



The unique neuropathological vulnerability of the human brain to aging

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ABSTRACT

Alzheimer's disease (AD)-related neurofibrillary tangles (NFT), argyrophilic grain disease (AGD), aging-related tau astroglialopathy (ARTAG), limbic predominant TDP-43 proteinopathy (LATE), and amygdala-predominant Lewy body disease (LBD) are proteinopathies that, together with hippocampal sclerosis, progressively appear in the elderly affecting from 50% to 99% of individuals aged 80 years, depending on the disease. These disorders usually converge on the same subject and associate with additive cognitive impairment. Abnormal Tau, TDP-43, and α -synuclein pathologies progress following a pattern consistent with an active cell-to-cell transmission and abnormal protein processing in the host cell. However, cell vulnerability and transmission pathways are specific for each disorder, albeit abnormal proteins may co-localize in particular neurons. All these alterations are unique or highly prevalent in humans. They all affect, at first, the archicortex and paleocortex to extend at later stages to the neocortex and other regions of the telencephalon. These observations show that the phylogenetically oldest areas of the human cerebral cortex and amygdala are not designed to cope with the lifespan of actual humans. New strategies aimed at reducing the functional overload of the human telencephalon, including optimization of dream repair mechanisms and implementation of artificial circuit devices to surrogate specific brain functions, appear promising.

1. Introduction

Heterogeneous pathologies are now known to contribute to cognitive impairment, behavioural and psychological deterioration, neuropsychiatric symptoms such as depression, and dementia in the elderly. For several decades, neuropathological and clinical studies have identified two main biological processes in human brain aging. On the one hand, there is the primary degeneration of nerve cells, mainly represented by neurofibrillary tangles and senile plaques culminating in Alzheimer's disease dementia. On the other, there is then the degenerative alteration of cerebral blood vessels, often occurring in parallel with the systemic

degeneration of large and medium size arteries, arterioles, venules, and capillaries that may result in various vascular deficits, including cognitive impairment and dementia of vascular origin. The two biological processes may occur with variable intensity in the same individual. In recent decades, several age-related neurodegenerative diseases have been newly identified in humans such as frontotemporal lobar degeneration (FTLD), now covering several separate entities, and dementia with Lewy bodies (DLB), along with others.

In addition, several brain neuropathological changes are linked to human brain aging, including argyrophilic grain disease (AGD), aging-related tau astroglialopathy (ARTAG), Lewy body disease (LBD), TDP-43

Abbreviations: ADD, Alzheimer's disease dementia; ADNC, Alzheimer disease neuropathological change; AGD, argyrophilic grain disease; APP, amyloid precursor protein; ARTAG, Aging-related tau astroglialopathy; CBD, corticobasal degeneration; CERAD, Consortium to Establish a Registry for Alzheimer's disease; DLB, dementia with Lewy bodies; ERK, extracellular regulated MAP kinase; fAD, familial Alzheimer's disease; FTLD, Frontotemporal lobe degeneration; GSK, glycogen synthase kinase; GVD, Granulovacuolar degeneration; LATE, Limbic age-related TDP-43 encephalopathy; LBD, Lewy body disease; MCI, mild cognitive impairment; NFT, neurofibrillary tangle; PART, Primary age-related tauopathy; PD, Parkinson's disease; PHF, paired helical filament; PiD, Pick's disease; PMCA, protein misfolding cyclic amplification; PS1, PSEN1, presenilin 1; PSP, progressive supranuclear palsy; RT-QuIC, real-time quaking-induced conversion; sAD, sporadic Alzheimer's disease; SAPK/JNK, stress-activated protein kinase/c-Jun N-terminal kinase; SP, senile plaque; TDP-43, TARDBP, TAR DNA-binding protein 43; TREM, triggering receptor expressed in myeloid cells; TSA, thorn-shaped astrocyte.

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encephalopathy (LATE), and hippocampal sclerosis. Due to the high prevalence of Alzheimer's disease-neuropathological change (ADNC), all of them are common in patients with sAD and may contribute to worsening the clinical symptoms of AD, but they may also occur as separate neuropathological neurodegenerative changes. Most occur in combination as co-morbidities.

ADNC, AGD, ARTAG, limbic α -synucleinopathy, LATE neuropathological change (LATE-NC), and hippocampal sclerosis will be discussed in this paper. Other age-related alterations such as lipofuscin accumulation, granulovacuolar degeneration, Hirano bodies, and corpora amylacea are not considered here in detail.

All these alterations are manifestations of brain aging, although none of them per se can be considered the only expression of brain aging. Currently, these alterations reflect the complexity of brain aging neuropathology. Moreover, all these neuropathological changes are prevalent in humans and poorly represented or absent in other species. The uniqueness of the neuropathological characteristics of human brain aging points to the specific vulnerability of the human brain to aging compared with other species. Efforts are needed to dissect and identify the mechanisms leading to such vulnerability in humans as well as to

discern the mechanisms preventing neurodegenerative changes in old individuals of other species.

2. Neurofibrillary tangles and senile plaques: Alzheimer's disease-neuropathological change (ADNC)

Neurofibrillary tangles (NFTs) and senile plaques (SPs) composed of a central core surrounded by dystrophic neurites, as first described by Alois Alzheimer and Oskar Fisher (Alzheimer, 1907; Fischer, 1907, 1910, 1912), are hallmark neuropathological lesions in human brain aging and AD, and named Alzheimer's disease neuropathological change (ADNC) (Fig. 1).

β -amyloid is the main component of cerebral amyloid in β -amyloid angiopathy and SPs (Glennner and Wong, 1984; Glennner et al., 1984; Masters et al., 1985; Iwatsubo et al., 1994; Masters and Beyreuther, 2006a). β -amyloid derives from the amyloid precursor protein (APP) which is a transmembrane protein that modulates brain cell adhesion, synaptic plasticity, and multiple intracellular signaling. Cleavage of APP through α - and δ -secretases leads to the non-amyloidogenic pathway of APP degradation, whereas the combined action of β - and δ -secretases

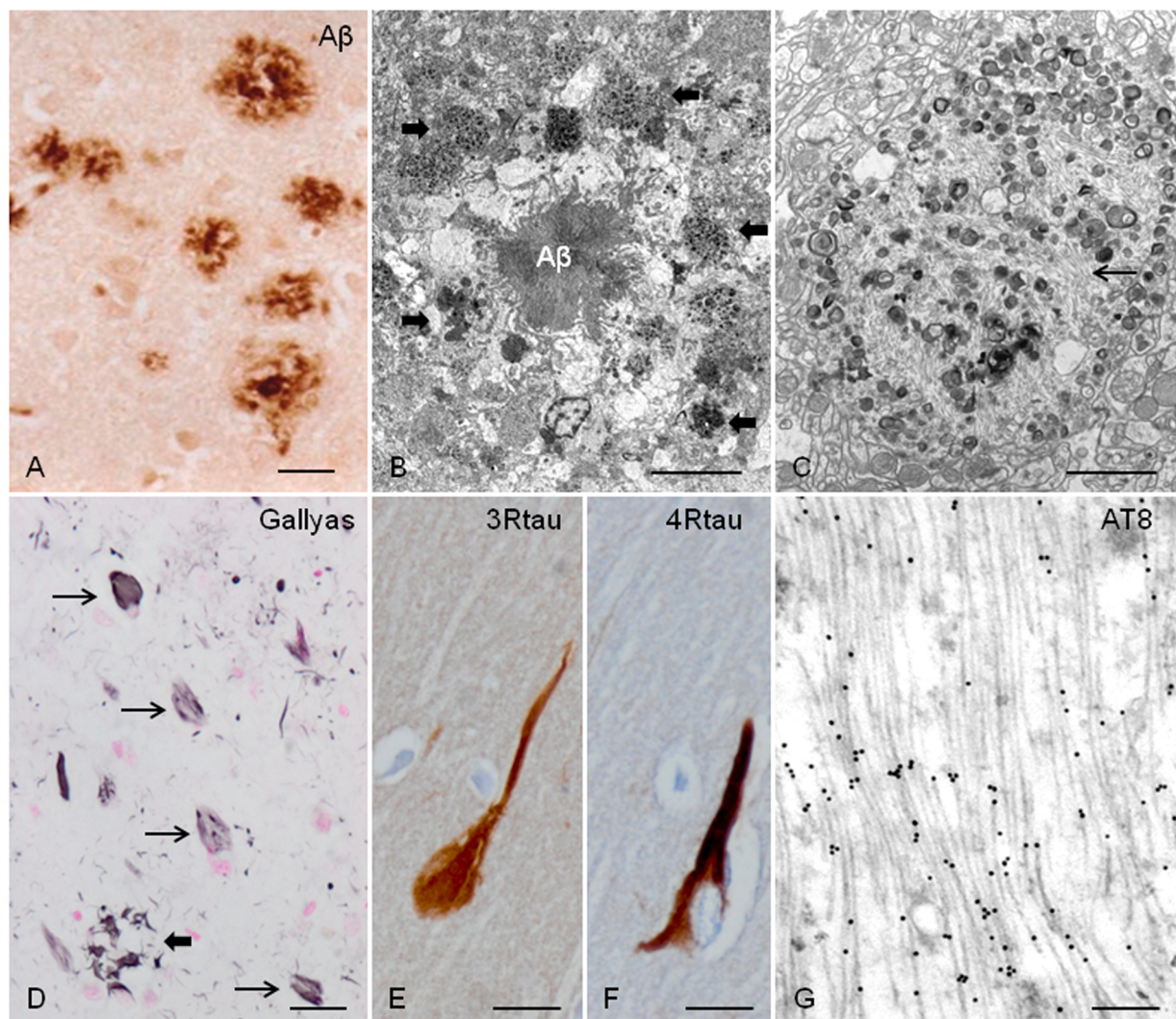


Fig. 1. Alzheimer's disease neuropathological change. A: senile plaques in the temporal cortex as seen with β -amyloid ($A\beta$) immunohistochemistry; B: senile plaque with a central core of β -amyloid (surrounded by dystrophic neurites (thick arrows); C: Dystrophic neurite containing paired helical filaments (thin arrow), abnormal mitochondria, and large numbers of polymorphic and dense inclusions and vesicles; D: Neurofibrillary tangles (NFT) (thin arrows) and one senile plaque (thick arrow) as seen with the Gallyas method in the temporal cortex; E: 3Rtau immunohistochemistry of a NFT; F: 4Rtau immunohistochemistry of a NFT; G: immunoelectronmicroscopy of paired helical filaments stained with the antibody AT8 showing the localization of phospho-tau deposition (black dots). A, D-F: paraffin sections; B, C, G: transmission electron microscopy. A, bar = 50 μ m; B, bar = 10 μ m; C, bar = 2 μ m; D, bar = 50 μ m; E, F, bar = 25 μ m; G, bar = 0.2 μ m.

generates truncated C-terminal peptides A β ₄₂ or A β ₄₀, and many other small forms (Beyreuther and Masters, 1991; Masters and Beyreuther, 2006b; Masters and Beyreuther, 2011; Masters and Selkoe, 2012; Chen et al., 2017). Seen under electron microscopy, β -amyloid is composed of fibrils with a high degree of conformational variability: α -helical intermediate conformation on the membrane, and structural transition to the β -conformation of amyloid fibrils. Cryo-electron microscopy reveals that A β ₄₂ fibril is composed of two intertwined protofilaments with specific morphology (Gremer et al., 2017; Yang et al., 2022a, 2022b) (Fig. 1A-C).

The main constituent of NFTs, dystrophic neurites of SPs, and neurofibrillary threads is abnormal tau (Delacourte and Defossez, 1986; Goedert et al., 1988; Kosik et al., 1986; Grundke-Iqbal et al., 1986a; Iqbal et al., 1986; Wischik et al., 1988; Buée et al., 2000; Iqbal et al., 2005; Mandelkow and Mandelkow, 2012; Spillantini et al., 2013; Arendt et al., 2016; Iqbal et al., 2016; Goedert and Spillantini, 2019). A combination of all six hyper-phosphorylated brain tau isoforms (3Rtau and 4Rtau expressed in brain), generated from alternative *MAPT* exon 10 splicing, is characteristic of AD tau with a ratio 1/1 (Goedert et al., 1982; Goedert et al., 1992; Delacourte et al., 1999). Western blots of sarkosyl-insoluble fractions show main bands of phospho-tau of 68 kDa, 64 kDa, and 60 kDa, an upper band of about 73 kDa, and several lower bands and smears of about 50 kDa and 30 kDa, as well as bands of lower molecular weight corresponding to truncated tau. Abnormal tau in sAD is characterized by various post-translational modifications including hyper-phosphorylation at different sites, glycosylation, acetylation, truncation at glutamic acid 391 and at aspartic acid 421, altered conformation, oligomerization, and β -sheet-rich fibril aggregation, among others (Grundke-Iqbal et al., 1986b; Weaver et al., 2000; García-Sierra et al., 2003; Hyman et al., 2005; Avila, 2006; Zilka et al., 2006; Luna-Muñoz et al., 2007; Mondragón-Rodríguez et al., 2008; Arendt et al., 2016; Avila, 2016; Iqbal et al., 2016; Goedert and Spillantini, 2019; Hernández et al., 2022). Tau hyper-phosphorylation is mediated by specific kinases accompanied by inhibition of phosphatases (Hanger et al., 2009; Wang et al., 2013; Arendt et al., 2016). Selected active kinases such as ERK1/2, p38, SAPK/JNK, and GSK3 β co-localize with abnormal tau deposits in brain tissue (Ferrer et al., 2001a, b; Ferrer et al., 2005).

Under electron microscopy NFTs are seen to be composed of paired helical filaments (PHF), whereas straight filaments occur in pre-tangles, and granular tau is composed of oligomers. Cryo-electron microscopy reveals a particular conformation profile of AD-tau (Fitzpatrick et al., 2017; Shi et al., 2021a, 2021b; Kametani and Hasegawa, 2022) (Fig. 1D-G).

Mechanisms of protein degradation and debris removal are also altered in human brain aging and sAD. The ubiquitin-proteasome system is defective, and ubiquitin and p62 are accumulated in tau-positive deposits (Riederer et al., 2011; Salminen et al., 2012; Lee et al., 2013; Weng and He, 2021). Moreover, misframed ubiquitin is expressed in abnormal tau-protein aggregates (Chadwick et al., 2012; Gentier and van Leeuwen, 2015), and the immunoproteasome is activated in sAD and APP/PS1 double-transgenic mice (Ferrer et al., 2004; Aso et al., 2012).

Autophagy, including mitophagy, is impaired in brain aging and sAD (Nixon et al., 2005; Lipinski et al., 2010; Pradeepkiran and Reddy, 2020).

Although the localization and distribution of NFTs progresses following a stereotyped pattern, the pace varies from one individual to another. NFTs have been identified in selected nuclei of the brain stem in young people in their twenties (subcortical stages a-c) (Braak and Del Tredici, 2011; Braak and Del Tredici, 2015; Arnsten et al., 2021). Later on, NFTs extend to the entorhinal and transentorhinal cortices (stages I-II), hippocampus, amygdala, inferior part of the temporal lobe and limbic system (stages III-IV), and finally to the diencephalon and most parts of the telencephalon (stages V-VI). Thus, the number of NFTs increases with age and affects about 85% of human beings at the age of 65, at least involving the entorhinal and transentorhinal cortex, and the

hippocampus, temporal cortex, and limbic system nuclei. About 98% of individuals have NFTs in the telencephalon at 80 (Braak and Braak, 1991; Braak and Braak, 1997; Braak et al., 2011; Ferrer, 2012; Arnsten et al., 2021; Ferrer, 2022a). However, SPs appear later, and their regional distribution also differs from NFT progression (Thal et al., 2002).

About 30% of people have SPs at age 65, and around 60% over 80. NFTs without SPs are detected in about 35% of individuals older than 90 (Braak et al., 2011; Ferrer, 2012; Arnsten et al., 2021; Ferrer, 2022).

Genetic factors modulate ADNC. The rarer familial forms of AD (fAD), which have an earlier onset, are linked to mutations in three genes which encode membrane proteins associated with membrane protein proteolysis and, in particular, with the amyloidogenic pathway: the gene encoding β -amyloid precursor protein named APP, presenilin 1 (PSEN1), and presenilin 2 (PSEN2); increased APP dosage is also causative of fAD and β -amyloid angiopathy (Goate et al., 1991; Chartier-Harlin et al., 1991; Murrell et al., 1991; Levy-Lahad et al., 1995; Sherrington et al., 1995; Rogaev et al., 1995; Bertram and Tanzi, 2011).

Sporadic AD (sAD) is the most common cause of dementia in the elderly. The prevalence of dementia in 65–69 years olds is about 1–5:100 individuals; over the age of 85, between 25% and 30% of individuals suffer from dementia (Knopman et al., 2011). Between 50% and 80% of cases with dementia have sAD (Knopman et al., 2011). AD dementia (ADD) is preceded by mild cognitive impairment (MCI), and by pre-clinical AD that is characterized by the presence of ADNC and positive biological markers without apparent cognitive impairment (Knopman, 2011; Sperling et al., 2011; Knopman et al., 2012). Dementia in AD occurs at advanced stages of NFT pathology (stages V-VI) accompanied by β -amyloid deposition at advanced Thal's phases (Hyman et al., 2012; Montine et al., 2012).

Individuals with Down syndrome, caused by the presence of all or part of the third copy of chromosome 21, have large numbers of SPs and NFTs at the age of 40 (Gomez et al., 2020; Fortea et al., 2021).

Apolipoprotein E epsilon 4 (ApoE ϵ 4) was the first low-penetrating genetic risk factor of sAD identified (Corder et al., 1993; Saunders et al., 1993; Strittmatter et al., 1993; Jun et al., 2010). More than seventy genetic risk factors have been identified in cases with AD dementia. These include HLDL receptor related protein 1 (LRP1), low density lipoprotein protein receptor 1 (LDLR), interleukin 1 α (IL1A), clusterin (CLU), phosphatidylinositol binding clathrin assembly protein (PIC-ALM), complement component (3b/4b) receptor 1 (CRI), bridging integrator 1 (BIN1), triggering receptor expressed on myeloid cells 2 (TREM2), sortilin-related receptor 1 (SORL1), ADAM metalloproteinase domain 10 (ADAM10), ATP binding cassette subfamily A member 7 (ABCA7), Spi-1 proto-oncogene (SPI1), paired immunoglobulin like type 2 receptor alpha (PILRA), membrane-spanning 4-domains subfamily A (MSA4), CD2-associated protein (CD2AP), and ephrin receptor A1 (EPHA1) (Harold et al., 2009; Lambert et al., 2009; Seshadri et al., 2010; Jun et al., 2010; Jones et al., 2010; Hollingworth, Lambert et al., 2011, 2013; Naj et al., 2014; Sims et al., 2017; Pimenova et al., 2018; Jansen et al., 2019; Kunkle et al., 2019; Andrews et al., 2020; Jansen et al., 2019; Tansey et al., 2018; Bellenguez et al., 2022).

However, individuals with NFT stages I-IV with absent β -amyloid burden, suffering from the so called primary age-related tauopathy (PART), show a lower prevalence of ApoE ϵ 4, rs28834970 *PTK2B*, rs6733839 in the *BIN1*, and *CRI* genes, and a higher prevalence of ApoE ϵ 2 (Bell et al., 2019; McMillan, 2018; Robinson et al., 2020a, 2020b).

Clinical and post-mortem neuropathological changes during human brain aging and sAD progression are similar although with augmented intensity and amplified distribution of ADNC in parallel with the cognitive and mental impairment (Hubbard et al., 1990; Crystal et al., 1988; Braak and Braak, 1991; Braak and Braak, 1997; Hulette et al., 1998; Price and Morris, 1999; Knopman et al., 2003; Bennett et al., 2006; Braak and Del Tredici, 2011; Braak et al., 2011; Ferrer, 2012;

Tsartsalis et al., 2018; Arnsten et al., 2021). For this reason, a continuum of brain aging with ADNC, and sAD has been proposed (Ferrer, 2022, 2023). The present comments should not be taken to imply that sAD pathology is synonymous with brain aging, as brain aging is manifested by additional neuropathological changes (and molecular modifications) not linked to ADNC. Moreover, progeric syndromes are not manifested with ADNC (Nelson et al., 2011a, 2011b).

Altered proteostasis in brain aging AD is not restricted to tau and β -amyloid. Whole proteomics studies have shown progressive deregulation of protein expression in the elderly, with marked individual variations and regional differences within the same age range; moreover, altered expression levels affect multiple structures and metabolic pathways (Musunuri et al., 2014; Hondius et al., 2016; Yu et al., 2018; McKetney et al., 2019; Wingo et al., 2019; Mendonça et al., 2019; Ping et al., 2020; Wingo et al., 2021; Velásquez et al., 2021; Gao et al., 2022).

Phosphoproteomics analyses in cases with MCI and AD dementia have identified deregulated protein phosphorylation of multiple proteins involved in a variety of molecular pathways (Tan et al., 2015; Triplett et al., 2016; Dammer et al., 2015; Sathe et al., 2020; Ping et al., 2020; Bai et al., 2020; Ferrer et al., 2021). Importantly, deregulated phosphorylation occurs in cases at early stages of ADNC (Braak stages I-II) in the frontal cortex in which NFTs and SPs are absent (Ferrer et al., 2021). Phosphoproteins deregulated in sAD are structural components of cell membranes and membrane signaling, cytoskeleton, synapses (including neurotransmitter receptors), serine-threonine kinases, proteins involved in energy metabolism, and RNA processing and splicing. Although deregulated protein phosphorylation is more pronounced at stages III and IV, and it is maintained at advanced stages of sAD, deregulated phosphorylation precedes tau and β -amyloid deposition in human brain aging (Ferrer et al., 2021).

β -amyloid plaques and β -amyloid angiopathy may be found in old dogs, bears, pinniped species, dolphins and other cetaceans, monkeys, and higher non-human primates. β -amyloid plaques are usually diffuse whereas SPs are exceptional (Price et al., 1991; Giannakopoulos et al., 1997; Borrás et al., 1999; Head, 2011; Morelli et al., 1996; Yu et al., 2011; Languille et al., 2012; Pérez et al., 2013; Uchiyama et al., 2016; Edler et al., 2017; Takaichi et al., 2021; Schultz et al., 2021a, 2021b).

Phosphorylated-tau deposits in neurons are rarely encountered in most aged mammals; tau deposits have the characteristics of pre-tangles rather than NFTs, as in aged dogs (Borrás et al., 1999) and mouse lemurs (Giannakopoulos et al., 1997). Intracytoplasmic tau inclusions in neurons, astrocytes, and oligodendrocytes are found in aged baboons (Schultz et al., 2000a, 2000b), but only rarely in aged gorillas (Pérez et al., 2013) and chimpanzees (Edler et al., 2017). In baboons, a combination of neuronal and glial tau pathology preferentially affects limbic brain areas, including the hippocampal formation; no apparent relationship was noted between the density and distribution of tau pathology and β -amyloid deposits (Schultz et al., 2021a and b). Tau accumulation in the brain of old sea lions, seals, and walrus forms argyrophilic fibrillar 3Rtau and 4Rtau aggregates in the neuronal somata and neurites; few tau aggregates are found in oligodendrocytes and microglia; their abundance and distribution largely differs from that seen in AD (Takaichi et al., 2021). A unique 4Rtauopathy without β -amyloid deposits mainly involving neurons of the neocortex but not the hippocampus, accompanied by widespread coiled bodies in the cerebral white matter, has been reported in aged domestic cats (Poncelet et al., 2019). *Octodon degus* is proposed as a valuable natural model of sAD (Hurley et al., 2018). However, ADNC largely differs in *O. degus* when compared with sAD; moreover, ADNC has not been identified in *O. degus* bred in captivity (Steffen et al., 2016).

Rather than discussing whether AD is restricted to humans, the available information points to a link between brain aging and abnormal tau and APP metabolism in many species, including dogs, bears, pinnipeds, primates, and cetaceans. Yet, in none of them (excepting baboons) do SPs, and more precisely NFTs, show the prevalence, localization, and widespread distribution they manifest in human beings culminating in a

clinical and neuropathological state consistent with AD dementia.

Several transgenic animal models are used to mimic AD, most of them transgenic mice bearing simple, double, or triple mutations of genes involved in the β -amyloid pathway. All of them replicate some aspects of β -amyloidopathy including the development of β -amyloid plaques and β -amyloid angiopathy. Yet the addition of mutations in the tau gene is needed to generate both SPs and NFTs. Although mice bearing multiple mutations covering the β -amyloid pathway and tau resemble fAD, the translation of most beneficial therapeutic strategies in these models fail to prove effective in humans (Drummond and Wisniewski, 2017; Gotz et al., 2018; McKean et al., 2021; Takeuchi et al., 2011; Vitek et al., 2021). The TgF344-AD rat expresses human APP with the Swedish mutation and human presenilin 1 with the Δ E9 mutation on the Fischer 344 background. These rats show A β plaques, NFTs, cognitive deficits, neuronal loss, reactive astrocytosis, chronic neuroinflammation, and reduced expression of triggering receptor expressed on myeloid cells-2 (TREM2) (Cohen et al., 2013; Bac et al., 2022). Further studies are needed to learn whether transgenic rats are suitable models to be used to test new therapies for AD.

3. Associated proteinopathies

Since sAD is a prevalent human age-related disorder, it is not uncommon for sAD to be associated with other age-related proteinopathies which have and additive effect on cognitive and neuropsychiatric impairment in old age (Higashi et al., 2007; Brayne et al., 2009; Kovacs et al., 2013; Kovacs et al., 2015; Elobeid et al., 2016; Spires-Jones et al., 2017; Robinson et al., 2018a, 2018b; Wennberg et al., 2019; Robinson et al., 2021; Montine et al., 2022). Co-morbidities are also common in the younger-old (Beach and Malek-Ahmadi, 2021).

3.1. Argyrophilic grain disease (AGD)

AGD is an age-related tauopathy characterized by argyrophilic granules or comma-shaped dendritic protrusions that contain phosphorylated 4Rtau, which are accompanied by pre-tangles, in the entorhinal cortex, hippocampus, amygdala, and neighbouring temporal cortex (Braak and Braak, 1987, 1989; Tolnay et al., 1997a; Tolnay and Clavaguera, 2004; Jellinger, 1998; Tolnay and Probst, 2008; Grinberg and Heinsen, 2009; Ferrer et al., 2008).

The frequency of AGD increases with age; it is present in about 20% and 40% of individuals at the age of 90 and 100, respectively (Braak and Braak, 1998; Ding et al., 2006; Rodriguez and Grinberg, 2015; Rodriguez et al., 2016). AGD occurs in about 25% of AD cases (Yokota et al., 2018). Other studies go further: tau-positive grains are always present in centenarians' hippocampus (Pham et al., 2011).

Argyrophilic grains are dendritic protrusions usually containing tau, and lacking spines, as revealed with combined tau immunohistochemistry and the Golgi method (Tolnay et al., 1998; Ferrer et al., 2008). In addition, tau-positive coiled bodies in oligodendrocytes and thorn-shaped astrocytes are found in the temporal white matter (Botez et al., 1999; Ikeda et al., 2018) (Fig. 2).

Ballooned neurons containing neurofilaments and α B-crystallin in the amygdala are constant features in AGD (Tolnay and Probst, 1998), but they may also occur in AD (Fujino et al., 2004).

Tau pathology in AGD has a particular phospho-tau pattern characterized by two bands of 68 kDa and 64 kDa that can be modified by the presence of additional bands in cases with concomitant AD pathology, with a ratio 3 R/4 R = 1/2 (Togo et al., 2002a, 2002b; Tolnay et al., 2002; Zhukareva et al., 2002; Ferrer et al., 2008). Tau deposits in AGD may be recognized by different antibodies directed to phospho-tau sites, including Ser262, conformational modifications, and truncated tau (Ferrer et al., 2002; Ferrer et al., 2014). Tau filament AGD-fold differs from tau filament AD-fold but resembles the four-layered fold of corticobasal degeneration (CBD) identified by cryo-electron microscopy (Shi et al., 2021a, 2021b; Kametani and Hasegawa, 2022).

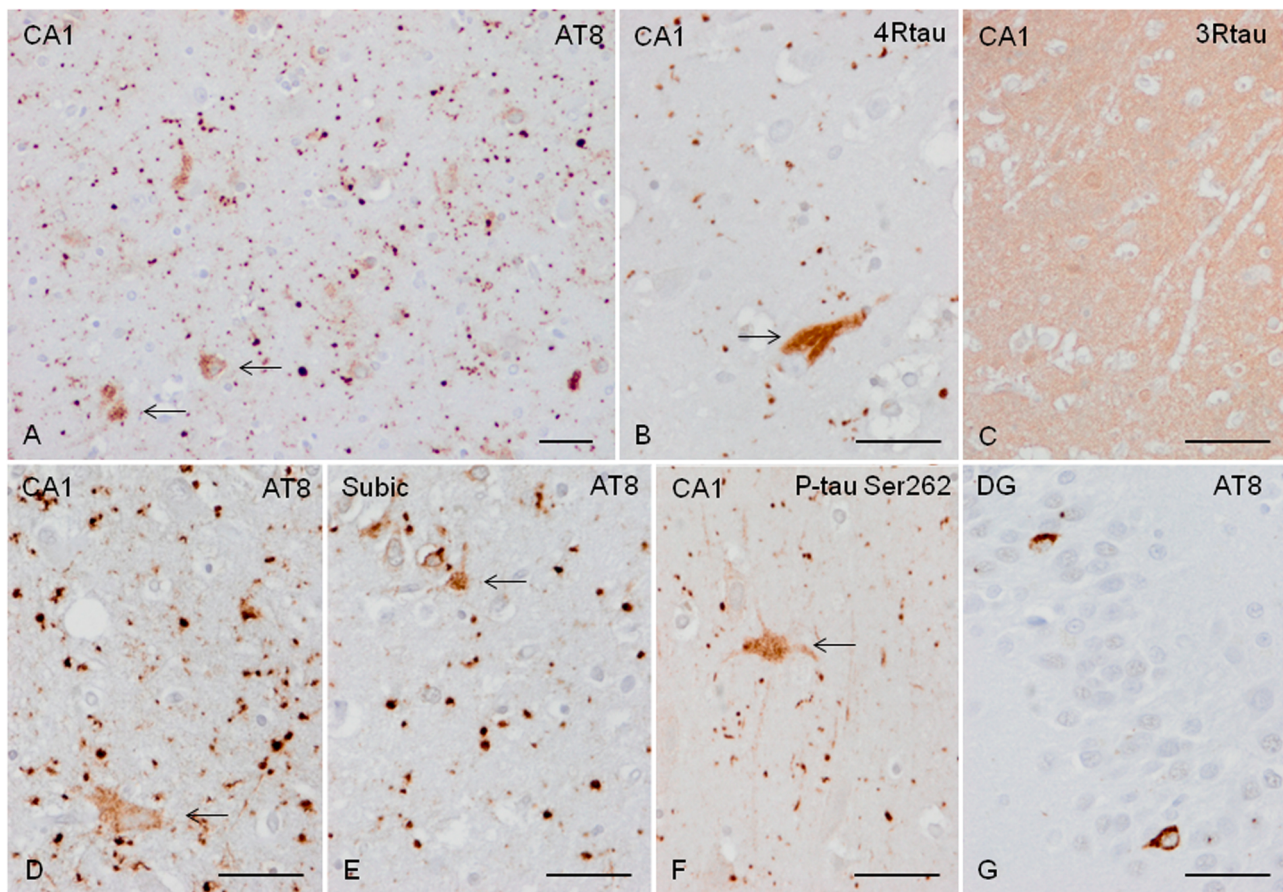


Fig. 2. Argyrophilic grain disease (AGD). A: Argyrophilic grains and neurons with pre-tangles (thin arrows) in the CA1 region of the hippocampus, as seen with AT8 immunohistochemistry; B: 4Rtau immunohistochemistry showing positivity of grains and pre-tangles (thin arrow); C: grains and pretangles are not stained with anti-3Rtau antibodies; D and E: phospho-tau-immunoreactive grains and pre-tangles in CA1 and subiculum (subic) seen with the AT8 antibody; F: grains and pre-tangles (thin arrow) stained with anti-phospho-tau Ser262 antibody; G: phospho-tau containing neurons and absence of grains in the dentate gyrus (DG). Paraffin sections slightly counterstained with haematoxylin, A, bar = 50 μ m; B-G, bar = 50 μ m.

Phospho-tau and active tau kinases co-localize in grains, pre-tangles, and ballooned neurons (Leroy et al., 2007; Ferrer et al., 2003; Ferrer, 2004; Ferrer et al., 2005), thus linking kinase activation and tau hyper-phosphorylation. The presence of acetylated tau in AGD is controversial (Grinberg et al., 2013; Irwin et al., 2013). Grains also contain markers of the sequestosome/p62, ubiquitin, and mutant ubiquitin (Fischer et al., 2003; Scott and Lowe, 2007; Ferrer et al., 2008). Mitochondrial dysfunction, oxidative and endoplasmic reticulum stress, and reduced neuronal haemoglobin also occur in AGD (Ilieva et al., 2011; Ferrer et al., 2011).

AGD is associated with apolipoprotein E epsilon 2 allele (*ApoEε2*), but not with *ApoEε4* allele (Ghebremedhin et al., 1998; Togo et al., 2002a, 2002b). Curiously, *ApoEε2* allele is protective against sAD. AGD is also associated with polymorphisms in α 2-macroglobulin and low-density lipoprotein receptor-related protein genes (Ghebremedhin et al., 2002). Although AGD is currently viewed as sporadic, AGD-like neuropathology has been reported in cases carrying *MAPT* S305S and *MAPT* S305I mutations (Kovacs et al., 2008; Rönnbäck et al., 2014).

AGD may follow successive stages of local and regional progression: stage I: anterior entorhinal cortex, mild involvement of the cortical and basolateral nuclei of the amygdala, and mild involvement of the hypothalamic lateral tuberal nucleus; stage II: entorhinal cortex, anterior CA1, transentorhinal cortex, cortical and basolateral nuclei of the amygdala, presubiculum, hypothalamic lateral tuberal nucleus, and dentate gyrus; stage III: entorhinal cortex, CA1, perirhinal cortex, presubiculum, amygdala, dentate gyrus, hypothalamic lateral tuberal nucleus, mild involvement of CA2 and CA3, mild involvement of the

subiculum, mild involvement of other nuclei of the hypothalamus (e.g. mammillary bodies), mild involvement of the anterior temporal cortex, insular cortex, anterior cingulate gyrus, orbitofrontal cortex, nucleus accumbens, and septal nuclei, and rare grains in the midbrain; and stage IV: moderate to severe additional involvement of the neocortex and brainstem (Saito et al., 2004; Ferrer et al., 2008). The gyrus ambiens is severely affected in cases with dementia (Saito et al., 2002). The involvement is asymmetric (Adachi et al., 2010; Sakurai et al., 2019).

AGD may occur as an isolated condition (Braak et al., 1987; 1989; Rodriguez et al., 2016; Wurm et al., 2020), but it is often accompanied by NFT pathology and advanced AD, and may occur in combination with other tauopathies like progressive supranuclear palsy (PSP), CBD, and Pick's disease (PiD), as well as α -synucleinopathies (Martinez-Lage and Munoz, 1997; Sabbagh et al., 2009; Nelson et al., 2010; Rodriguez et al., 2016; Yokota et al., 2018). AGD can occur as an incidental post-mortem neuropathological lesion, but it is frequently associated with cognitive impairment and dementia. When present in combination with early stages of NFT pathology of AD type, cognitive impairment and dementia are more prevalent than in cases with the same stage of NFT pathology alone (Tolnay et al., 1997b; Thal et al., 2005).

It has been suggested that there is no support for independent association between cognitive impairment linked to aging and AGs (Sabbagh et al., 2009; Nelson et al., 2010). However, dementia has been reported in AGD without co-morbidities, and the degree of cognitive impairment depends on the extension of lesions in the limbic system and neocortex (Braak and Braak, 1987; Braak and Braak, 1989; Tolnay et al., 1997; Ikeda et al., 2000; Probst and Tolnay, 2002; Tolnay and

Clavaguera, 2004).

AGD has not been reported in natural conditions in species other than humans. Deafferentation of the hippocampus in rats generates phospho-tau positive grain deposits in the molecular layers of the dentate gyrus on the lesioned side, as revealed with the AT8 antibody (Mudher et al., 2001). However, the origin of the granules (dendritic or axon terminals) and the characteristics of tau deposits (argyrophilia, only 4Rtau immunoreactivity) were not described in the original paper. Therefore, deafferentation of the hippocampus is likely not the cause of AGD.

3.2. Aging-related tau astrogliopathy (ARTAG)

Thorn-shaped astrocytes (TSAs) are a subpopulation of fibrillary astrocytes containing hyper-phosphorylated tau that appear in the human aged brain in subependymal, subpial, perivascular, white matter, and grey matter locations; 4Rtau are the only tau isoforms deposited in TSAs (Ikeda et al., 1995; Schultz et al., 2004; López Gonzalez et al., 2013; Okamoto et al., 2019). In the age-range of 75–98 years, TSAs are found in approximately 50% of all individuals (Schultz et al., 2004). TSAs are prevalent in the brain of the oldest-old or supercentenarians (Takao et al., 2016; Rogalski et al., 2019).

TSAs are frequent in the brain of individuals affected by tauopathies including sAD, AGD, FTLD-tau, PSP, and chronic traumatic tauopathy

(Schultz et al., 2004; Kovacs et al., 2017; Nolan et al., 2019; McCann et al., 2021; Kovacs et al., 2020; Arena et al., 2020a, 2020b; Ameen-Ali et al., 2022). In sAD, TSAs are not related to Braak neurofibrillary tangle or hippocampal tangle pathology stages (Schultz et al., 2004; Lace et al., 2012). TSAs are associated with argyrophilic grains (Lace et al., 2012), coiled bodies in oligodendrocytes (Lace et al., 2012; Forrest et al., 2022), and limbic-predominant age-related TDP-43 encephalopathy (Forrest et al., 2022). TSAs are also frequent in DLB (Liu et al., 2016). An extreme case of combined prominent ARTAG, AD, cerebral β -amyloid angiopathy, LBD, and TDP-43 proteinopathy has been reported (Klotz et al., 2021).

TSAs show deposition of phosphorylated tau at different sites, recognized with phospho-specific anti-tau antibodies Thr181, Ser202, Ser214, Thr231, Ser396, Ser422, and clones AT8 and PHF-1, and conformational changes revealed with Alz50 and MC-1 antibodies. However, TSAs are only seldom stained, or not stained at all, with phospho-specific tauSer262, and with Tau-C3 antibody directed against tau truncation at aspartic acid 421 (López-González et al., 2013; Ferrer et al., 2018). TSAs are also decorated with antibodies against tau N-terminal, C-terminal, and tau 100 (Ferrer et al., 2018). TSAs are also immunostained with antibodies to active tau kinases MAPK/ERK-P, SAPK/JNK-P, p38-P, and GSK-3 β , thus suggesting a functional role of active tau kinases in the hyper-phosphorylation of tau in TSAs (López-González et al., 2013). Finally, western blotting of

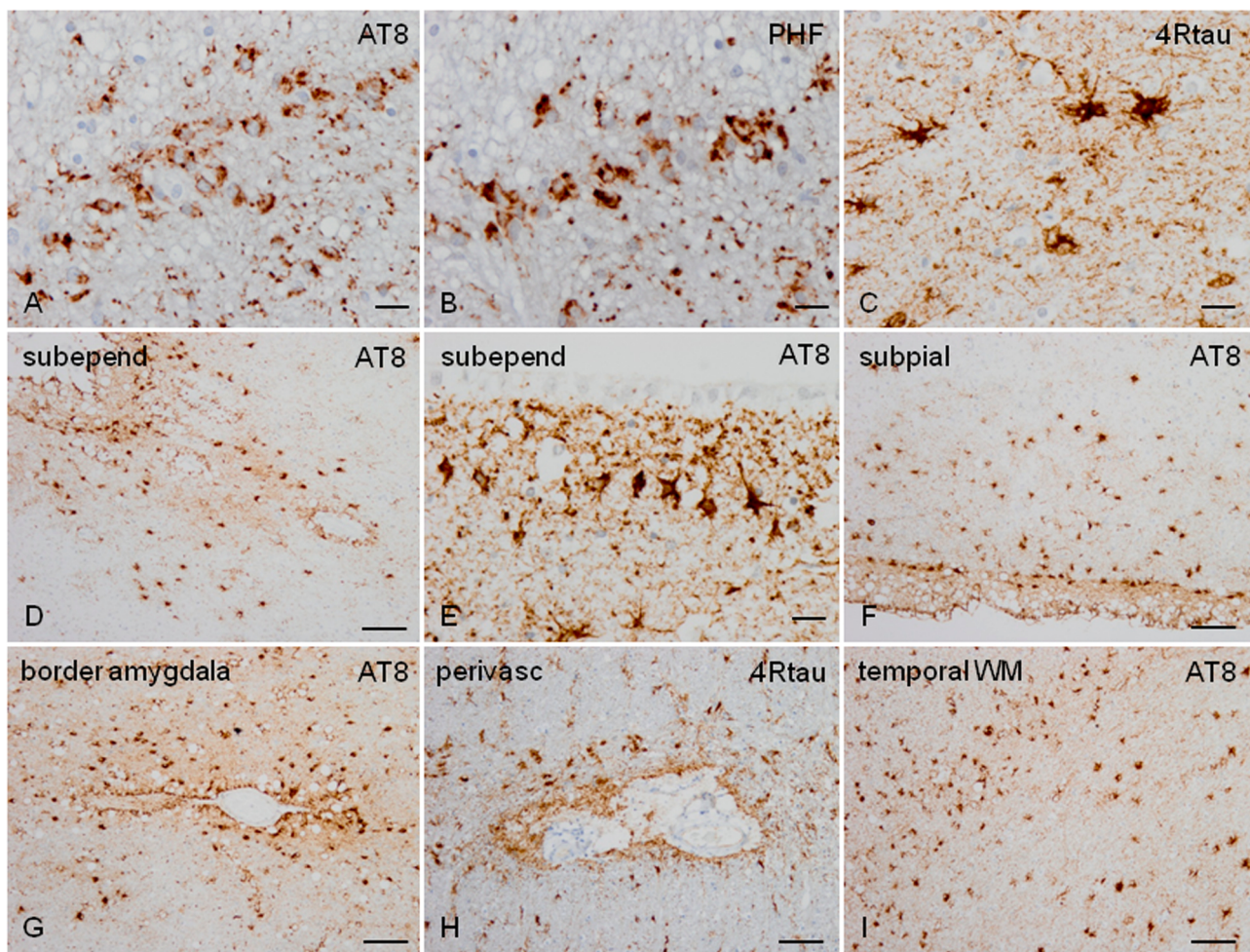


Fig. 3. Aging-related tau astrogliopathy (ARTAG); characteristics and localization of thorn-shaped astrocytes (TSAs). A-C: TSAs in the deep temporal white matter visualized with antibodies AT8 (A), PHF (B), and 4Rtau (C) showing characteristic fibrillar and short branched morphology; E: TSAs are also visualized in the subependymal region of the temporal ventricles; D, F-I: lower magnification showing TSAs in the subependyma of the temporal ventricle (D), subpial localization in the deep temporal cortex (F), border of the amygdala (G), perivascular in the white matter (H), and temporal white matter (I). Paraffin sections, slightly counterstained with haematoxylin, A-C and E, bar = 30 μ m; D, F, G-I, bar = 45 μ m.

sarkosyl-insoluble fractions from the temporal lobe in cases with only TSAs reveals two phospho-tau bands of 68 kDa and 64 kDa, identified with the phospho-specific tau Ser422 antibody, and several lower bands of variable molecular weight consistent with C-terminal truncated tau (Ferrer et al., 2018).

TSAs are negative for ubiquitin, mutant ubiquitin, and p62 (López-González et al., 2013).

The term aging-related tau astrogliopathy (ARTAG) was coined to describe a 4 R tauopathy composed of TSAs, and solitary or clustered granular/fuzzy astrocytes (GFAs) in the gray matter (Kovacs et al., 2016). TSAs in ARTAG are localized in subpial, subependymal, perivascular, white matter, and gray matter domains, and mainly in the temporal lobe, lobar, subcortical, and brainstem (Kovacs et al., 2016). ARTAG patterns are categorized into different stages regarding the distribution of TSAs (Kovacs et al., 2018a, 2018b) (Fig. 3). The stages differ depending on the localization of TSAs (subpial, white matter, and grey matter), and associated pathologies (for example PSP, CBD, and PiD) (Kovacs et al., 2018a, 2018b). However, TSAs in aging brain, not associated with PSP, CBD, or PiD, usually appear first in basal brain regions including subependyma of the temporal horn, temporal white matter, subpial of the entorhinal cortex, and amygdala. GFAs also occur in other tauopathies in the elderly (Ferrer et al., 2014). Whether ARTAG, or the presence of TSAs in the white matter, has any clinical manifestation is controversial (Munoz et al., 2007; Mesulam et al., 2008; Wharton et al., 2016; Resende et al., 2020). Cortical ARTAG is associated with dementia, but limbic and brainstem ARTAG is not (Robinson et al., 2018a, 2018b).

The proximity of TSAs to the subachnoidal, subventricular, and perivascular spaces prompted the suggestion that astrocytes in these areas might have a potential effect on brain-fluid interfaces; connexin-43 immunoreactivity is increased in ARTAG independently of tau pathology, and aquaporin 4 only in the white matter and grey matter, but associated with increased AT8 immunoreactivity in white matter and perivascular areas (Kovacs et al., 2018a, 2018b). However, aquaporin 4 is expressed in AT8-immunoreactive and AT8-negative astrocytes in the subependymal and perivascular regions in another study (Ferrer et al., 2018). Moreover, SOD1 and GLT1 are equally expressed in TSAs and neighboring astrocytes in ARTAG (Ferrer et al., 2018). Interestingly, TSAs express YKL40, thus pointing to an inflammatory profile for these astrocytes (Ferrer et al., 2018).

Phosphoproteomics of dissected brain regions enriched in TSAs as the only neuropathological change identifies increased phosphorylation marks in a large number of proteins in ARTAG compared with controls, including glial fibrillary acidic protein (GFAP), aquaporin 4, several serine-threonine kinases, microtubule associated proteins, and other neuronal proteins. These data reveal a hyper-phosphorylation background that affects several molecules, including many kinases and proteins that are components of various cell compartments and cell types (Ferrer et al., 2018). Therefore, deregulated protein phosphorylation is not restricted to tau hyper-phosphorylation in TSAs, but rather is a widespread altered molecular setting in ARTAG (Ferrer et al., 2018).

Several tau transgenic mice have been used as models of human tauopathies, including transgenic mice expressing either murine 3Rtau and 4Rtau, or the longest human brain 4Rtau isoform (Alz17 mice), or 1N4Rtau containing the P301S mutation, or high levels of human 3Rtau and lower 4Rtau in a KO murine tau background (hTau mice), or human 3Rtau and 4Rtau at a ratio 1:1 in a KO murine tau background (6hTau mice) (Allen et al., 2002; Andorfer et al., 2003; Yoshitama et al., 2007; Frank et al., 2008; Takeuchi et al., 2011; Götz and Götz, 2019; Hosokawa et al., 2022). All these mice present neuronal tauopathy and variable tau deposition in glial cells resembling FTLD-tau, but none of them exhibit neuropathological patterns similar to those seen in human sporadic tauopathies including ARTAG and AGD. Transgenic rats bearing the P301S mutation also mimic human tauopathy but not AGD or ARTAG (Janice et al., 2019).

3.3. α -synuclein pathology (limbic predominant Lewy body disease)

Lewy bodies and neurites are composed of normal, misfolded, and truncated proteins, principally α -synuclein, which is abnormally phosphorylated at Ser129, nitrated and oxidized, has altered crystallographic structure and abnormal solubility, and is prone to the formation of aggregates and insoluble fibrils with predominant β -pleated sheet conformation; in addition, Lewy bodies associate proteins of the ubiquitin-proteasome system and autophagy that become deficient to degrade the abnormal products (Spillantini et al., 1997; Wakabayashi et al., 1997; Arima et al., 1998; Baba et al., 1998; Hashimoto and Masliah, 1999; Duda et al., 2000; Goedert, 2001b; Giasson et al., 2002; Fujiwara et al., 2002; Iwatsubo, 2003; Saito et al., 2003; Anderson et al., 2006; Schults, 2006; Leverenz et al., 2007; Uversky, 2007; Wakabayashi et al., 2007; Bandyopadhyay and Cuervo, 2007; Engelender, 2008; Xia et al., 2008; Uchiyama and Giasson, 2016).

Several kinases may phosphorylate α -synuclein, including casein kinase II, leucine-rich repeat kinase 2, G-protein-coupled receptor kinase, and polo-like kinase (Kawahata et al., 2022).

Under electron microscopy, classical Lewy bodies have a central core of granular material and a peripheral halo composed of radiate fibrils. Dense Lewy bodies are composed of lipid membranes, vesicles, dysmorphic organelles, filaments interspersed between the membranes, and organelles. Clear or hyaline inclusions are mainly composed of granular material and vesicles (Roy and Wolman, 1969; Forno and Norville, 1976; Forno, 1986; Gibb et al., 1991; Galloway et al., 1992; Fukuda et al., 1993; Spillantini et al., 1998; Arima et al., 1998; Galvin et al., 1999; Schults, 2006). The use of combined methods shows a more complex structure and composition of Lewy bodies; Lewy bodies consists of vesicular structures, dysmorphic organelles, rare filaments, granules and lipid membranes (Shahmoradian et al., 2019). Cryo-electron microscopy has disclosed that α -synuclein filaments in Lewy bodies are made from two protofilaments formed by a polar fibril of staggered β -strands (Li et al., 2018; Guerrero-Ferreira et al., 2020; Yang et al., 2022a, 2022b; Kametani and Hasegawa, 2022).

Lewy bodies and neurites define Lewy body diseases (LBD), mainly represented by Parkinson's disease (PD) and DLB (Forno, 1996; Kosaka and Iseki, 1996; Goedert et al., 2001a; McKeith et al., 2004; Fujishiro et al., 2008a, 2008b; Dickson et al., 2009; Kosaka and Iseki, 2011; Ince, 2011).

LB pathology in PD progresses from the myenteric plexus and medulla oblongata (and olfactory bulb) to the midbrain, diencephalic nuclei, and neocortex (Braak et al., 2002; Braak et al., 2003; Braak et al., 2004). Stage 1 is manifested by Lewy bodies and neurites in the dorsal IX/X motor nuclei and/or intermediate reticular zone, and myenteric plexus. Stage 2 affects, in addition, the medulla oblongata and pontine tegmentum; the olfactory bulb is also involved. Stage 3 adds midbrain lesions, particularly in the substantia nigra pars compacta. Stage 4 includes basal prosencephalon and mesocortex (cortical involvement confined to the transentorhinal region and allocortex, and CA2 plexus). Stage 5 extends to sensory association areas of the neocortex and prefrontal neocortex. Stage 6 includes Lewy bodies and neurites in first-order sensory association areas of the neocortex and pre-motor areas, as well. Braak staging is well-accepted regarding typical PD progression (Dickson et al., 2010). A simplified version has been proposed for DLB, and categorized as LBD brainstem predominant, limbic, and neocortical (McKeith et al., 2017). More recently, an improved classification with higher reproducibility has been proposed based on the McKeith system, but applying a dichotomous approach for the scoring of Lewy pathology and including amygdala-predominant and olfactory-only stages (Attems et al., 2021).

Lewy pathology is frequent (about 30%–50%) in cases with mild cognitive impairment and AD dementia, and in brain aging with ADNC (Jellinger, 2004; Spina et al., 2021; Robinson et al., 2021). Conversely, the majority of patients with DLB have AD pathology, usually at NFT stages III–V, and abundant diffuse and SPs (Marui et al., 2002; Iseki et al.,

2003). Interestingly, there is an association of ApoE ϵ 4 and Lewy bodies in sAD (Tsuang et al., 2005).

An atypical but common form of LBD in the human aged brain is amygdala-predominant LBD, accompanied by Lewy bodies in the olfactory bulb, in about 30% of cases with sAD and Down syndrome (Uchikado et al., 2006) (Fig. 4A-C).

Severe Braak NFT stage, high CERAD (Consortium to Establish a Registry for Alzheimer's Disease) score, and ApoE ϵ 4 are significantly associated with amygdala-predominant LBD, but not with the caudo-rostral progression pattern of PD. This observation suggests two distinct LBD patterns of α -synuclein pathology origin and progression in the elderly, one of them characteristic of PD and DLB, the other of amygdala-predominant LBD (Raunio et al., 2019). This observation leads to the LOC model (body-first versus brain-first model of Lewy body

disorders) that proposes the enteric nervous system origin of Lewy body pathology with secondary spreading to the brain in most cases of LBD, and the central origin of Lewy body pathology in some patients with amygdala-predominant LBD with secondary spreading to the lower brainstem and peripheral autonomic nervous system (Borghammer, 2021; Borghammer et al., 2021).

Co-localization of phospho-tau and α -synuclein is not uncommon in Lewy bodies and neurites in selected neurons (Arima et al., 1999; Iseki et al., 1999; Ishizawa et al., 2003; Fujishiro et al., 2008a, 2008b; Clarimón et al., 2009). Another study in DLB shows co-localization of NFTs and Lewy bodies in the same neurons, most frequently in the subiculum-pre-CA1; phospho-tau and α -synuclein co-exist in terminal axons of the perforant pathway, and tau accumulates not in paired helical filaments but in the periphery of α -synuclein-positive components

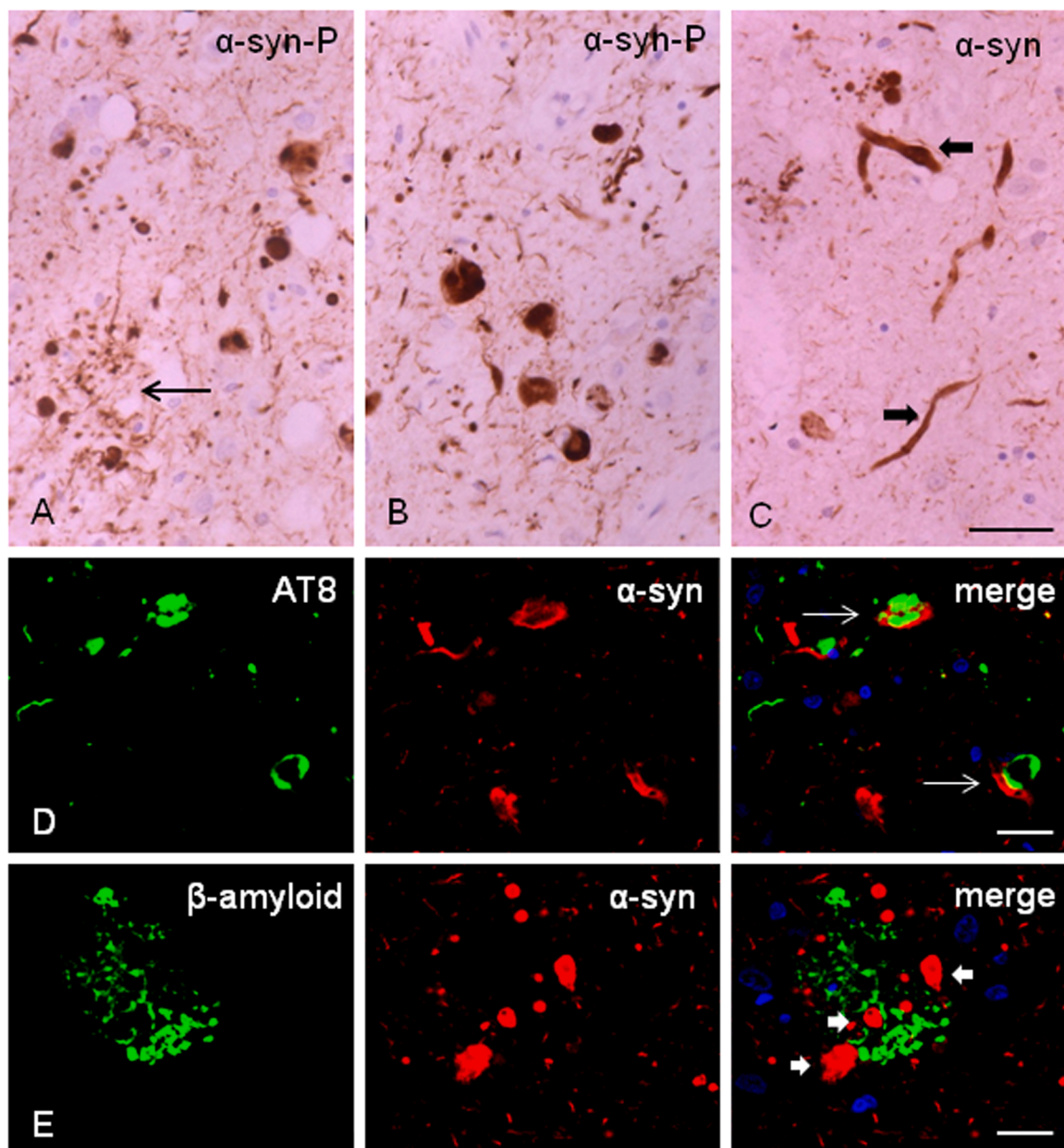


Fig. 4. Amygdala-predominant Lewy body disease. A-C: Lewy bodies, dystrophic neurites in senile plaques (thin arrow), and Lewy neurites (thick arrows) in the amygdala as seen with anti-P- α -synuclein Ser129, and non-phosphorylated α -synuclein antibodies; D: double-labelling immunofluorescence and confocal microscopy with AT8 (green) and anti- α -synuclein (red) antibodies showing co-localization of phospho-tau and α -synuclein in neurofibrillary tangles (thin arrows); E: double-labelling immunofluorescence and confocal microscopy with anti- β -amyloid (green) and anti- α -synuclein (red) antibodies showing α -synuclein-immunoreactive neurites surrounding β -amyloid deposits (thick arrows); nuclei are stained with (blue). Paraffin sections, A-C, bar = 25 μ m; D, E, bar = 20 μ m.

(Iseki et al., 2002) (Fig. 4D). Tau co-localizes with α -synuclein in the striatum (Wills et al., 2011) and post-synaptic spines in TgA53T mice (Teravskis et al., 2018; Singh et al., 2019). Molecular studies have also shown co-existence of phosphorylated tau and phosphorylated α -synuclein in synaptic-enriched fractions in AD, PD, and DLB (Muntané et al., 2008). *In vitro* studies have shown that tau and α -synuclein can interact and promote aggregation (Giasson, 2003) through the C-terminus of α -synuclein (Dasari et al., 2019). However, the functional consequences of tau/ α -synuclein interactions in pathology remain controversial (Pan et al., 2021). β -amyloid and α -synuclein may participate in SPs, but such proteins are expressed in different compartments (Fig. 4E).

Finally, LBDs are restricted to humans. Several animal models have been generated to re-create certain aspects of PD and DLB, including drug-induced α -synuclein aggregation in the substantia nigra of baboons, as well as multiple pharmacological treatments, and transgenic mouse models bearing PD- and DLB-related human mutations. Unfortunately, none of them reproduces Lewy pathology as seen in human diseases (Kowall et al., 2000; Duty et al., 2011; Koprich et al., 2017; Hamadjida et al., 2019; Lama et al., 2021). However, overexpression of human tyrosinase in rat substantia nigra results in age-dependent production of human-like neuromelanin within nigral dopaminergic neurons which above a specific threshold is associated to an age-dependent PD phenotype, including hypokinesia, Lewy body-like formation and nigrostriatal neurodegeneration (Carballo-Carbajal et al., 2019).

3.4. TDP-43 pathology and limbic-predominant age-related TDP-43 encephalopathy (LATE)

TAR DNA-binding protein 43 (TDP-43, TARDBP) usually resides in the nucleus but can shuttle to the cytoplasm; TDP-43 acts as a transcription factor, but also exerts multiple functions such as regulation of splicing, stabilization of RNA, microRNA processing, and protein-protein interaction. TDP-43 phosphorylation on serine 379 (S379), S403, S404, S409, S410, and abnormal cleavage and formation of C-terminal fragments results in abnormal TDP-43 aggregation in the nucleus, cytoplasm, and cell processes; abnormal TDP-43 deposits are

ubiquitinated as a result of dysfunctional constitutive and inducible UPS in TDP-43 proteinopathies (Neumann et al., 2006; Bendotti et al., 2012). Abnormal TDP-43 deposits in neurons and glial cells are characteristic of frontotemporal lobar degeneration with TDP-43 deposits (FTLD-TDP) and amyotrophic lateral sclerosis (ALS) (Gao et al., 2018; Prasad et al., 2019; Tziortzouda et al., 2021; Corbet et al., 2021; Liao et al., 2022; Keating et al., 2022).

TDP-43 inclusions are characterized by bundles of 10–20 nm diameter straight filaments with electron dense granular material within nuclear, cytoplasmic, and neuritic deposits, in most cases of FTLD-TDP, ALS, and AD (Lin and Dickson, 2008). Cryo-electron microscopy shows the structure of TDP-43 filaments from ALS and FTLD as a single protofilament that adopts a double-spiral-shaped fold, with no similarity to TDP-43 filaments formed *in vitro* (Arseni et al., 2022).

TDP-43-immunoreactive neuronal inclusions and threads are common in the hippocampus in brain aging over the age of 65, and in advanced sAD, often accompanied by hippocampal sclerosis (Geser et al., 2010; Davidson et al., 2011; Uchino et al., 2015; Josephs et al., 2015; Josephs et al., 2017; Smith et al., 2018; Nag et al., 2018; Huang et al., 2020; Gauthreaux et al., 2022). TDP-43 inclusions occur in up to 57% of sAD cases, most often in a limbic distribution, with or without hippocampal sclerosis; TDP-43 deposits can be found in neurons with NFTs (Meneses et al., 2021). Other studies estimate TDP-43 pathology to be present in up to 70% of symptomatic sAD cases (Koper et al., 2022) (Fig. 5).

TDP-43 pathology linked to sAD has been categorized into six stages: stage 1: amygdala; stage 2: entorhinal cortex and subiculum; stage 3: dentate gyrus of the hippocampus and occipitotemporal cortex; stage 4: insular cortex, ventral striatum, basal forebrain, and inferior temporal cortex; stage 5: substantia nigra, inferior olive, and midbrain tectum; and stage 6: basal ganglia and middle frontal cortex (Josephs et al., 2016). Subsequent contributions point to a simplified classification, and discriminate cases at stage 6 as FTLD-TDP (Nelson et al., 2019, see later). Similar categorization has been proposed in PART excepting for the involvement of the gyrus dentatus and the omission of advanced TDP-43 stages (Zhang et al., 2019).

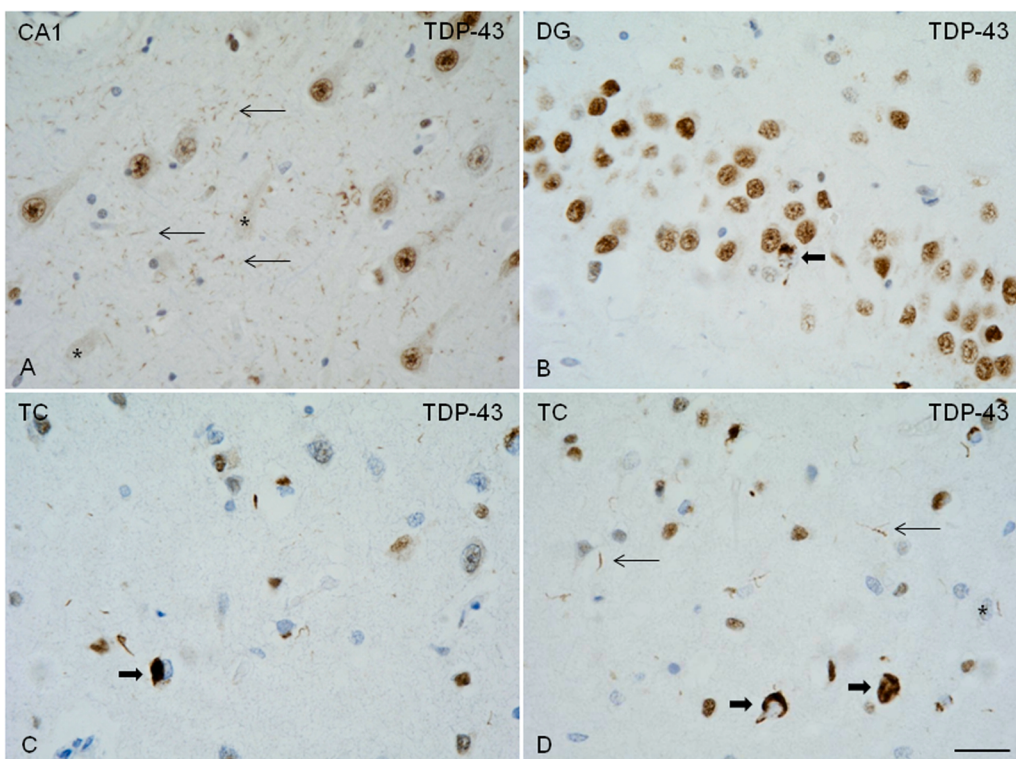


Fig. 5. Limbic-predominant age-related TDP-43 encephalopathy neuropathologic change (LATE-NC). TDP-43 immunoreactivity in normal nerve cells is mainly localized in the nucleus. A-D: Reduced TDP-43 expression in the nucleus (asterisk) is accompanied by abnormal localization of TDP-43 in neuropil threads (A, D, thin arrows), and in dense cytoplasmic inclusions (B, C, D) (thick arrows) in TDP-43 proteinopathy involving the hippocampus (CA1) dentate gyrus (DG) and deep regions of the temporal cortex (TC). Paraffin sections, slightly counterstained with hematoxylin, A-D, bar = 25 μ m.

TDP-43 pathology in the amygdala and hippocampus also occurs in fAD and Down syndrome (Lippa et al., 2009; Davidson et al., 2011; Ichimata et al., 2022), thus linking ADNC to TDP-43 pathology in those brain regions. TDP-43 pathology co-exists with α -synuclein and tau pathology in AD and DLB (Higashi et al., 2007).

TDP-43 proteinopathy is common in AGD; phospho-TDP-43 and phospho-tau co-localize only in some but not all neuronal cytoplasmic inclusions, grain-like structures, and pre-tangles (Fujishiro et al., 2009). TDP-43 pathology in CBD and PSP is reminiscent of TDP-43 proteinopathy in ALS (Riku et al., 2022), but limbic-predominant TDP-43 encephalopathy has also been described in PSP, often in association with hippocampal sclerosis (Yokota et al., 2010). Limbic-predominant TDP-43 encephalopathy has been exceptionally reported in globular glial tauopathy (Rusina et al., 2019).

The relationship between TDP-43 and tau is puzzling (Jamerlan and An, 2020). TDP-43 and tau appear to behave independently of one another (Smith et al., 2018; Buciu et al., 2020a; McAleese et al., 2020). Yet, combined human (h) Tau and TDP-43 expression in *C. elegans* results in severe degeneration consistent with a synergistic, rather than simply additive, interaction between hTau and hTDP-43 neurodegeneration (Latimer et al., 2019). Moreover, cytoplasmic TDP-43 accumulates in the presence of soluble human recombinant tau oligomers in cellular and murine models (Montalbano et al., 2020). Widespread co-localization of phospho-tau and phospho-TDP-43 deposits occurs in a rare form of familial astroglial predominant tauopathy (Gelpí et al., 2021).

TDP-43 proteinopathy is common in old-age hippocampal sclerosis (Nelson et al., 2016; Wang et al., 2022; Gauthreaux et al., 2022), and in cases with more severe non- β -amyloid vessel wall pathologies (Gauthreaux et al., 2022). Interestingly, neuron loss leading to old-age hippocampal sclerosis associated with TDP-43 pathology predominates in the subicular end of CA1 is more common than the end-stage of old-age hippocampal sclerosis alone (Hokkanen et al., 2018).

The term cerebral age-related TDP-43 with (hippocampal) sclerosis (CARTS) was proposed to categorize robust TDP-43 pathology in the hippocampus of individuals older than 85 at death, and includes cases with hippocampal sclerosis in aging, and hippocampal sclerosis with sAD pathology (Nelson et al., 2016).

Later, the term limbic-predominant age-related TDP-43 encephalopathy (LATE) was coined to designate an entity characterized by the presence of TDP-43 pathology localized in the amygdala and hippocampus, and extending to the limbic system in aged individuals usually with sAD. LATE differs from FTLTDP. LATE is associated with hippocampal sclerosis in some cases (Nelson et al., 2019; Robinson et al., 2020a, 2020b; Nelson, 2021; Nelson et al., 2022), but may also occur in isolation (Besser et al., 2020). LATE's prevalence is very high in old-aged individuals as it occurs in about 35%–50% of individuals over the age of 80 (Nelson, Sajjadi et al., 2019, 2022). LATE neuropathological change (LATE-NC) staging is classified as stage 1: amygdala only, stage 2 plus hippocampus, and stage 3 plus frontal cortex.

Clinically, LATE may be manifested with episodic memory loss and amnesic dementia syndrome (Nag et al., 2017; Nelson et al., 2019). No differences are apparent between black and white decedents, at least in one North American community (Nag et al., 2020). When associated with sAD, LATE-NC worsens cognitive decline in sAD and psychiatric symptoms (Vatsavayi et al., 2014; Josephs et al., 2015; Sennik et al., 2017; Nelson et al., 2019; Latimer et al., 2019; Kapasi et al., 2020; Buciu et al., 2020b; Sajjadi et al., 2022; Gauthreaux et al., 2022). Yet TDP-43 pathology did not increase the risk of neuropsychiatric symptoms in another study (Liu et al., 2020).

Brain atrophy at early stages of sAD seems to be supported by concomitant LATE-NC (Josephs et al., 2019). This is further supported by recent MRI and PET studies showing patterns of limbic-predominant atrophy on MRI and hypometabolism on 18 F-fluorodeoxyglucose PET in LATE-NC plus sAD are greater than expected for levels of local sAD pathology alone (Duong and Wolk, 2022).

ApoE ϵ 4 is associated with increased risk for LATE-NC (Yang et al., 2018). Subsequent studies have identified five genes with risk alleles for LATE-NC: granulin precursor (*GRN*), transmembrane protein 106b (*TMEM106B*), ATP binding cassette subfamily C member 9 (*ABCC9*), potassium calcium-activated channel subfamily M regulatory beta subunit 2 (*KCNMB2*), and *ApoE* (Nelson et al., 2019). *TMEM106B*, *GRN*, and *ApoE* are associated with both LATE and hippocampal sclerosis, whereas *ABCC9* is associated with hippocampal sclerosis only. None of these genes except *ApoE* is associated with Alzheimer's-type pathology (Dugan et al., 2021; Meneses et al., 2021). Mutations in *GRN* are linked to FTLTDP (Cruts et al., 2006; Baker et al., 2006; Wauters et al., 2017), and *TMEM106B* is associated with amyloid formation in several neurodegenerative diseases (Feng et al., 2021; Schweighauser et al., 2022; Chang et al., 2022).

Abnormal TDP-43 in TDP-43 proteinopathies forms neurotoxic fibrils with variable structure depending on the origin of the fibrils, the core, C-terminal fragments, or the entire low complexity domain of TDP-43 (Chen et al., 2010; Cao et al., 2019; Li et al., 2021a, 2021b). Amyloid fibrils in FTLTDP are composed of *TMEM106B* and not TDP43; however, amyloid fibrils occur in combination with non-fibrillar aggregated TDP-43 (Chang et al., 2022; Jiang et al., 2022).

LATE-NC is also associated with tau pathology in glial cells. Thus, ARTAG and tau oligodendroglialopathy (mainly in the form of coiled bodies) are frequently associated with LATE (Forrest et al., 2022).

LATE-NC also occurs in combination with amygdala/limbic-predominant LBD, and more rarely with neocortical LBD (Besser et al., 2020; Agrawal et al., 2021a, 2021b; Uemura et al., 2022). Fine neurites composed of C-terminal truncated TDP-43 in CA2 mainly occur in association with LBD whereas neuronal cytoplasmic inclusions predominate in cases with combined sAD (Uemura et al., 2022). LATE-LBD also associates with the genetic risk variants of *TMEM106B* rs1990622 and *GRN* rs5848 (Uemura et al., 2022).

TDP-43 pathology co-exists with α -synuclein and tau pathology in AD and DLB (Higashi et al., 2007). The interaction between α -synuclein and TDP-43 is poorly understood. However, the prion-like C-terminal domain (PrLD) of TDP-43 interacts with α -synuclein to form toxic aggregates that co-localize in the cytosol of neuroblastoma cells and induce synaptic dysfunction in primary neurons (Dhakal et al., 2021a, 2021b; Dhakal et al., 2022). Moreover, electron microscopy of TDP-43 inclusions in AD and LBD shows co-localization of TDP-43-immunoreactive filaments and granular material with tau filaments in NFTs in AD, or α -synuclein filaments in Lewy bodies in LBD (Lin and Dickson, 2008).

Four LATE-NC subtypes have been identified. Pattern 1 is characterized by TDP-43-immunoreactive processes and pre-inclusion pathology in cortices of the amygdala region, and hippocampal sclerosis; pattern 2 shows neurofibrillary tangle-like TDP-43 neuronal cytoplasmic inclusions together with high AD pathology; pattern 3 is recognized by round neuronal cytoplasmic inclusions and thick neurites in amygdala, and frequent LBD; and pattern 4 is characterized by tortuous TDP-43-immunoreactive processes in subpial and white matter regions, rare AD-related pathology, and rare hippocampal sclerosis (Cykowski et al., 2022). The different morphology and distribution of TDP-43 pathology suggest molecular particularities of TDP-43 deposits among subtypes. In this line, TDP-43 aggregates in sAD vary in their composition, suggesting different molecular profiles of TDP-43 pathology (Tomé et al., 2020).

Other studies have suggested distinct clinicopathological clusters of patients with TDP-43 proteinopathy. Cluster 1 contained FTLTDP, clinically manifested by different frontotemporal dementia clinical phenotypes. Cluster 2 consisted of LATE-NC patients without severe neuritic amyloid plaques. Subjects in Clusters 3 and 4 had severe ADNC + LATE-NC. However, Cluster 4 was distinguished by earlier disease onset, rapid clinical course, more LBD, less neocortical TDP-43 proteinopathy, and a trend for increased C9orf72 risk SNP rs3849942 T allele (Katsumata et al., 2020). About 98% of subjects dying past age 85

years lacked clinical features of FTLD thus differentiating FTLD-TDP and LATE-NC (Katsumata et al., 2020).

Quadruple misfolded proteins (represented by NFTs, SPs, Lewy bodies and TDP-43 proteinopathy) in the same brain were detected in nearly 20% of individuals with mean age at death 86.9; triple proteinopathy in 38.1%. The prevalence of dementia was higher (89%) in cases with quadruple proteinopathy (Karanth et al., 2020; Karanth et al., 2021).

LATE-NC also commonly associates with microvascular disease including cerebral β -amyloid angiopathy (Besser et al., 2020; Agrawal et al., 2021a, 2021b; Robinson et al., 2021; Harrison et al., 2021; Wang et al., 2022).

In contrast to humans, LATE-NC has not been observed in aged macaques (Darricau et al., 2021). No evidence of hippocampal/limbic TDP-43 pathology has been identified to date in other animal species.

4. Hippocampal sclerosis

Neuron loss and reactive astrogliosis in the CA1 region of the hippocampus, subiculum, and amygdala that is out of proportion to ADNC in the same structures characterizes hippocampal sclerosis of aging (Dickson et al., 1994; Jellinger, 1994; Leverenz et al., 2011; Nelson et al., 2011a, 2011b; Montine et al., 2012). Hippocampal sclerosis in aging occurs in about 30% of nonagenarians (Dickson et al., 1994; Nelson et al., 2011a, 2011b; Zarow et al., 2012; Nelson et al., 2013). Hippocampal sclerosis is commonly asymmetrical and, occasionally, segmentary (Nelson et al., 2013; Ighodaro et al., 2015). It can be presented alone or, currently, in association with AD, LBD, other tauopathies, and ALS (Dickson et al., 1994; Zarow et al., 2012; Yokota et al., 2010). The extent of hippocampal atrophy is more severe in cases with associated hippocampal sclerosis than in cases with AD alone (Zarow et al., 2012).

TDP-43 pathology is found in nearly 90% of cases with hippocampal sclerosis when compared with about 10% in cases without hippocampal sclerosis (Nelson et al., 2013), and it is usually associated with ADNC (Amador-Ortiz et al., 2007; Yokota et al., Nag et al., 2015). Aberrant TDP-43 pathology in hippocampal sclerosis is usually characterized by TDP-43 immunoreactive neurites and neuronal cytoplasmic inclusions (Nelson et al., 2011a, 2011b; Nelson et al., 2013; Gauthreaux et al., 2022a, 2022b). Usually, TDP-43 pathology is not restricted to the sclerotic regions (Nelson et al., 2013). Moreover, neuron loss leading to hippocampal sclerosis in aging starts from the subicular end of CA1 when it is associated with TDP-43 pathology; this neurodegenerative process is likely to be significantly more common than "end-stage" hippocampal sclerosis alone (Hokkanen et al., 2018).

The clinical manifestations due to hippocampal sclerosis are difficult to dissect because of the co-morbid pathology; memory impairment and dementia occur in patients with hippocampal sclerosis, an expected secondary consequence of the hippocampal circuit damage (Leverenz and Lipton, 2008; Leverenz et al., 2002; Onyike et al., 2013).

GRN, *TMEM106B*, *KCNMB2*, and *ABCC9* variants are identified as risk genes of hippocampal sclerosis (Nelson et al., 2014; Nelson et al., 2015a, 2015b; Neltner et al., 2016; Katsumata et al., 2017). These are the same genetic risk factors as those identified for LATE. In contrast, there is no association between *ApoE4* and hippocampal sclerosis dementia (Troncoso et al., 1996).

The cause of hippocampal sclerosis in aging is not known. Although there is a close association between hippocampal sclerosis and arteriolosclerosis, it is not clear whether hypoxic/ischaemic insults are the cause of hippocampal sclerosis in the elderly (Neltner et al., 2014; Walker, 2015). The possibility that altered cell cycle re-entry may play a role in the pathogenesis of hippocampal sclerosis, as happens in AD (Arendt, 2003; Arendt, 2005; Arendt et al., 2007), should be considered.

5. Centenarians/the oldest-old

Centenarians are resistant and resilient to sAD or have very low progression to advanced Braak stages of tau and β -amyloid pathology (Arenaza-Urquijo and Vemuri, 2018; Andersen, 2020; Beker et al., 2021). ADNC in the oldest-old population also shows a particular neuropathological distribution, including high densities of NFTs, mainly in the hippocampus, without apparent significant clinical deficiencies (Giannakopoulos et al., 1993; Giannakopoulos et al., 1995; Braak et al., 2011; Rogalski et al., 2019; Xuereb et al., 2000). ADNC appears to peak around 95 years of age, while other common pathologies continue to increase with age (Farfel et al., 2019). Co-morbidities, including TDP-43 proteinopathy and mesial sclerosis, reduce resilience (Aiello Bowles et al., 2019; Buciu et al., 2020a and b). In contrast, resilient oldest-old individuals without dementia have less cerebrovascular disease, no hippocampal sclerosis, and less cortical ARTAG, TDP-43, and Lewy pathology (Latimer et al., 2022; Robinson et al., 2018a, 2018b).

Genetic factors participate in cognitive and neuropathological resilience (Tavana et al., 2018; Nguyen et al., 2018; Nygaard et al., 2019; Dumitrescu et al., 2020; Seto et al., 2021; Leng et al., 2021).

LYST (lysosomal trafficking regulator), *MDN1* (meiotic nuclear divisions 1), and *RBMXL1* (RNA binding motif protein X-linked (RBMX)-like 1) burden are associated with extreme aging (Nygaard et al., 2019). *ATP8B1* encodes a protein that modulates phospholipid composition within cellular membranes; a variant on chromosome 18 upstream of *ATP8B1* is associated with unimpaired cognition in the oldest-old; the top variant at this locus (rs2571244) is associated with methylation in prefrontal cortex tissue at multiple CpG sites, including one just upstream of *ATP8B1* (Dumitrescu et al., 2020). A *RAB10* locus is associated with AD resilience (Tavana et al., 2018).

RORB (RAR-related Orphan Receptor B) encodes a transcription factor that drives the development of layer IV neurons in the neocortex but is also expressed in other cell layers. *RORB* depletion is associated with vulnerability to NFT formation in excitatory neurons of the entorhinal cortex (Leng et al., 2021). Decreased expression of genes involved in homeostasis also occurs in reactive astrocytes (Leng et al., 2021).

Non-genetic factors are differentially predictive of resilience in women and men (McDermott et al., 2017). Indeed, many genes in chromosome X predict resilience; increased expression in 19 genes is associated with slower cognitive decline in women; however, increased expression of 3 genes is associated with neuropathological tau burden in men but not women (Davis et al., 2021).

Other factors are involved in neuronal resilience in old age. Some are linked to glycolytic function and individual molecular modulators such as epigenetic regulation (Tesi et al., 2020; Zhang et al., 2021a, 2021b). Additional elements are related to neuroinflammation: expression levels of chemokines decrease, and trophic factors increase in the oldest old (Barroeta-Espar et al., 2019; Tesi et al., 2020).

Finally, there is a heterogeneous group of factors that constitute the cognitive reserve, linked to educational and occupational acquisition, social networks, and leisure activities in later life, which have a protective effect (Stern, 2012; Lesuis et al., 2018; Montine et al., 2019; Weisenbach et al., 2019; Peng et al., 2022).

6. Seeding and spreading of abnormal protein aggregates

Several studies postulate that the progression of AD, tauopathies, LBD, and other diseases with abnormal protein aggregates occurs in a similar way to prions in prion diseases (Uchiyama and Giasson, 2016; Mudner et al., 2017; Volpicelli-Daley and Brundin, 2018; Fuster-Matanzo et al., 2018; Dujardin and Hyman, 2019; Tarutani and Hasegawa, 2019; Goedert et al., 2020; Peng et al., 2020; Chen and Mitchell, 2021).

Tau secretion mainly occurs trans-synaptically, but vesicular (microvesicles and exosomes) and non-vesicular transport by direct translocation across the plasma membrane may also take place; nanotubules are also implicated in tau transfer from one cell to another (Chai

et al., 2012; Dujardin et al., 2014a; Dujardin et al., 2014b; Wang et al., 2017; Katsinelos et al., 2018; Polanco et al., 2018; Merezko et al., 2018; Ruan and Ikezu, 2019; Zhang et al., 2021a, 2021b). Tau is then internalized via endocytosis, pinocytosis, and membrane fusion, with the contribution of heparan sulfate proteoglycans, bridging integrator 1 (Bin1), LDL receptor-related protein 1 (LRP1), and muscarinic receptors (Wu et al., 2013; Holmes et al., 2013; Rauch et al., 2018; Cooper et al., 2021; Vasili et al., 2019; Rauch et al., 2020; Zhao et al., 2021).

Mechanisms of release, transfer, and uptake of α -synuclein and its aggregates are similar, and include exocytosis by exosomes/secretory vesicles, tunnelling nanotubes composed of F-actin, endocytosis, and uptake by cell surface receptors with heparan sulfate proteoglycans facilitation (Lee et al., 2005; Lee et al., 2008; Emmanouilidou et al., 2010; Danzer et al., 2012; Uchiyama and Giasson, 2016; Vasili et al., 2019; Tofaris, 2022). Formation of pore-like structures may permit α -synuclein release but no similar mechanism is proved for tau (Vasili et al., 2019). Cell death also allows the transfer of tau and α -synuclein from one cell to another (Vasili et al., 2019).

In cell cultures, TDP-43 is extruded from the cytoplasm via exosomes, axon terminals, or independently of vesicles (Feiler et al., 2015; Iguchi et al., 2016; Sackmann et al., 2020). The mechanisms of TDP-43 uptake are probably linked to microvesicles; studies using microfluidic neuronal devices suggest both anterograde and retrograde trans-synaptic transmission of TDP-43 (Feiler et al., 2015).

In vitro and *in vivo* studies show β -amyloid transmission by axonal processes and retrogradely transported to neuronal cell bodies (Song et al., 2014). β -amyloid transmission is facilitated in regions with strong network connectivity (Pignataro et al., 2017).

6.1. β -amyloid seeding

The intracerebral injection of diluted extracts from AD brains or from old AD transgenic mice, and particularly soluble forms of β -amyloid, accelerates β -amyloid deposition in transgenic mice bearing *APP* and/or *PSEN1* mutations (Walker et al., 2002; Meyer-Luehmann et al., 2006; Langer et al., 2011; Rosen et al., 2012; Morales et al., 2012; Hamaguchi et al., 2012; Hérard et al., 2020). Widespread β -amyloid deposits, focal tau hyper-phosphorylation, synaptic loss, and glial reactivity occur in cynomolgus macaques following intraventricular injection of A β oligomers (Forny-Germano et al., 2014). Intravenous or peripheral inoculation of β -amyloid induces cerebral β -amyloidosis and β -amyloid angiopathy (Eisele et al., 2010; Burwinkel et al., 2018).

β -amyloid seeding has also been reported in humans. β -amyloid deposits are found in the brain of patients with iatrogenic Creutzfeldt-Jakob disease (CJD) contaminated with cadaveric dura mater grafts, or following treatment with human growth hormone obtained from hypophysis of CJD-affected donors (Duyckaerts et al., 2018; Lauwers et al., 2020).

6.2. Tau seeding from AD

Neuropathological studies in humans reveal the beginning of telencephalic tau pathology in aging and sAD in the transentorhinal and entorhinal cortex; from these regions tau spreads to the hippocampus and other regions of the limbic system, and then progresses to the whole telencephalon (Braak and Braak, 1991; Braak and Braak, 1997; Braak et al., 2011; Ferrer, 2012; Furman et al., 2017; Kaufman et al., 2018; Arnsten et al., 2021; Ferrer, 2022). Tau-PET neuroimaging studies further support tau spreading along the functional connectivity networks not only "downstream" (i.e., along the expected sequence of the established Braak stages) but also in part "upstream" or "retrograde" (Seemiller et al., 2021).

Tau seeding and then spreading is produced following the intracerebral inoculation of recombinant full-length tau or truncated tau containing four microtubule binding repeats in P301S and P301L transgenic mice overexpressing mutant human tau (Iba et al., 2013; Peeraer et al.,

2015).

Tau seeding and spreading is produced following the intracerebral inoculation of fibrillar tau-enriched fractions from AD homogenates containing hyper-phosphorylated tau in wild-type (WT) mice and transgenic mice bearing murine or human tau (Ahmed et al., 2014; Clavaguera et al., 2013a, 2013b; Boluda et al., 2015; Hu et al., 2016; Guo et al., 2016; Narashiman et al., 2017; Ferrer et al., 2020a and b; Andrés-Benito et al., 2022; Ferrer et al., 2022). Tau phosphorylation is needed for tau seeding and spreading (Hu et al., 2016). Propagation in these models occurs through connectivity rather than proximity (Ahmed et al., 2014). Several studies have shown that homogenates from different tauopathies generate disease-specific patterns of seeding and spreading, and involve different cell types, thereby mimicking the original human tauopathies (Clavaguera et al., 2013a, 2013b; Boluda et al., 2016; Narashiman et al., 2017; Ferrer et al., 2022). These findings support the proposal that tau strains lie behind the different phenotypes and progression of human tauopathies (Goedert et al., 2017; Mudner et al., 2017; Goedert and Spillantini, 2017; Goedert, 2020; Vaquer-Alicea et al., 2021).

However, this assumption must be approached with caution. Oligodendroglial tau-containing inclusions (coiled bodies) are generated following the inoculation of sAD homogenates whereas coiled bodies are never seen in AD unless AD is accompanied by other tau co-morbidities. Tau seeding and spreading also occur in oligodendrocytes in WT mice following inoculation of sarcosyl-insoluble fractions in the hippocampus and corpus callosum of human brain homogenates from other tauopathies (Narasimhan et al., 2018; Ferrer et al., 2019). The inoculation of pure ARTAG homogenates generates tau deposits in neurons and oligodendroglia but rarely if present in astrocytes (see later). Since these observations are obtained in WT mice, possible by-products linked to different promoters used to deliver transgens in genetically-manipulated mice (for example, the use of *prnp* promoters that may deliver the transgen to neurons and glial cells) are not applicable. The morphology of tau deposits also depends on the site of inoculation and the characteristics of the host tau (Götz and Götz, 2019; Ferrer et al., 2020b; Andrés-Benito et al., 2022).

Different tau strains are reported in AD brains (Li et al., 2021a, 2021b); thus, different tau strains may contribute to the clinical heterogeneity in sAD and fAD (Dujardin et al., 2020; Wesseling et al., 2020; Sepulveda-Falla et al., 2021).

Finally, abnormal tau may also be transmitted to humans in parallel to iatrogenic Creutzfeldt-Jakob disease after treatment of growth hormone from a cadaveric source (Duyckaerts et al., 2018).

6.3. Tau seeding from AGD

Staging of tau pathology in AGD is consistent with the hypothesis of prion-like cell-to-cell transmission of abnormal tau (Clavaguera et al., 2013a, 2013b; Rábano et al., 2014). Indeed, AGD-tau has the capacity for seeding and spreading when inoculated into the hippocampus of WT mice (Ferrer et al., 2020). Abnormal hyper-phosphorylated tau deposits are found in ipsilateral hippocampal neurons, grains (dots) in the hippocampus, and threads, dots and coiled bodies in the fimbria, as well as coiled bodies and threads in the ipsilateral and contralateral corpus callosum (Ferrer et al., 2020).

6.4. Tau seeding from ARTAG

Brain homogenates of pure ARTAG cases unilaterally inoculated in the hippocampus and corpus callosum of WT mice have the capacity for tau seeding and spreading in the ipsilateral hippocampus and corpus callosum and distant regions such as the contralateral corpus callosum (Ferrer et al., 2018; Ferrer et al., 2019; Ferrer et al., 2020). Hyper-phosphorylated tau deposits are found in neurons, neuronal threads, dots, and oligodendroglial cells; in contrast, astrocytes do not contain abnormal tau deposits in long-term inoculated mice. This

pattern is similar, although with variable intensity, to that following inoculation of human brain homogenates from sAD and other tauopathies in WT mice (Ferrer et al., 2018; Ferrer et al., 2019; Ferrer et al., 2020).

6.5. α -synuclein seeding from Lewy body diseases (LBD)

Recombinant α -synuclein amyloid fibrils that resemble human pathological α -synuclein have been used in a large number of α -synuclein seeding studies in cellular and animal models. Various types of α -synuclein aggregates are found in host cells, as well as in transgenic mice expressing wild-type or mutant α -synuclein and WT mice. α -synuclein aggregates in mice have been observed following intracerebral and peripheral inoculation of pre-formed fibrillar α -synuclein precursors (Luk et al., 2012; Sacino et al., 2014a, 2014b; Breid et al., 2016; Ayers et al., 2017; Griboaud et al., 2019). The amount and type of aggregates largely depend on the type of fibrils and characteristics and age of the host (Uchihara and Giasson, 2016). Moreover, α -synuclein strains cause distinct synucleinopathies after local and systemic administration (Peelaerts et al., 2015), and have differing structural and functional effects (Bousset et al., 2013; Holec and Woerman, 2020).

Intrastriatal injection of amyloidogenic α -synuclein aggregates in human α -synuclein transgenic mice leads to widespread α -synucleinopathy independent of neuronal connectivity (Sorrentino et al., 2017). The presence of intra-astrocytic α -synuclein deposits in inoculated mice suggests that glial cells participate in α -synuclein transmission (Sorrentino et al., 2017). The inoculation of phosphorylated α -synuclein at Ser129 fibrils in the striatum of WT mice augments α -synuclein pathology in the substantia nigra and cerebral cortex when compared with mice injected with non-phosphorylated and phosphorylation-incompetent S129 fibrils (Karampetsou et al., 2017). However, the enhancer effect of phosphorylated α -synuclein at Ser129 on α -synuclein aggregation is not supported by other studies; aggregation indeed precedes α -synuclein phosphorylation (Ghanem et al., 2022).

Clinical studies have shown that Lewy bodies occur in grafted embryonic and fetal neurons in subjects with PD thus suggesting host-to-graft propagation (Kordower et al., 2008; Li et al., 2008; Chu and Kordower, 2010). Similar results have been reproduced in grafted dopaminergic neurons in cultured human cells and rats (Hansen et al., 2011; Angot et al., 2012).

The intracerebral injection of Lewy body extracts from PD patients in WT mice and macaques produced α -synuclein deposits (but not Lewy bodies) and nigrostriatal degeneration (Recasens et al., 2014). However, PD homogenates inoculated in transgenic mice expressing mutated A53T α -synuclein did not show α -synuclein conversion at one year post-inoculation (Prusiner et al., 2015). This latter observation is in striking contrast to the effective transmission of multiple system atrophy (MSA) prions to transgenic mice carried out by the same researchers (Watts et al., 2013; Prusiner et al., 2015). Other studies have shown transmission of soluble and insoluble α -synuclein from LBD brain homogenates in BDF1 transgenic mice that over-express human wild type α -synuclein under the regulatory control of the platelet-derived growth factor (PDGF- β) promoter (Jones et al., 2015); and incidental LBD (and MSA) homogenates in Tg(SNCA)1Nbm/J mice expressing human wild-type synuclein (Bernis et al., 2015). Induction of α -synuclein aggregates is also generated following intracerebral injection of brain-derived exosomes from DLB patients in wild-type mice (Ngolab et al., 2017).

Transmissible α -synuclein seeding has also been produced up to 600 days following inoculation of brain and stomach homogenates from PD patients in TgM83^{+/+} mice which express the mutant human A53T α -synuclein under the direction of the mouse prion protein promoter (Thomzig et al., 2021).

Capacities for seeding and spreading of α -synuclein depend on the source (strain) from PD, incidental LBD, DLB, and MSA (Peelaerts et al.,

2018). In the same line, a comparison of the seeding and spreading capacities of α -synuclein obtained from DLB cases, AD/amygdala-predominant LBD, and recombinant α -synuclein fibrils inoculated in the brain of transgenic mice overexpressing human wild-type α -synuclein, or human α -synuclein with the A53T mutation, shows differing phenotype and course of the spreading depending on the α -synuclein inoculum (Lloyd et al., 2022).

6.6. TDP-43 seeding from TDP-43 proteinopathies

Staging of TDP-43 pathology in LATE suggests the progression of abnormal TDP-43 from cell-to-cell transmission in a prion-like manner. *In vitro* and *in vivo* studies have shown TDP-43 transmission across axon terminals, and TDP-43-derived from FTLD-TDP and ALS spreading with sub-type specific characteristics (Nonaka et al., 2013; Feiler et al., 2015; Smethurst et al., 2015; Smethurst et al., 2016; Porta et al., 2018; De Rossi et al., 2021; Porta et al., 2021; Jo et al., 2020). To date, no similar studies assessing seeding capacities of TDP-43 from LATE cases are available.

7. *In vitro* seeding assays in clinical practice

The capacity for seeding can be analyzed in biological samples using methods that amplify abnormally conformed proteins using the corresponding natural proteins as templates. The real-time quaking-induced conversion (RT-QuIC) method shakes and breaks abnormal aggregates which are incubated with fragments of corresponding basal recombinant proteins as substrate and then amplifies the amount of misfolded abnormal protein. The protein misfolding cyclic amplification (PMCA) technique is based on the sonication of abnormally folded proteins into smaller fragments; this is followed by the incubation step in which normal proteins are recruited and converted into abnormally conformed forms. These methods, first created for the study of prion diseases, are helpful to detect small amounts of other abnormally conformed proteins in tissues and body fluids, and may be applied to the clinical diagnosis of AD, α -synucleinopathies, tauopathies, and TDP-43 proteinopathies (Saijo et al., 2019; Kraus et al., 2019; Saijo et al., 2020; Metrick et al., 2020; Tennant et al., 2020; Rossi et al., 2020; Scialò et al., 2020; Arnold et al., 2022; Yoo et al., 2022; Standke and Kraus, 2022). The PMCA method has also been helpful for detecting α -synuclein seeding in formalin-fixed post-mortem nervous system tissue (Fenyi et al., 2021). Abnormal tau seeding can also be detected in formalin-fixed tissue using a new biosensor method (Kaufman et al., 2017).

8. Role of seeding and spreading in the progression of age-related proteinopathies

Tau can propagate from one neuron to another under physiological conditions, and the process is stimulated by neuronal activity (Pooler et al., 2013; Yamada et al., 2014; Wu et al., 2016). Tau seeding and spreading is also influenced by sleep deprivation; human CSF tau increases more than 50% during sleep deprivation; and tau seeding and spreading is increased following sleep deprivation in an animal model (Holth et al., 2019). Sleep deprivation promotes AD-like pathology in another paradigm (Lv et al., 2022).

The transmission of β -amyloid is also facilitated by neuronal activity (Pignataro and Middei, 2017). Likewise, neuronal activity increases α -synuclein aggregation and spreading in organotypic cell cultures and it exacerbates α -synuclein pathology following injection of preformed α -synuclein protofibrils in the striatum of WT mice (Wu et al., 2020).

The capacity of anomalous proteins to potentiate each other's' aggregation has been contemplated in several studies. Cellular prion protein facilitates interneuronal β -amyloid transmission (Del Río et al., 2018 8), and facilitates the uptake of tau amyloid fibrils (De Cecco et al., 2020). β -amyloid enhances pathological tau seeding accompanied by increased levels of the 25 activator of CDK5 kinase in AD-tau-inoculated

4xFAD transgenic mice (Vergara et al., 2019). The inoculation of pre-formed α -synuclein fibrils in 5xFAD Tg mice, expressing mutations in APP (K670N/M671L [isoform 770] + I716V + V717I) and PS1 (M146L + L286V), with abundant β -amyloid plaques promotes seeding and spreading of α -synuclein and tau hyper-phosphorylation throughout the brain (Bassil et al., 2020). Therefore, these results suggest that β -amyloid facilitates α -synuclein and tau seeding. APOE status also modulates α -synuclein's effects: α -synuclein aggregates from patients with AD plus LBD with ApoE4 are highly toxic to iPSc-derived neurons compared to aggregates from AD APOE4⁻, AD APOE4⁺, and AD+LB APOE4⁻ (Jin et al., 2022).

α -synuclein also impacts tau aggregation. Different recombinant α -synuclein fibril strains differentially promote tau inclusions in neurons (Guo et al., 2013). α -synuclein oligomers from PD cases administered to hTau mice accelerate tau oligomer formation (Castillo-Carranza et al., 2018). Intracellular tau aggregation is promoted by α -synuclein seeds in tau mouse models (Waxman and Giasson, 2011), but the opposite does not occur in α -synucleinopathy models (Williams et al., 2020).

Although mechanisms of release and uptake of abnormal aggregates are documented, the modifications of the host protein by the pathologic seed are not clearly understood. Abnormal tau triggers a series of molecular processes that include activation of several tau kinases, hyper-phosphorylation, nitration, and altered tau conformation, as well as recruitment of additional substrates in tau deposits (Ferrer et al., 2018; Ferrer et al., 2019; Ferrer et al., 2020a, 2020b; 2020c; Ferrer et al., 2022). However, there is no evidence that the conformation of abnormal tau generated in the host is the same as the conformation of the inoculated tau. Indeed, hyper-phosphorylation of recruited tau appears before altered tau conformation and tau truncation, which affect a subpopulation of phospho-tau containing neurons. Thus, pathogenic aggregated tau triggers a complex response in the host that follows similar steps to those occurring during the genesis of abnormal tau in the donor. This phenomenon may explain why the characteristics of tau deposits at short time points after inoculation are similar independently of the strain. Similarly, differences in host tau may lie behind the variable pace of tau transformation following injection of similar inocula.

In vitro studies aimed at monitoring the internalization and aggregation of externally added synthetic fibrils and AD brain extracts have shown, using real-time conversion of microtubule-binding domain of tau fused to a fluorescent marker into aggregates, colocalization of ubiquitin and p62 in the aggregates (Chastagner et al., 2020). The inoculation of AD-tau into the hippocampus of THY-Tau22 transgenic mice induced tau-positive grain-like inclusion in subregions of the hippocampus at three months after injection; these inclusions were immunoreactive with the antibodies phospho-tau, 4Rtau, misfolded tau, ubiquitin, and p62 (Audouard et al., 2016). However, no ubiquitin or p62 deposits have been observed following intracerebral inoculation of homogenates from several human tauopathies into WT mice at three and six months after injection (Ferrer et al., 2020c). These differences may be explained by differing states of abnormal tau deposition depending on the type of inoculum and characteristics of the host.

Another interesting point is the capacity to recruit 3Rtau following injection of 4Rtau, or 4Rtau following inoculation of 3Rtau. PSP- and CBD-tau do not induce 3Rtau in 3Rtau-expressing mice, and PiD does not induce 3Rtau in 4Rtau-expressing mice, whereas AD-tau induces 3Rtau and 4Rtau deposits in 3Rtau- and 4Rtau-expressing mice (He et al., 2020). However, other studies have shown small amounts of 3Rtau deposition, in addition to 4Rtau, following inoculation of homogenates from 4R-tauopathies, and a few 4Rtau deposits following inoculation of human 3Rtau homogenates; AD-tau inoculation gives rise to 3Rtau and 4Rtau deposits in WT and hTau transgenic mice (Ferrer et al., 2018; Ferrer et al., 2019; Ferrer et al., 2020a, 2020b). These results point to the possibility that foreign abnormal tau might modulate *mapt* exon 10 splicing (Ferrer et al., 2022). In this line, tau splicing modifier CKL1 is expressed in the ipsilateral dentate gyrus in AD- and GGT-inoculated hTau mice but not in hTau inoculated with vehicle

alone (Ferrer et al., 2022).

Another important point is the characteristics of tau spreading in the human brain that seem to skip over obligate regions on the basis of cell connectivity. The dentate gyrus does not show tau pathology in AD and other 3R+ 4R tauopathies without co-morbidities, but the dentate gyrus is commonly affected in 3R- and 4R-tauopathies. Alternatively, the following sequence has been proposed: tau pathology progresses from pre- α cells to distal dendrites in the prosubiculum and CA1; then, from CA1 or prosubicular pyramids to CA2 principal cells and CA3/CA4 mossy cells; and finally, from CA4 mossy cells to dentate granule cells (Braak and Del Tredici, 2020).

As a matter of fact, tau and α -synuclein seeding and spreading circumvent regions that should be involved according to the hypotheses of either neuronal connectivity or neuronal proximity. These observations suggest that neuronal subpopulations are able to transfer abnormal tau from one neuron to the next in the connecting pathway without recruiting host tau and forming local aggregates within themselves. In this line, tau seeding has been documented in regions with little or no apparent accumulation of phospho-tau in AD brains (Stopschinski et al., 2021).

Finally, there is no single origin of tau, β -amyloid, and α -synuclein seeding (Uchihara and Giasson, 2016; Kaufman et al., 2018). Moreover, seeding and propagation pathways of tau and α -synuclein differ in AD, other tauopathies, and α -synucleinopathies (Braak and Braak, 1991; Braak and Braak, 1995; Braak et al., 2002; Braak et al., 2003; Braak et al., 2004; McCann et al., 2016; Hoenig et al., 2018; Schwarz et al., 2018; Franzmeier et al., 2022).

Microglia and the status of neuroinflammation in brain aging and its role in the pathogenesis of AD are well documented. The involvement of microglia in tau seeding and spreading has also been assessed in animal models. Tau is internalized by microglia *in vivo* and *in vitro* (Bolós et al., 2015), but tau seeding by cultured adult microglia from AD cases and a mouse model of tauopathy is apparently not very efficient, as revealed with a sensitive fluorescence resonance energy transfer (FRET) bio-sensing cell line for tau seeding and aggregation (Hopp et al., 2018).

Other studies offer divergent results. Rapid tau propagation from the entorhinal cortex to the dentate gyrus was generated via an adeno-associated virus vector driving transgene expression of human P301L tau, in P301S tau transgenic mice; microglia depletion reduced tau propagation in this model (Asai et al., 2015).

TREM2 activation exacerbated β -amyloid-associated tau seeding and spreading around amyloid plaques in 5xFAD mice (overexpressing mutant human A β precursor protein with K670N-M671L, I716V, and V717I mutations and human PS1 harboring M146L and L286V mutations) (Jain et al., 2023). Yet TREM2 deletion and microglia ablation enhanced tau seeding and spreading around plaques in the same (5xFAD) transgenic model of β -amyloidopathy (Gratuze et al., 2021).

TREM2 deletion increased tau seeding and spreading *in vivo* at short time points post-inoculation of AAV-P301L tau vectors in Trem2 knockout compared with wild-type mice, and enhanced intraneuronal dispersion of tau *in vitro* between neuronal layers cultured in a microfluidic device (Zhu et al., 2022). In contrast, TREM2 deficiency in microglia resulted in greater accumulation of tau in THY-Tau22 transgenic mice at late stages following inoculation (Vautheny et al., 2021). The study was carried out by crossing THY-Tau22 heterozygous mice expressing the 1N4Rtau and the G272V and P301S point mutations, with Trem2^{-/-} or Trem2^{+/+} littermate mice to generate two groups: Trem2^{+/+}, Tau22 and Trem2^{-/-}, Tau22 mice (Vautheny et al., 2021).

These discrepancies are difficult to explain, unless we consider the many facets of microglia as comprehensively discussed by others (Odfalk et al., 2022).

9. Human brain aging vulnerability as revealed by the regional convergence of age-related proteinopathies

The most vulnerable regions in human brain aging to sAD (including

PART), AGD, and LATE are the archicortex, followed by the paleocortex and other parts of the limbic system. TSAs in ARTAG, not associated with other tauopathies excepting sAD, chiefly appear in different locations of the temporal lobe including the subependyma of the hippocampus, subpial region of the entorhinal cortex, amygdala, and temporal white matter. Amygdala-predominant LBD in the elderly usually linked to sAD also centers on the limbic system. Other neuropathological changes associated with brain aging such as Hirano bodies and granulovacuolar degeneration (GVD) also first appear in the same regions.

Hirano bodies are eosinophilic, rod-shaped inclusions derived from an abnormal organization of the neuronal cytoskeleton mainly localized in pyramidal neurons of the hippocampus in aging and sAD (Galloway et al., 1987). Hirano bodies do not express markers of the proteasome and autophagosome, but rather ubiquitin-1, which mediates the translocation of polyubiquitinated proteins to the proteasome for degradation (Satoh et al., 2013).

GVD is characterized by the presence of vacuolar cytoplasmic lesions with a dense central core. The molecular composition of cytoplasmic granules in GVD suggests a convergence of altered proteostasis, protein hyper-phosphorylation with enhanced tau-kinase activity, altered proteolysis, an impaired ubiquitin-proteasome system, abnormal reticulum stress responses, altered endocytic and autophagic pathways, and mitophagy (Okamoto et al., 1991; Ghanevati and Miller, 2005; Barrachina et al., 2006; Hoozemans et al., 2009; Funk et al., 2011; Hu et al., 2020; Hondius et al., 2021; Andrés-Benito et al., 2021). Phospho-tau and phosphorylated TDP-43 are common components of GVD (Andrés-Benito et al., 2021; Koper et al., 2022). Moreover, LATE-NC aggravates GVD-mediated necroptosis in AD, as revealed by the increased expression of the phosphorylated necroptosis executioner mixed-lineage kinase domain-like protein (pMLKL) (Koper et al., 2022).

GVD appears in neurons of CA1 and CA2, and the subiculum in stage 1; this is followed by the entorhinal cortex, and CA4 neurons in stage 2; temporal neocortex in stage 3; amygdala and/or the hypothalamus in stage 4; and cingulate, frontal, and parietal cortices in stage 5 (Thal et al., 2011).

The particular vulnerability of the archicortex followed by the paleocortex indicates that these regions cannot cope with the physiological demands made over the whole lifespan of actual humans. Physiological failure is manifested by variable and progressive wear of neuronal and glial proteostasis with production and accumulation of abnormal protein aggregates, followed by nerve cell demise first and foremost arising in these regions. This applies to tau aggregates in NFTs, pre-tangles, and grains in neurons; TSAs in ARTAG; and coiled bodies in oligodendrocytes; as well as α -synuclein in neurons and neuritis; and TDP-43 in neurons, neurites, and glial cells.

This scheme does not apply to β -amyloid deposition, as β -amyloid has no early predilection for these phylogenetically old regions, but it involves first the convexity of the telencephalon and then progresses to other brain places.

The reason for the particular vulnerability is not known but it can be linked to the advanced development of the neocortex in primates and particularly in humans when compared with other species (Crosby and Schnitzlein, 1982; Gall, 1990; Jones and Peters, 1990; Hodoss and Butler, 1996; Kaas, 2017). Other gyrencephalic species such as cetaceans have highly developed and convoluted telencephalon, but they do not show the same age-related regional vulnerability seen in humans. Therefore, differences might be associated with neuron and glial cell numbers, and synapses, but more likely with the complexity of interneural connections and the variety of neuronal subpopulations in the human neocortex and subcortical nuclei, which confer unique functional activities in humans (Herculano-Houzel, 2012; Triarhou, 2017; Briscoe and Ragsdale, 2019).

Serotonergic neurons of the raphe, noradrenergic neurons of the locus ceruleus, and dopaminergic neurons of the substantia nigra pars compacta, together with cholinergic neurons of Meynert's basal nucleus of the prosencephalon, are involved in the α -synucleinopathy at early

Braak stages (mainly I-III) of Lewy body in pre-motor cases of PD; interestingly, neurons in these regions show hyperbranched axons, and they therefore support a high demand of the corresponding neurotransmitter innervation mainly to the whole telencephalon (Kanazawa et al., 2008; Sulzer and Surmeier, 2013; Uchiyama and Giasson, 2016). The same types of neurons are also vulnerable at early stages of NFT pathology (stages a-c of Braak) in the elderly and in AD (Braak and Del Tredici, 2015; Arnsten et al., 2021).

10. Therapeutic implications

Current strategies to cure AD are based on the assumption that i) β -amyloid triggers tau pathology in AD and therefore, β -amyloid is the first target to combat AD; ii) tau pathology parallels cognitive impairment, and then tau is the second target to reduce AD pathology; iii) other factors, such as inflammation, membrane integrity, neurotransmitter alterations, are complementary targets to reduce neuronal damage in AD. However, all these strategies have failed to some degree as i) β -amyloid vaccination does reduce the β -amyloid burden but not tau pathology and disease progression (this is a significant point against the amyloid cascade hypothesis as the origin of sAD); ii) tau vaccination has to decide what the critical tau isoform or aggregate, among the multiple pathological tau species, is the crucial target for therapeutic intervention; iii) anti-tau phosphorylated agents (mainly anti-active kinases) act on multiple molecules that are vital to the normal cell functions; iv) other drugs directed to replace neurotransmitter deficits have transient and mild effects; v) therapies aimed at clearing abnormal proteins in the blood (i.e., plasmapheresis) are still in a preliminary phase; vi) available gene therapies in humans have demonstrated little benefit; vii) the use of shuttles including exosomes to deliver selected molecules into the cells is still at the early stages; and viii) all these procedures are implemented at the middle or advanced stages of the neurodegenerative process.

So far, no therapies have been proposed regarding AGD, LATE-NC, ARTAG, amygdala-predominant LBD, and hippocampal sclerosis.

The present scenario of human brain aging implies the need for new therapeutic attempts based on new targets altered at earlier stages of the neurodegenerative processes. One of the first points is to gain an understanding of the differential vulnerability of the human brain to aging when compared with other species based on genetic and epigenetic factors that may determine the early fragility of the human archicortex and paleocortex when compared with other species; and the dramatic progression of pathological changes, although with different individual pace, once initiated the pathological processes. Another point is to consider that NFT (and β -amyloid) pathology is not the only neurodegenerative change in the elderly, but instead that tau and β -amyloid pathology are part of a complex abnormal proteostasis; in this line, tau pathology differs in AD, ARTAG, and AGD; moreover, TDP-43 and α -synuclein pathologies are also relevant in human brain aging. Finally, alterations in other molecular pathways, including those compromising i) lipid composition of membranes, membrane proteins, and membrane signaling, ii) mitochondria and energy metabolism, iii) DNA and RNA metabolism integrity and regulation, iv) neuroinflammation, v) glial cells senescence, and vi) blood vessel dysfunction, also participate in human brain aging (Ferrer, 2022).

Another conclusion of the present review postulates that the human archicortex and paleocortex are not designed to endure a functional overload during the human lifespan. Biological cell reprogramming may cover different areas, including brain DNA editing, optimization of mitochondrial function, and pharmacological combined protection of lipid-protein interactions. Improvement in the efficiency of reparative sleep functions (program resetting during stages of sleep) may also be specifically explored. In addition to biological procedures, the rapid growth of artificial intelligence (AI) may offer excellent opportunities to use advanced technologies. Intelligent devices and "external" memories may be designed and implemented to delegate (and even expand) expensive (in terms of energy and molecular consumption) tasks of the

vulnerable phylogenetically older circuits. Implanting microdevices may facilitate cooperative human-machine function. External electrical or wave-based signals may reduce the energy consumption of essential neuronal networks.

Brain reprogramming would likely be undertaken before the beginning of the slow-paced functional decline in middle-aged adults. Improvement of brain function in aging and sAD has a chance of applying high-throughput molecular technology, AI, and robotics (Ferrer, 2022).

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Declaration of Competing Interest

No competing interests to declare.

Data availability

No data was used for the research described in the article.

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