HS-Aging, HpScl, or HS dementia. Thus, whatever final terminology is adopted, it should not be simply “HS” because this is clearly not a disease-defining pathologic endpoint. Here, we describe what is known about this disease including data germane to a useful new terminology.

HS-Aging Is a Common High-Morbidity Disease of Advanced Old Age

The disease referred to as “HS-Aging” affects up to 25% of individuals beyond 85 years of age (53, 56, 116, 117, 135, 136, 147). The reported prevalence varies across cohorts, perhaps because the “sclerosis” is diagnosed subjectively. Further, 40%–50% of the HS-Aging cases have unilateral HS pathology on hematoxylin and eosin (H&E) stain (116, 147). Because this unilateral pathology is associated with cognitive impairment (34), there would be a large number of false-negatives reported if only one side of the brain were evaluated. Another very important variable is study design. Among research cohorts that are linked to dementia clinics, the samples have tended to be enriched with “pure” AD and FTLN cases, whereas in community-based cohorts, FTLN is quite rare and there are greater numbers of cognitively intact subjects as well as those with dementia due to cerebrovascular disease and HS-Aging (22, 25, 33, 61, 62, 116, 117, 148–153).

Research from many centers has found that HS-Aging-type pathology is associated with impaired cognition (15, 34, 42, 44, 53, 56, 119, 122–124, 136, 147, 154–162). Lacking more specific biomarkers, some studies have demonstrated associations between HS-Aging pathology and particular cognitive domains (116, 119, 135, 136). A cognitive profile in patients with autopsy-confirmed HS-Aging was described with relatively impaired Logical Memory Delayed Recall, yet with preserved verbal fluency (116). These findings were validated in a separate sample to differentiate cognitive impairment with HS-Aging pathology, versus AD or FTLN pathologies, at the group level (15).

HS-Aging is generally misdiagnosed in living individuals as AD because of the presence of a memory impairment and cognitive deterioration (15, 124). Put another way, a relatively large proportion (>10%, increased in advanced age) of “clinical AD” is actually HS-Aging. This may improve as some individuals with SNAP (36), based on clinical biomarkers, are removed from clinical AD cohorts. However, identification of HS-Aging cases will remain challenging in the large group of individuals with comorbid AD and HS-Aging pathologies because they are not SNAP (15, 53, 116, 163). Indeed, HS-Aging was found in 2 (9%) of the first 22 subjects followed to autopsy among intensely longitudinally studied subjects with clinical AD in the AD Neuroimaging Initiative (ADNI) cohort (164), whereas only 4 (18%) of these cases had pure AD pathology (165).

HS-Aging: Clues About Pathogenesis and the Preclinical State

Although the pathogenesis of HS-Aging is incompletely understood, some prior findings suggest that ischemia or other

vascular dysfunction may contribute to the disease phenotype. As stated by Zarow et al (117), “HS has long been hypothesized to result from ischemic–hypoxic insult to the brain”. The CA1 sector is fed by small end-arterioles from the anterior choroidal and posterior cerebral arteries and is known to be susceptible to hypoxic injury (166). In a study of 13 aged individuals with HS, Dickson et al reported severe “arteriosclerosis” in 12 of the 13 cases (121), and others have also published data compatible with a link between HS-Aging and cerebrovascular disease (117, 123, 157, 167, 168). Subsequent studies have provided a more specific focus. We found that among vascular neuropathologies, only arteriolosclerosis is associated with HS-Aging pathology (169). The association between HS-Aging and arteriolosclerosis pathology throughout the brain was confirmed in a subsequent study (24) and is discussed further below.

In apparent contradiction to the hypothesis that HS-Aging is purely associated with cerebrovascular disease, HS-Aging brains also demonstrate characteristics that are indicative of a neurodegenerative condition. The clinical course of HS-Aging tends to follow the trajectory of a neurodegenerative disease (53, 116). A key pathologic biomarker for HS-Aging is aberrant hippocampal TDP-43 pathology that often resembles the pathologic pattern observed in FTLN-TDP (140, 141, 146, 170–172). In both HS-Aging and FTLN-TDP, slender TDP-43-immunoreactive neurites are observed in hippocampus, subiculum, and amygdala (termed “Type A” TDP-43 pathology) (86, 140, 170). Some gene variants that are associated with increased risk for HS-Aging (53, 124, 144, 173, 174) were previously associated with increased risk for FTLN (175, 176).

Thus, HS-Aging has been suggested to reflect both cerebrovascular dysfunction and abnormal proteostasis leading to protein misfolding, a mechanistic leitmotif of neurodegenerative processes (177, 178). Although these dual vascular and proteostasis mechanisms may seem contradictory, there is increasing evidence of synergistic “mixed” mechanisms that could lead to neurodegeneration (179–181). Analyzing this requires insights into TDP-43 pathology, which is the most specific marker for HS-Aging (116, 117, 140).

TDP-43 pathology was discovered in the context of brains along the clinical/genetic/pathologic spectrum that includes both amyotrophic lateral sclerosis (ALS) and FTLN (141); however, TDP-43 pathology is not specific for ALS/FTLN spectrum disorders. TDP-43 pathology has been reported in Alexander disease, Cockayne syndrome, Down syndrome, Guam ALS-parkinsonism-dementia, a subset of Lewy body disorders, low-grade glial neoplasms, inclusion body myositis, and chronic traumatic encephalopathy (97, 120, 142, 182–187). As such, TDP-43 pathology in some cases must represent a secondary (“downstream”) manifestation of diverse neurodegenerative, developmental, and “reactive” influences. Moreover, monogenic, early onset familial AD is frequently comorbid with hippocampal TDP-43 pathology (120, 188), which indicates molecular synergy for specific misfolded proteins, likely due to abnormal proteostasis. These observations argue strongly that conditions outside the ALS/FTLN spectrum may include TDP-43 pathology. A staging schema has been proposed to describe how TDP-43 pathology

is distributed in brains with comorbid AD pathology, many of which also had HS-Aging (189, 190). Notably, in multiple cohorts of aged persons, TDP-43 pathology is far more strongly linked to HS-Aging than early AD pathology (15, 53, 116, 136, 191). However, within the amygdala of subjects with advanced AD, protein misfolding of tau, A β , α -synuclein, and TDP-43 pathologies tends to occur (61, 192, 193). Accounting for the existing uncertainties, the above findings collectively indicate that multiple mechanisms can result in hippocampal TDP-43 pathology. The challenge is to define a unique condition with both TDP-43 (TDP[+]) and HS (HS[+]) pathologies.

For determining “boundary zones” that are meaningful for pathology-based classification, a key goal is to understand the disease in its preclinical stage(s). Current knowledge derives predominantly from cross-sectional data, and here we are referring mostly to autopsy series that include subjects over 85 years of age. The term “pre-HpScl” was used to describe hippocampal pathology characterized by none to minimal neuronal loss yet with abundant TDP-43 pathology (170). This partially overlaps with “segmental” HS-Aging, where only select portions of the TDP[+] hippocampal formation showed evidence of neuronal loss on H&E despite extensive additional sampling (194). Notably, in cases with unilateral HS according to H&E evaluation, the contralateral side is almost always positive for TDP-43 pathology (116).

Prior autopsy studies that reported a relatively high proportion of cases with HS[-]TDP[+] pathology (136, 61, 195), in contrast to studies with a higher proportion of HS[+]TDP[+] cases (116, 147), reflect the lack of universally applied diagnostic criteria for aging-related TDP-43 or HS-Aging pathologies. Thus, what one group may call HS[+]TDP[+], another would categorize as HS[-]TDP[+]. Yet taken together, the published studies are compatible with a progressive disease with limbic TDP-43 pathology in the early stages and HS in later stages.

Do TDP[+] cases in advanced age represent a subtype of FTLTDP-TDP? This is debatable, but there are reasons to consider TDP[+] in older subjects to be separate from FTLTDP-TDP. TDP-43 pathology seen in HS-Aging cases does not appear to progress to full-blown frontotemporal dementia (clinically) or FTLTDP-TDP (pathologically) when evaluated in community-based cohorts (25, 26, 135, 151, 61). TDP-43 pathology is rare before 65 years but allocortical TDP-43 pathology (i.e. within amygdala, hippocampus, entorhinal cortex) is common in octogenarians and nonagenarians (136, 196, 197). In a high-quality community-based cohort ($n = 544$, average age of death 89.0 years), 52% had limbic TDP-43 pathology but none had FTLTDP-TDP (198). Likewise, in the largest neuropathologic study to date of centenarians, there was not a single example of FTLTDP-TDP (24). The enormous difference in prevalence (Fig. 2) is a key point: FTLTDP-TDP affects approximately 20 000 individuals in United States (62), whereas HS-Aging afflicts well over 10 times as many if one extrapolates from large autopsy series (15, 56, 116, 117, 120, 135, 157, 199). In Figure 4, we provide cognitive, neuroimaging, and neuropathologic data on a patient with clinical “probable AD” yet whose autopsy showed HS[+]TDP[+] pathology by our criteria, and with very minimal A β deposition. To make prog-

ress in studying this common disease phenotype, it is critical to generate consensus about the disease-defining criteria. These efforts will be aided by clinical studies because there currently is no validated animal model.

In a recent neuroimaging study, Kotrotsou et al found that in elderly individuals dying with eventual autopsy-proven HS-Aging, premortem MRI studies showed extensive brain atrophy outside of the hippocampal formation, particularly in the frontal lobes (200). Furthermore, in the AD Neuroimaging Initiative (ADNI) data set (164), the HS-Aging risk alleles (described below) were associated with widespread MRI-detected brain atrophy outside of the hippocampus (201). Previous pathologic observations are compatible with the hypothesis that HS-Aging is actually a generalized disease that is often comorbid with pan-cerebral arteriosclerosis pathology, rather than one localized to medial temporal lobe structures (15, 56, 136, 158, 169, 194).

We interpret these prior findings to indicate that there is a common cerebral disease, affecting persons in advanced age, characterized by a spectrum of pathologies:

preclinical disease \rightarrow TDP - 43 pathology
 \rightarrow TDP - 43 pathology with HS and cerebral atrophy.

In other words, the signal feature of the disease is TDP-43 pathology, rather than HS. Yet, there are more complexities. Perhaps analogous to the many non-AD diseases that are associated with hippocampal NFTs (202–204), some rare diseases, fundamentally different from HS-Aging, also show the HS[+]TDP[+] pattern (127, 132, 205, 206). To understand what makes HS-Aging unique, further knowledge is required about its specific pathogenesis.

Genetics of HS-Aging

Genetic risk factors can provide insights into disease-specific mechanisms. For example, *APOE* gene variants are not associated with altered risk for either TDP[+] or HS[+] neuropathology (15, 116, 124, 135, 207). This supports the hypothesis that HS-Aging is a separate disease entity from AD.

Genotypes linked to HS-Aging pathology have now been identified (Table 3). Potential risk alleles were first analyzed in 2 specific genes (*GRN* and *TMEM106B*), in line with the hypothesis that HS-Aging is related pathogenetically to FTLTDP-TDP. The first gene variant linked to HS-Aging pathology was rs5848, a single nucleotide polymorphism (SNP) located in the 3'UTR of *GRN* (173). This SNP is also associated with altered expression of *GRN* (144, 211). Whereas many different *GRN* mutations cause FTLTDP-TDP (212–216), the HS-Aging SNP (rs5848) is apparently a disease-modifying allele that impacts the manifestation of multiple different diseases rather than specifically of HS-Aging. For example, rs5848 has been linked to AD, Parkinson disease, *C9ORF72* neurodegeneration, and bipolar disorder (173, 217–221), whereas several groups have reported that rs5848 is not linked to FTLTDP (208, 222).

The *TMEM106B* SNP rs1990622 is a risk allele for FTLTDP-TDP, as determined using a genome-wide association study (GWAS) (223), and the same SNP is linked to a coding variant and altered protein expression (224). *TMEM106B*

Case Report: Patient followed longitudinally (>20yrs) with neurocognitive testing, brain MRI, and autopsy

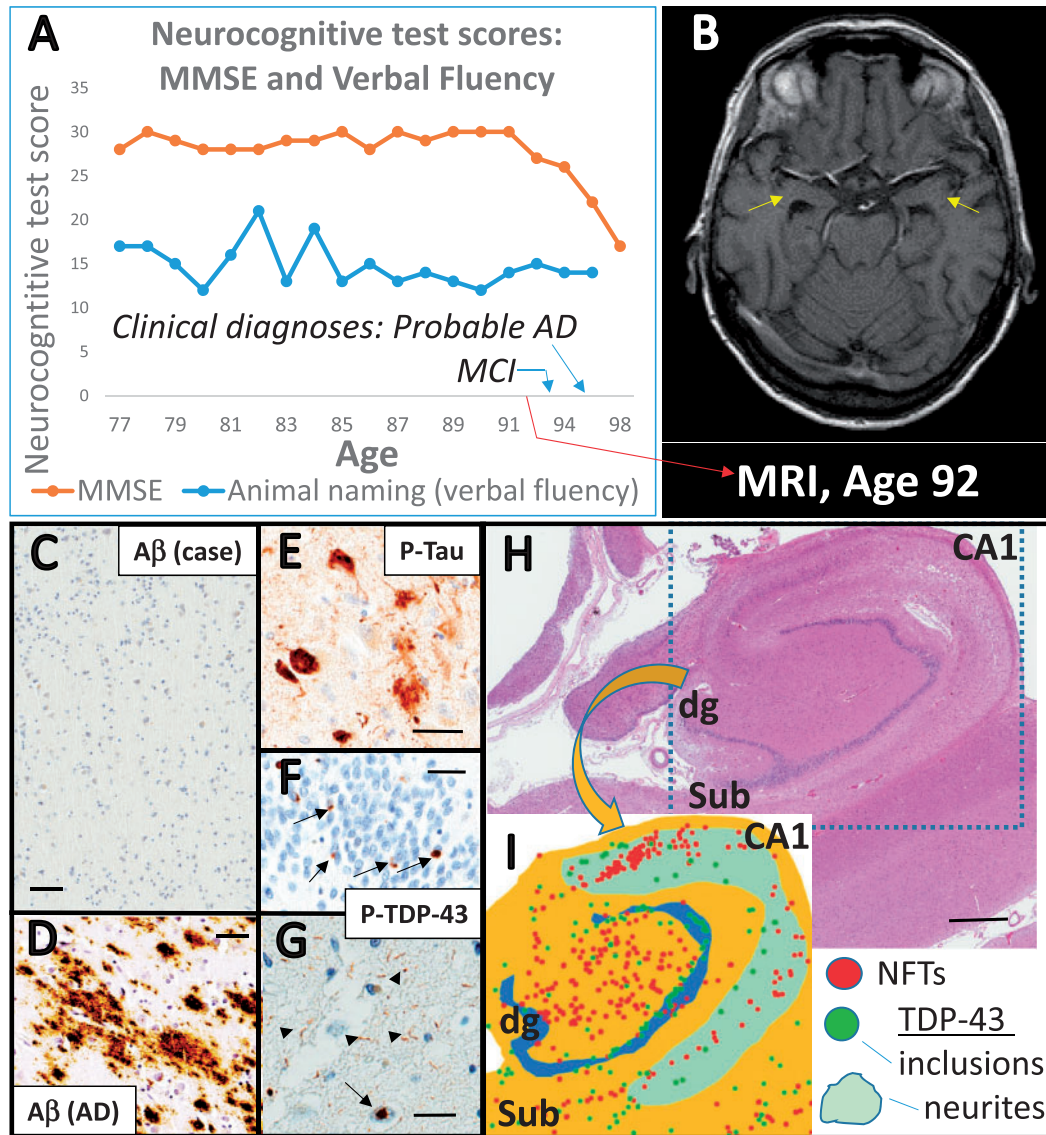


FIGURE 4. Case study illustrates clinical and neuropathologic features of common comorbid diseases. The female subject was followed from 77 years until death at age 102 years. Detailed neurocognitive tests were performed until age 98 years; MCI was diagnosed clinically at age 93, “Probable Alzheimer Disease” at age 95. *APOE* genotype was $\epsilon 3/\epsilon 3$. **(A)** Panel shows results of MMSE (global cognition) and animal naming (verbal fluency) results; note that the verbal fluency was relatively stable even after global cognitive status was impaired. A brain MRI (horizontal plane) 10 years before death **(B)** showed hippocampal atrophy (arrows). Immunohistochemistry demonstrated extremely sparse A β amyloid pathology in temporal neocortex **(C)** and no neuritic plaques. A β amyloid in AD brain **(D)** is shown for comparison. In the hippocampal formation there was Braak NFT stage II tauopathy **(E)** and PART and HS-Aging were both diagnosed. Note that the hippocampal sclerosis is diagnosed according to consensus-based criteria (2): “cell loss and gliosis out of proportion to plaques and tangles,” rather than complete destruction of the structure. TDP-43 pathology was present in the hippocampus; **(F)** shows dentate gyrus with inclusions (arrows) and **(G)** shows subiculum with neuronal inclusion (arrow) and slender nontapering TDP-43 neurites (arrowheads). Widespread brain arteriolosclerosis pathology was also observed (Fig. 5). Panel **(H)** is a low-power photomicrograph showing the hippocampal formation including CA1, dentate granule (dg), and subiculum (Sub) regions. Adjacent sections were stained for phospho-Tau (P-Tau) and P-TDP-43 and the pathology was depicted schematically (inset I) using an Aperio ScanScope as described previously (56): red dots for NFTs, green dots for P-TDP-43 inclusions, and cyan region shows area with P-TDP-43 neurites. As noted previously (56), the tauopathic distribution in TDP[+]HS[+] cases is slightly different from “classic” early Braak NFT stages. Scale bars: **C**, 100 μ m; **D**, 80 μ m; **E**, 40 μ m; **F**, 30 μ m; **G**, 70 μ m; **H**, 2 mm.

TABLE 3. Genes and Single Nucleotide Polymorphisms Associated With Risk for Hippocampal Sclerosis of Aging

Gene	SNP	Experiment that Linked the Gene to HS-Aging: SNP-Focused or GWAS	Replicated?	References
<i>GRN</i>	rs5848	SNP-focused	Yes	(124, 144, 173, 174)
<i>TMEM106B</i>	rs1990622	SNP-focused	Yes	(170, 174, 194, 196, 208, 209)
<i>ABCC9</i>	rs704180	GWAS	Yes	(24, 151, 174, 58) ^a
<i>KCNMB2</i>	rs9637454	GWAS	No	(210)

^aReference (58) refers only to *ABCC9* association with brain arteriolosclerosis.

polypeptide is a lysosomal protein that apparently affects *GRN* expression (225–227). The risk allele is associated with increased vulnerability to ALS and for neurodegeneration linked to *C9ORF72* repeat expansions (209,228). Further, in SNP-focused studies, rs1990622 status was found to be associated with HS pathology (53, 151, 229), altered AD phenotype (210, 229, 230), and cognition independent of AD or HS pathologies (196).

The studies on specific *GRN* and *TMEM106B* gene variants due to their link with other diseases left unaddressed the possibility of genotypes associated specifically with HS-Aging. A complementary experimental approach is GWAS, which is unbiased by prior mechanistic hypotheses. GWASs have now identified 2 putative HS-Aging risk genes, both of which encode potassium channel regulators: *ABCC9* and *KCNMB2* (151, 231).

The association between *ABCC9* SNP rs704180 and HS-Aging pathology attained genome-wide significance in the GWAS paper (151), and has since been replicated (174), although not as extensively as *GRN* and *TMEM106B*. This intronic SNP is associated with altered *ABCC9* mRNA expression (232), and nearby *ABCC9* gene variants are also linked to other neurologic diseases such as sleep disorder and depression (233–235). The *ABCC9* gene encodes proteins that regulate potassium channels (233, 234), serving as a metabolic “sensor” relevant to vascular responses to hypoxia, ischemia, and inflammation (236). There are published studies that support direct connections between *ABCC9* and neurodegenerative disease mechanisms (237–244).

A second gene linked through GWAS to HS-Aging pathology is *KCNMB2* (231). Intriguingly, Zarei et al found that the *KCNMB2* gene product could be relevant to hippocampal physiology (245). As yet, the finding of association between the *KCNMB2* SNP rs9637454 and HS-Aging remains to be replicated.

In summary, genomic studies provided meaningful indications about what may cause or protect against HS-Aging. The associations for both *GRN* and *TMEM106B* SNPs with HS-Aging risk have now been replicated, providing strong support for a mechanism relevant to both HS-Aging and FTLT-DTP. However, these HS-Aging risk SNPs are risk-modifying alleles in multiple diseases, thereby begging the question about the disease-specific “upstream” factors. The impact of these particular gene variants may be analogous to the *MAPT* H1 haplotype that confers increased risk for PART, progressive supranuclear palsy, and other “sporadic” tauopathies (57, 105, 108, 246, 247), as opposed to *MAPT* mutations

that directly cause familial FTLT-MAPT (248–250). As with PART in comparison to FTLT-MAPT, the ultimate manifestations of HS-Aging and FTLT-TDP are also profoundly different from each other in terms of clinical (i.e. course and age range) and pathological features (15, 56). Although it is an important insight that particular *GRN* and *TMEM106B* SNPs can increase risk for TDP-43 pathology in multiple diseases, the experiments that discovered these phenomena were blind to the disease-specific “upstream” mechanisms involved in a disease that is far more common than FTLT-TDP. Published genome-wide analyses have implicated *ABCC9* gene variants specific to HS-Aging. Because genomics information provides insights into pathogenesis, this may help in the delineation of the disease phenotype, shifting the focus to another brain pathology, namely aging-related brain arteriolosclerosis (B-ASC).

Previously Unsuspected Pathologic Synergies: B-ASC and HS-Aging

B-ASC describes pathologic thickening of the walls of brain arterioles not due to brain amyloid (58, 63, 169, 251–255). This subtype of small vessel pathology is very common in the brains of older individuals and is associated with impaired cognitive status, independent of other pathologies (255). In prior studies by us and others, it was implied that B-ASC represents a well-defined and classifiable subtype of vascular pathology in the CNS.

However, we have much to learn about brain arterioles in healthy and disease states. A recent review made trenchant points: “The term arteriolosclerosis actually does not define a lesion at all. It is a generic term meaning ‘hardening of small arteries’. In fact, the term encompasses 2 distinct lesions: (1) a fibromuscular proliferation of the intima, the ‘hyperplastic type’ and (2) a deposition of amorphous material in the arteriolar wall, the ‘hyaline type’” (256). Moreover, the current classification of arteriosclerosis is not based on a consensus document by a major cerebrovascular, cardiovascular, or pathology organization (256). Despite progress in the field, relatively little is known about the neuropathology of elements that comprise brain arterioles, a complicated arrangement of endothelial cells, pericytes, smooth muscle cells, basement membrane, astrocyte end-feet, and extracellular matrix (64, 255, 257–261). Small blood vessels participate in energy exchange, removal of waste, blood pressure regulation, neuroglial activity, and neuroimmune functions and it seems clear that we still have much to learn.

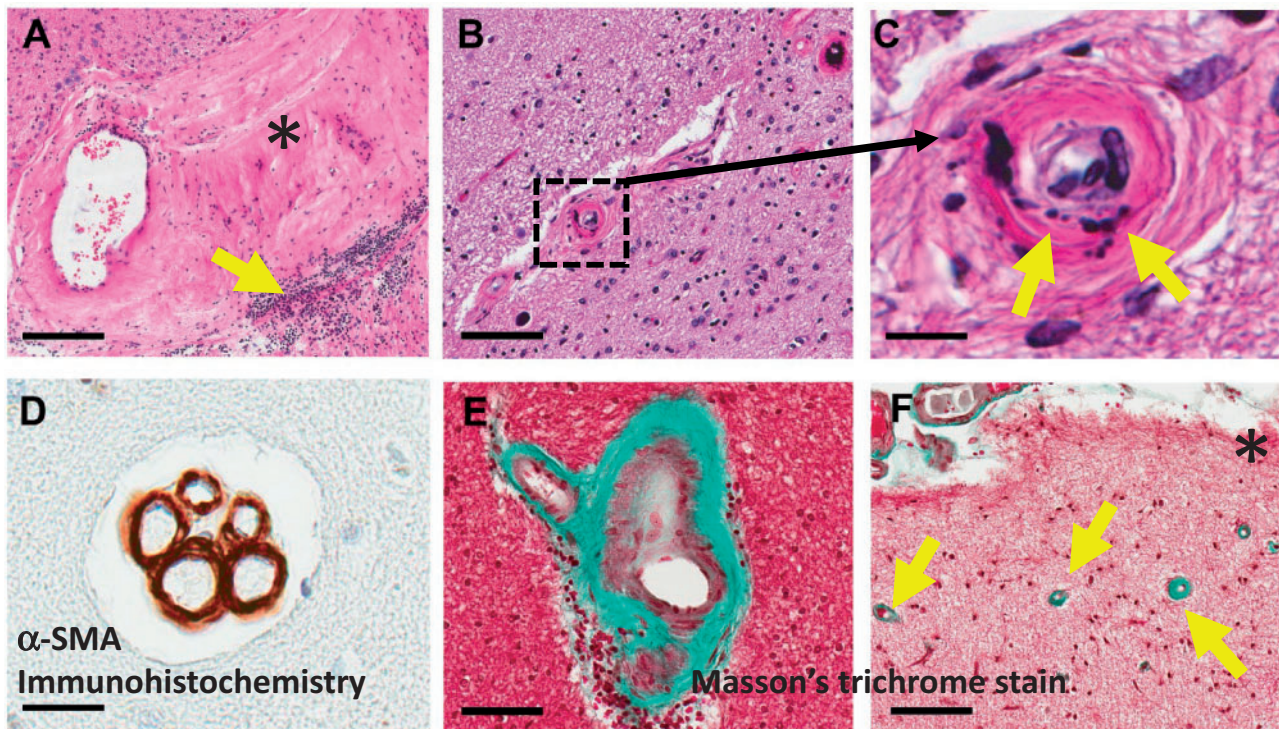


FIGURE 5. Brain arteriolosclerosis (B-ASC) pathology is a complex phenotype. These panels show B-ASC vascular profiles in brains from different aged individuals to provide a small sampling of the heterogeneity of B-ASC. (**A–C**) Panels show hematoxylin and eosin staining. Panel (**A**) is a low-power photomicrograph depicting a vessel in the amygdala of a person with advanced AD and cerebrovascular disease. Note the large expanse of hyalinized material (*) that extends from the vessel wall, along with a patch of lymphocytic inflammation (arrow). By contrast, in the hippocampus of the case study (Fig. 4) there is a smaller blood vessel (boxed in **B**, magnified in **C**) that shows a vascular profile with apparent fibrinoid necrosis and/or microcalcifications in the paucicellular vessel wall. Another pattern we have seen in many cases is multiple vascular profiles in the same vessel bed, as shown in panel (**D**) (arterioles are here visualized using α -SMA immunohistochemistry). Collagen can be visualized using a trichrome stain (panels **E**, **F** are separate HS-Aging cases); a B-ASC profile is shown in **E** with the collagen labeled green. Cases with hippocampal TDP-43 in our experience often show neocortical B-ASC as visualized by the green-staining arterioles (arrows) in this low-power photomicrograph near the pia (*) of frontal neocortex, Brodmann Area 9. Scale bars: **A**, 200 μ m; **B**, 90 μ m; **C**, 10 μ m; **D**, 25 μ m; **E**, 70 μ m; **F**, 100 μ m.

Photomicrographs to convey some of the heterogeneity of vascular changes that may be diagnosed as B-ASC at autopsy are shown in Figure 5. In aged brains, arteriolar morphologies include pathologic variants other than “hyperplastic” and “hyaline”-type changes. For example, some arterioles show degenerative changes in smooth muscle cells, whereas other arteriolar structures comprise multiple lumens (262, 263). Future work may better capture the heterogeneity of arteriolar disease phenotypes and provide the basis for robust clinical-pathologic correlations.

Although many unknowns remain in the study of B-ASC, insights have been gained. Studies of organs outside the brain indicate that arteriolosclerosis is associated with metabolic or cardiovascular disorders such as diabetes and hypertension (57, 256, 264–267). Ighodaro et al recently tested risk factors of B-ASC among 2390 persons who had come to autopsy with known B-ASC status using the National Alzheimer’s Coordinating Center data set (255, 268). These analyses indicated that advanced age at death was associated with B-ASC severity. Self-reported hypertension was only associated with B-ASC in the <80 years age at death group.

Interestingly, in the ≥ 80 years age at death group, the *ABCC9* gene variant rs704180, previously associated with HS-Aging, was also associated with B-ASC (255). By contrast, neither *GRN* nor *TMEM106B* SNPs were associated with B-ASC (255). The hypothesis that *ABCC9* is associated with arteriolosclerosis pathology throughout many different brain regions was supported in analyses of centenarians’ brains (24). Intriguingly, Lim et al recently reported that B-ASC is associated with “sleep fragmentation,” (269) and *ABCC9* gene variants have been linked to sleep problems (235, 270, 271).

The observation that the same *ABCC9* gene variant is associated with risk for both B-ASC and HS-Aging pathologies in old age provides the basis for a novel hypothesis combining cerebrovascular and neurodegenerative paradigms (255). One exciting aspect of implicating *ABCC9* in disease pathogenesis is that *ABCC9* gene product-modifying drugs (both agonists and antagonists) are widely used in the human pharmacopeia (272–275). We emphasize that the findings of *ABCC9* require further validation; this is still a new hypothesis that requires more study.

HS-Aging/CARTS:

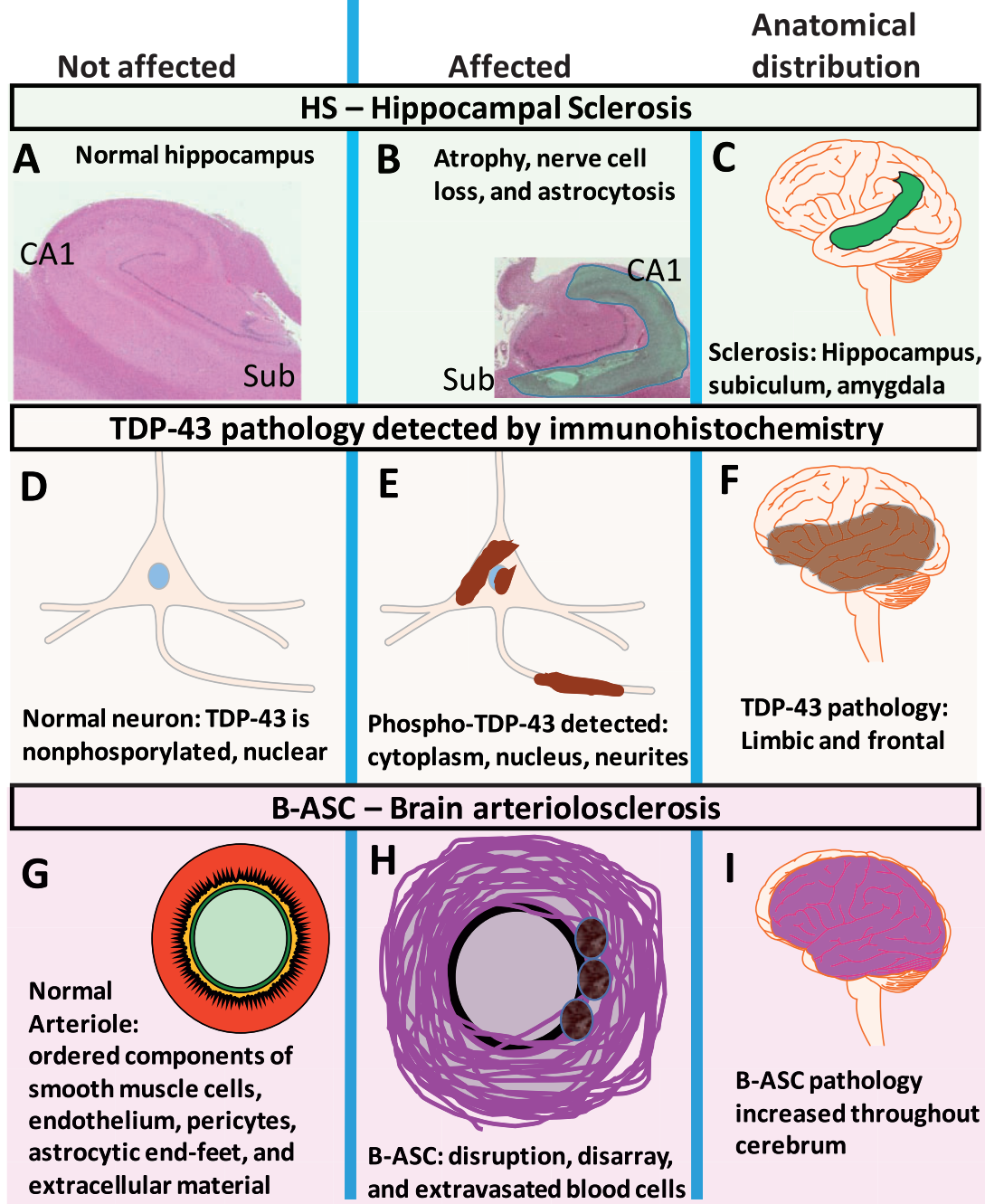


FIGURE 6. The disease we have referred to as hippocampal sclerosis of aging (HS-Aging) is a complex phenotype that includes hippocampal sclerosis (**A-C**), TDP-43 pathology (**D-F**), and brain arteriolosclerosis (**G-I**). Features of pathologically unaffected compartments are shown (**A**, hippocampus; **D**, neurons; and **G**, arterioles) in contrast to the compartments (**B**, **E**, **H**) and brain areas (**C**, **F**, **I**) affected in this disease. Because the extant classification is suboptimal, we propose a new terminology to classify this disease: cerebral age-related TDP-43 and sclerosis, CARTS.

Any hypothesis to conceptualize the aging-related disease that was previously labeled HS-Aging or HS dementia must include TDP-43 pathology. In each of the many conditions associated with TDP-43 pathology there is a chronic

genetic and/or environmental insult to the brain. It is possible that a subtype of chronic vascular insult(s) could induce TDP-43 phosphorylation and misfolding. Numerous studies indicate that TDP-43 pathology does not appear to arise following

TABLE 4. Proposed Staging of Disease Referred to as HS-Aging or “CARTS”

Disease Stage	Genetic risk factors	Pathology
Preclinical	<i>ABCC9</i>	Brain arteriolosclerosis (B-ASC)
↓		+
Early clinical		Amygdala/limbic TDP-43 pathology
↓	<i>GRN/TMEM106B</i>	+
Late clinical		TDP-43 outside the amygdala Hippocampal sclerosis Cerebral atrophy

Inclusion:

- o >85 years of age at death.
- o TDP-43 pathology in limbic structures, preferably in more than one region. Amygdala, subiculum, hippocampus proper, parahippocampal gyrus.
- o Hippocampal sclerosis and arteriolosclerosis should be evaluated but are not required for diagnosis.

Exclusion:

- o Exclude cases with frontotemporal dementia (FTD)-spectrum, including behavioral variant FTD, semantic dementia, progressive nonfluent aphasia, and logopenic aphasia (on clinical grounds and optimally on neuropsychological testing).
- o Exclude cases with predominantly amygdala TDP-43 in the context of advanced Alzheimer disease pathology (Braak NFT stages V/VI).

acute hypoxic/ischemic neuronal injury (116, 117, 140, 142). This would be directly analogous to brain trauma, where a single traumatic event is not associated with TDP-43 pathology (276), yet approximately 80% of brains with chronic traumatic encephalopathy are positive for TDP-43 pathology (127). If chronic vascular dysfunction can lead to TDP[+] disease phenotype, then that disease may constitute a novel targetable cause of dementia. An intriguing possibility is that epidemiologic phenomena previously attributed to AD (65, 66) are related instead to this common, high-morbidity, but hitherto largely ignored disease.

Revised Terminology: A Recommendation

Whatever the pathogenetic mechanisms are, new terminology is required. Neither “HS-Aging,” nor any other extant term, is truly applicable. A terminology that focuses on FTLT, TDP-43, or HS in isolation would not be accurate based on the experimental data. Because the disease preferentially affects the “oldest-old,” often includes TDP-43 pathology and arteriolosclerosis well beyond the hippocampus, and may evolve to HS, we recommend the term “cerebral age-related TDP-43 and sclerosis” (CARTS). Features seen in CARTS are illustrated in Figure 6.

A diagnosis of CARTS indicates robust TDP-43 pathology in the hippocampus of persons aged >85 years at death and would otherwise incorporate the current TDP[+] cases termed HS-Aging, HpScl, and HS dementia. As stated above, it is relevant that both HS and arteriolosclerosis are often parts of the phenotype. We recommend that HS is not necessary for the diagnosis of CARTS because HS is ill-defined, nonspecific, and often segmental and, therefore, sampling bias would be considerable. Although B-ASC may well play a role in pathogenesis,

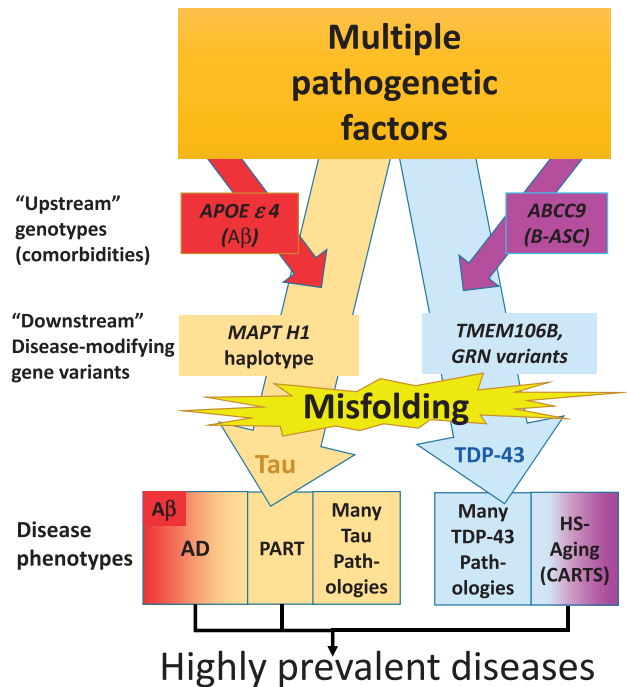


FIGURE 7. Pathogenesis helps guide classification of neurodegenerative diseases. This schematic depicts hypotheses about the multiple genetic and environmental factors that promote tau and TDP-43 pathologies. These may include comorbid pathologies such as amyloid plaques (associated with *APOE* ε4 allele) or brain arteriolosclerosis (B-ASC, associated with *ABCC9* gene variant). There also are “downstream” genetic risk modifiers, such as *GRN* (rs5848), *TMEM106B* (rs1990662), and *MAPT* H1 haplotype, which appear to influence many different disease phenotypes each. Ultimately, protein misfolding contributes to symptomatic manifestations. While there are large number of rarer conditions, the common tau and TDP-43 diseases linked to cognitive impairment in advanced old age are AD, PART, and HS-Aging/CARTS.

the current diagnosis of B-ASC is too inconsistent to be practical as part of the diagnostic rubric at this time. The TDP-43 pathology frequently extends outside the hippocampus, but CARTS should not have the extremely dense subcortical TDP-43 pathology that occurs in FTLT-TDP. A hypothetical staging schema is presented in Table 4. Some older FTLT-TDP cases may be challenging to discriminate from CARTS in the absence of other biomarkers, but CARTS affects a virtually nonoverlapping age group in comparison with FTLT-TDP. AD and CARTS pathologies are both common pathologies and thus are expected to be comorbid frequently, although distinct ‘boundary zones’ will require further research.

CONCLUSION

High-quality, large autopsy cohorts and collaborative efforts among neuropathologists have enabled recent advances in the field of disease classification relevant to dementia. There are diagnostic “border zones” that need to be clarified and a better understanding of the “mixed” pathologies that are typical in advanced old age is needed. As these challenges are

addressed, the diagnoses increasingly reflect the biologic complexity and should help in efforts to identify appropriate patient groups for clinical trials. Particular diagnostic categories are in different stages of scientific “maturity,” with some having been studied in thousands of published papers, whereas others will require substantial additional work to achieve an accurate nosology. TDP-43 pathologies appear to be analogous to tau tangles, “upstream” factors and comorbid pathologies can disturb protein homeostasis, especially with the added influence of gene variants that increase risk across different diseases (Fig. 7). Categorizing the “downstream” pathology is complex because of the overlapping pathologic phenotypes. This is particularly true for CARTS because TDP-43, HS, and B-ASC pathologies all occur in multiple conditions. The recently revised pathologic concepts are not all truly novel. On the contrary, investigators had previously reported many of the manifestations of the brain diseases but lacked adequate contextual data. It is safe to assert that for all prior advances, current data are imperfect and skepticism should be sustained in considering the current diagnostic terms and criteria. Categorization of brain diseases of aging is still a work in progress.

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