Contents lists available at ScienceDirect

Neuroscience Letters

journal homepage: http://ees.elsevier.com



Minireviews

Aging and Alzheimer's disease connection: Nuclear Tau and lamin A

Laura Gil¹, Sandra A. Niño², Gabriela Capdeville³, María E. Jiménez-Capdeville^{2,*}

¹ Departamento de Genética, Escuela de Medicina, Universidad "Alfonso X el Sabio", Madrid, Spain

² Departamento de Bioquímica, Facultad de Medicina, Universidad Autónoma de San Luis Potosí, Mexico

³ Escuela de Medicina, Universidad Panamericana, Mexico

ARTICLE INFO

Keywords Alzheimer's disease Aging Tau protein Nuclear lamin Lamin A Hippocampal neuron Chromatin

ABSTRACT

Age-related pathologies like Alzheimer's disease (AD) imply cellular responses directed towards repairing DNA damage. Postmitotic neurons show progressive accumulation of oxidized DNA during decades of brain aging, which is especially remarkable in AD brains. The characteristic cytoskeletal pathology of AD neurons is brought about by the progressive changes that neurons undergo throughout aging, and their irreversible nuclear transformation initiates the disease. This review focusses on critical molecular events leading to the loss of plasticity that underlies cognitive deficits in AD. During healthy neuronal aging, nuclear Tau participates in the regulation of the structure and function of the chromatin. The aberrant cell cycle reentry initiated for DNA repair triggers a cascade of events leading to the dysfunctional AD neuron, whereby Tau protein exits the nucleus leading to chromatin disorganization. Lamin A, which is not typically expressed in neurons, appears at the transformation from senile to AD neurons and contributes to halting the consequences of cell cycle reentry and nuclear Tau exit, allowing the survival of the neuron. Nevertheless, this irreversible nuclear transformation alters the nucleis machinery as well as the nuclear lamina and cytoskeleton structures, leading to neurofibrilary tangles formation and final neurodegeneration.

1. Introduction

Aging is a universal and holistic biological process underlying the declining health of cells and tissues. This damage leads to irreversible systemic dysfunction bringing about diseases and finally death. Four primary causes within the cellular origin of aging have been established: genomic instability, telomere attrition, epigenetic alterations, and loss of proteostasis [1]. Three out of them directly affect nuclear chromatin structure and function [2], and they are related to cumulated DNA damage throughout cellular life [3].

The genesis of highly prevalent pathologies such as Alzheimer's disease (AD) and cancer is closely related to aging [4]. Decades of research have succeeded in the treatment of some types of cancer, but minimal achievements have been reached concerning effective AD therapies [5]. In this respect, AD research has been overwhelmingly focused on aberrant neuronal cytoplasm and neuropile alterations related to tau and β -amyloid misfolded proteins, respectively [6]. In this review, we analyze the progressive changes that hippocampal neurons undergo throughout aging and the irreversible nuclear transformation that originates the cytoskeletal pathology in AD. The discussion is centered on the role of nuclear lamin (NL) and tau protein.

2. Neuronal aging and nuclear lamin dysfunction in AD

2.1. Nuclear lamin and Alzheimer's disease

Nuclear lamin (NL) is a flexible multimeric protein network conforming the nuclear structural scaffold. It connects the nucleoskeleton with the cytoskeleton through a platform of intermingled proteins called A, C, B1, and B2 lamins, each of them with different mechanical properties [7]. These proteins spread from the nuclear periphery throughout the nucleoplasm, creating an anchoring net for chromatin [8]. Not every cell has a NL consisting of all four lamin proteins, but each cellular type has a specific composition and organization of them [9–11]. The degree of stiffness and flexibility of NL required by each cell is conferred by the specific array of lamins [12–14]. NL regulates genic expression since it is directly or indirectly related to DNA replication, transcription, and reparation, as well as to the control of the cell cycle. In consequence, NL is intimately related to basic and complex biological processes such as development, differentiation, and aging [15].

Lamin B1 and B2 are the main components of human neuronal NL, although a minor contribution of Lamin C cannot be discarded [16].

https://doi.org/10.1016/j.neulet.2021.135741

^{*} Corresponding author at: Departamento de Bioquímica, Facultad de Medicina, UASLP, Av. Venustiano Carranza 2405; San Luis Potosí, Mexico. *E-mail address:* mejimenez@uaslp.mx (M.E. Jiménez-Capdeville)

Received 25 August 2020; Received in revised form 12 January 2021; Accepted 11 February 2021 Available online xxx 0304-3940/© 2021.

The constant presence of Lamin B1 allows the NL to maintain the nuclear shape [14,7]. Nevertheless, increased expression of Lamin B2 during aging seems to be required in order to reinforce the NL [17]. Last decade, the studies from Frost and collaborators in a *Drosophila melanogaster* model of AD demonstrated that NL plays a decisive role at the starting point of the disease [18], defining AD as an acquired laminopathy [19]. Recently, altered conformations of NL associated to aging as well as to Alzheimer's pathology have been reported in hippocampal neurons [17]. Human postmitotic neurons usually display a characteristic absence of Lamin A at their NL, and a unique and large nucleolus which congregates most of the nucleolus organizing regions (NORs) [20,21]. The absence of Lamin A confers greater flexibility to the nucleoskeleton, favoring the fluid interaction between the cytoskeleton and the nucleus required for neuronal plasticity [22–24].

Interestingly, Lamin A is involved both in physiological aging and in an accelerated aging process leading to very premature death, namely Hutchinson-Gilford syndrome (HGPS). A dysfunctional NL of fibroblasts and the subsequent DNA damage underlie HGPS. Therefore, it is considered a genetic laminopathy. The affected children present connective tissue alterations, which result in pathologies that would generally occur in advanced biological age in several organs such as bone, muscle, skin, blood vessels, and subcutaneous tissues. Nevertheless, not all organs are affected, the brain is spared given the absence of Lamin A in postmitotic neurons and does not present characteristic signs of neurodegeneration associated with advanced age such as AD [25].

Sporadic AD is a multifactorial disease whose etiology remains unknown, but where the main risk factor is aging [6]. Old neurons display a more complex and less flexible NL than young neurons but still with a certain degree of plasticity, allowing mechanical interaction between the aged nucleus and cytoplasm [22,23,14]. Recently, it has been demonstrated that in aged AD brains, postmitotic hippocampal cells express Lamin A from the initial stages of the disease [16]. The NL structure of AD neurons is even more complex than in healthy aged neurons, since it expresses at least 3 intermediate filaments type V, Lamin B1, B2, and also Lamin A [17]. The presence of Lamin A fortifies the NL, providing greater rigidity and viscosity that prevents nuclear deformation [14]. These findings suggest that a dysfunctional NL is implicated in both aging and AD [19], whereby the up regulation of Lamin A expression is one of the most significant differences between healthy senile and AD brains [16].

2.2. Lamin A and neuronal aging

An exciting relationship between Lamin A, HGPS and normal aging has been recently demonstrated. In prematurely aged fibroblasts from HGPS patients, NL dysfunction is due to a dominant punctual mutation in the LMNA gene (1874C-T). This change generates a truncated Lamin A lacking 50 aminoacids in its C-terminus, which is permanently farnesylated (Lamin A50/progerin) [26–28]. Lamin A50 becomes abnormally associated with the membrane and organizes a dysfunctional pseudo-structure of type V filaments that accumulates in the nuclear periphery [29,30]. The resultant defective NL does not provide the adequate restrain deformation rate and strength required by the cell nucleus to anchor and stabilize peripheral and nucleoplasmic heterochromatin [31]. Instead, it forms a weak and viscous interaction with heterochromatin [32,33], which lacks the mechanical dynamics with the robust cytoskeleton resulting in pathologic alterations of the nucleus and chromatin [14].

Normal aging is also associated to the presence of Lamin A50, through alternative splicing of the LMNA gene. This has been established by demonstrating the presence of mRNA of Lamin A50 in fibroblasts from young and old subjects [34]. Although the expression of Lamin A50 was 50 times higher in HGPS cells as compared with the healthy fibroblasts, this study indicates that healthy cells also contain Lamin A50 at much lower levels than HGSP cells. Cells from old subjects show 2 striking differences from those from young ones. First, they express low levels of Lamin A50, and second, while cells from young subjects express it throughout the nucleoplasm, these cells express Lamin A only at the rim of the nuclear membrane, which is a similar distribution of mutant lamin in HGSP cells. Importantly, this aberrant splicing event driving to a lack of nucleoplasmic Lamin A is associated with substantial changes in epigenetic markers and an increased amount of unrepaired DNA damage [34]. All this suggests that the truncated Lamin A isoform is physiologically related to aging, although its function is still unknown.

Lamin A is not present in the neuronal NL and is not implicated in their aging process either. Nevertheless, its expression plays a key role in the transformation from senile to AD neurons [16]. Besides, its position at the nuclear periphery is similar to that observed in HGPS fibroblasts, suggesting a non-canonical function. Early AD stages are characterized by radical structural and regulatory changes of the nucleus of hippocampal pyramidal neurons (Fig. 1). These changes progressively lead to cytoskeleton dysfunction, which can be observed years later in the form of neurofibrillary tangles [35]. Concerning the nuclear periphery, Lamin A appearance at the internal side of the aged NL generates an increased rigidity of the nuclear scaffold, mechanical changes of cytoskeleton-nuclear transduction and a different chromatin viscosity [14]. Future research will determine whether AD neurons express only normal length Lamin A or also the truncated Lamin A related to physiological aging.

3. Nuclear Tau: chromatin modifier in aging and Alzheimer's disease

Chromatin structure safeguards the integrity and expression of the genome. Its dynamics rule the temporal-cellular implementation of specific genetic programs that regulate the development and age-related changes of biological functions in cells and tissues [2]. Aging and progressive chromatin deterioration is associated with increased DNA damage in all tissues [36–39]. The main processes accounting for DNA damage both in proliferative and postmitotic aging cells [40] are the accumulation of unrepairable double-strand breaks [41,42], genome rearrangements [43] and the decrement of repair capacity with age [44,45].

3.1. Nuclear Tau and chromatin aging

Tau protein stands out among the proteins with an essential diversity of neuronal functions. In the cytoskeleton is a microtubule-associated protein, which stabilizes microtubules and promotes their assembly. Its phosphorylation is associated with a detachment from microtubules and is essential for neuronal plasticity in the healthy brain. Nevertheless, hyperphosphorylation drives Tau aggregation and the production of neurofibrillary tangles in pathological aging and tauopathies [35]. More recently, its nuclear presence and DNA binding have been widely demonstrated [46–50] as well as its protective role against oxidative and heat stress, which is related to Tau concentration [46,51,52].

Strand breaks caused by endogenous reactive oxygen species (ROS) are among the main causes of DNA damage. The high oxygen consumption rate of postmitotic neurons leads to a progressive accumulation of oxidized DNA during decades of brain aging, which is especially remarkable in AD brains [53,54]. In this context, the amount of one form of phosphorylated Tau, AT100 (p-The212-Ser214) in hippocampal CA1 and dentate gyrus (DG) neurons increases with age, reaching its higher levels in the oldest neurons and those subjected to oxidative stress [55,56]. Young neuronal nuclei display scarce, and weak AT100 positivity in a disperse punctuate pattern. As neurons age, the positivity zones increase in frequency and intensity, in particular close to the nu-



Fig. 1. Transformation from senile to AD pyramidal neurons. (A) Lamin A is not present in the neuronal nuclear lamina, the senile neurons display an increment of Lamin B2 in their NL, with redistribution to replication factories where it reinforces the LADs. (B) The addition of Lamin A to Lamin B1 and B2 will increase the stiffness of the nuclear lamina, resulting in a limited nuclear deformation and reduced chromatin mobility. Hence, the spatial chromatin organization, gene expression regulation, and nucleus-cytoplasm transport are modified in the AD neuron.

clear membrane and around the nucleolus, colocalizing with the rich DAPI stained heterochromatin regions [49,57,58]. The most significant finding is the vast presence of AT100 in the nuclei of old neurons interacting both with heterochromatin and euchromatin in the nuclear periphery and the nucleolus [56]. This progressive up-regulation of Tau in parallel with age–related DNA damage due to oxidation and rupture would confirm its participation, ensuring genome stability and function throughout healthy neuronal aging [59,43].

In addition to DNA strand breaks, the electron microscopy analysis of 30 nm chromatin fibers in aging fibroblasts shows a progressive loss of density [60,61], which indicates a decrease of chromatin compaction along with lifespan [62]. Heterochromatin regions like telomeres, pericentromeres, and those coding for ribosomal proteins undergo the most drastic changes with age [63-65]. One of the main causes of chromatin decompaction is the loss of histone proteins, which reaches a 50% diminution of the histone core [2,66,67]. Interestingly, Tau binds the minor groove of DNA forming a beads-on-a-string structure similar to histone binding [67]. Tau is predominantly present at the border of the nucleolus, where it colocalizes with H3K9me2, an epigenetic mark of constitutive heterochromatin [48]. Throughout neuronal aging chromatin fibers would loss nucleosomes, but their interaction with nuclear Tau increases in order to keep a functional compaction level. This behavior supports the hypothesis that Tau plays a protective role in stress situations such as physiological aging [55].

3.2. Nuclear Tau and global chromatin decondensation in AD neurons

Age-related chromatin changes increase the incidence of age-related diseases like AD. Postmortem histological analysis of hippocampal cells at early AD stages, previous to the presence of NFTs, reveals the presence of two characteristics that distinguish them from healthy senile brains. First, the anomalous presence of Lamin A described in the previous section, and second, the gradual appearance of Tau in the cytoplasm [68,69]. The nuclei of senile neurons from the CA1 and DG regions show high AT100 immunopositivity. The aged and damaged chromatin is thought to be protected and stabilized by this phosphorylated form of Tau [56]. At early AD stages, however, depletion of nu-

clear Tau advances gradually as AD progresses, and it reaches its maximum at late AD stages when AT100 immunopositivity is exclusively localized in neurofibrillary tangles (NFTs); and the nuclei are completely devoid of Tau [70]. Tau exit from neuronal nuclei induces global chromatin relaxation, namely extended fibers and fibers without nucleosomes [18]. This relaxed chromatin presents 1) important epigenetic changes [71], 2) dysregulation of euchromatin genes and 3) abnormal transcription of heterochromatin genes [18,57,72,73] and of transposable elements [74]. All these characteristics support a role of nuclear Tau in chromatin protection.

The decrease of marks associated to transcriptional silencing such as H3K9me2/me3 downstream nuclear Tau depletion [18,70] leads to constitutive heterochromatin decondensation at the pericentromeric and perinuclear regions called LADs (lamin associated domains) due to their close relationship with NL [56,57,75] and with nucleolar regions denominated NADs [48,58,50]. This decondensation is the consequence of a synchronized overall increase of activating epigenetic marks such the histones acetylations H4K16ac, H3K12ac and H3K9ac [17,70,71,76,77].

Tau is localized adjacent to the inner side of the NL [56,75] and regulates the nuclear pore complex (NPC). The progressive accumulation of Tau in the somatodendritic compartment along AD stages affects the structure of NL and disrupts nucleocytoplasm transport and results in the mislocalization of nuclear proteins in the cytoplasm [78]. The critical role of Tau on the structural and functional regulation of the genome has been revealed employing genoma-wide immunoprecipitation (ChiP) and microarray hybridation (ChiP-on-chip) assays [79]. Non-protein coding DNA sequences are targets of nuclear Tau, which binds to GAGA motifs distributed throughout the genome. The presence of GAGA repeats in the LADs associated to NL [80] confirms Tau participation in the organization of perinuclear heterochromatin. Therefore, the exit of Tau from the neuronal AD nuclei implies the destabilization of chromatin domains and the remodeling of LADs [18,56].

Significant amounts of Tau protein interact with DNA intergenic and intronic regions coding for long noncoding RNA (lncRNA), which are chromatin regulators [79,81]. These lncRNA act as molecular scaffolds through direct or indirect association with chromatin-modifying factors such as methyl and acetyltransferases, deacetylases and kinases [82–84]. Also, through their interaction with transcription factors, Tau and lncRNAs regulate the transcription state of chromatin and, indirectly, the expression of genes involved in cellular processes that are highly dysregulated during aging [2,67,85–87] and in AD [88–90]. Recent evidences point to the role of lncRNAs in AD [91,92].

Nucleolar dysfunction in AD has been widely documented [70,93,94]. Tau is present in the nucleolus, both in the euchromatic regions harboring ribosomal genes (rDNA) and in the NADs [17,48,50,56,95,96]. Nucleolar Tau depletion has been reported to affect rRNA synthesis and to destabilize rDNA loci [58]. In the hippocampus, Tau depletion decreases the ratio of mature rRNA 28 s and deregulates the expression of proteins involved in translation [70]. Altogether, nucleolar Tau presence is essential for NADs stability, rDNA transcriptional regulation, and the structure and function of the nucleolus.

In summary, Tau is a key player in the healthy aging of postmitotic hippocampal neurons. Its nuclear expression along decades protects genomic DNA and stabilizes the peripheral (LADs) and nucleolar (NADs) heterochromatin blocks [57,58,97], by allowing the required chromatin compaction in order to silence the repetitive DNA sequences and to warrant hippocampal gene regulation. Still, it has not been elucidated the precise stimuli that trigger Tau exit from the nucleus and the cascade of events leading to the dysfunctional AD neuron, whose characteristics are documented in detail as follows, 1) decondensed global chromatin [18]; 2) activation of previously silenced intergenic and non-coding sequences in heterochromatin regions [57,74,79,91,92,98]; 3) repression of characteristic postmitotic neuron genes and expression of new genes [71,79,88,90]; 4) dysfunctional transcription and translation [70,99]; 5) disorganized NL and nucleoskeleton resulting in abnormal nucleus-cytoplasmic transport [17,75]. The final consequence of these long-standing changes will be the main characteristics of AD, namely loss of neuronal plasticity and the presence of NFTs.

4. Lamin A rescues neurons from death following aberrant cell cycle reentry in AD

Neuronal aging underlies the neurodegeneration observed under sporadic AD. Terminally differentiated neurons are highly susceptible to oxidative DNA damage due to their high rate of oxidative metabolism [100]. High levels of damaged DNA have been detected at autopsy of hippocampal tissue both from healthy senile subjects and from AD patients [101]. Neuronal DNA damage at senile stages is markedly localized at the promoter regions of genes involved in learning, memory and neuronal survival, which already show a reduced expression after the age of 40 years [102]. In parallel, a reduction of markers of DNA repair [102,103] implicates a mismatch between patterns of damage and successful repair. Unrepaired or incorrectly repaired double-strand breaks are the most lethal damage that can occur to DNA.

4.1. Neuronal aging and cell cycle reentry

Reliable evidence indicates that the failure to repair DNA damage is the determinant factor leading to the activation of an aberrant cell cycle [104]. Aged neurons arriving at a particular "vulnerability" point require to express repairing proteins by activating the S checkpoint. In addition to AD, this phenomenon has been described in other neurodegenerative diseases such as Parkinson's disease and amyotrophic lateral sclerosis as well as in retinal degenerative disorders [105]. In fact, the activation of DNA repair pathways has been demonstrated following the G0-G1 transition of postmitotic neurons [106,107]. Even in absence of AD markers, the expression of cyclin E has been reported in elderly CA1 neurons [108]. Also, in the entorhinal cortex up to 10% of hyperploid pyramidal neurons have been quantified [109]. When cell cycle reentry is forced in cortical cultures, it has been demonstrated that although hyperploid neurons remain connected to normal diploid cells and seem to maintain their basic electrophysiological properties, excitability and spontaneous activity show an important decrease [110].

The study of cell cycle reentry in cultures of primary cortical neurons and animal models has revealed that it requires the presence of soluble Tau and beta amyloid $(A\beta)$ before they become incorporated into tangles and plaques, respectively [18,111-114]. A β has antioxidant properties [115,116]. Oxidative stress activates positive feedback between gamma and beta-secretase cleavage of beta-amyloid precursor protein (APP) and increases the expression and activity of beta-secretase [117,118]. On the other hand, nuclear Tau has a concentration-dependent protective role of DNA oxidation [46,51,52]. Throughout healthy neuronal aging, an up-regulation of nuclear Tau becomes evident through the progressive accumulation phosphorylated Tau in the site Thr212-Ser214 (AT100). The nucleus of senile neurons entering cell-cycle displays the highest presence of AT100 accompanied by a reorganization of NL, whereby Lamin B2 is redistributed from the nuclear envelops to the nucleoplasm [56,17]. Lamin B2 redistribution to replication factories takes place during the S phase [119], indicating a direct role in DNA synthesis [120] and the conversion of hyperploid neurons [109,121].

Once the genome has been replicated, the neurons continue to the G2-M phase, from which they are unable to progress [122]. Interestingly, although these hyperploid neurons present synaptic dysfunction, they continue integrated in networks with diploid neurons, which favors their survival. It has been hypothesized that these dysfunctional networks could be underlying the cognitive deficits found in AD [123]. Finally, hyperploid neurons end in cell death [108,124,125]. It is a fact that healthy aging involves neuronal loss, and aberrant cell-cycle reentry seems to provoke between 5 and 10% of hippocampal neuronal death [122]. It is also plausible that this neuronal loss slowly starts as soon as after age 40 when a reduced expression of genes responsible for neuronal survival and plasticity decreases [102]. Multiple in vitro studies employing cell cultures and in vivo research in murine AD models confirm that neuronal death is a consequence of cell cycle reentry [126-130]. A sustained neuronal loss takes place along 2-3 decades of healthy aging without a significant impact on cognitive skills [131].

4.2. Lamin A and nuclear Tau: crucial players blocking the consequences of cell cycle reentry

Notwithstanding this deadly pathway for aging neurons, why and how senile neurons that enter the aberrant cell cycle that leads them to death, transform themselves in dysfunctional AD neurons, which are able to survive through several years? We do not have a complete answer yet. For almost 30 years, it is known that two groups of neurons coexist in AD brains at initial stages. One of them suffers the abortive cell cycle and accounts for 75-90% of the neuronal loss by the time the disease progresses to later AD stages [128,132,133], while the second type of neurons do not die but triggers Tau hyperphosphorylation and aggregation, originating NFTs. These neurons suffer from a nucleo-cytoskeleton disruption, and even the extracellular matrix becomes invaded by protein aggregates, but these changes enable them to survive for years [108,134,135]. As commented above, the involvement of nuclear Tau at the beginning of AD has been demonstrated [70]. It is important to underline, however, that new nuclear Tau phosphorylation takes place in senile neurons, in addition to the AT100 site. The phosphorylation of the emblematic site Ser202-Thr205 (AT8) results in a paper clip conformation [136], which is the pathological structure characteristic for Tau in AD. Tau is an unfolded protein whose phosphorylation determines its structure and function [137]. The phosphorylated AT8 site is related to inhibition of replication [138], inactivation of rDNA transcription [96], and preservation of vulnerable neurons in G0 [108]. This clearly indicates a key role of nuclear Tau by blocking the cell cycle while keeping the vulnerable neurons in a viable, static G0-G1 in the aged hippocampus [17]. The phosphorylation of residues T205-T212-S214 of the proline-rich domain [136] are the characteristic of nuclear and cytoplasmic Tau forms during aging and neurodegeneration [139,140,136]. The structural change associated to phosphorylation of the same or different nuclear Tau isoforms [141,142] is involved not only in neuronal differentiation but also in cellular stress [96,143]. Altogether, these versatile functions of nuclear Tau suggest that it protects heterochromatin stability and is able to modify DNA expression [144].

The senile and vulnerable neurons that had enriched their nuclei with hyperphosphorylated Tau also display an increment of Lamin B2 in their NL, where it reinforces the LADs and immobilizes the shortened telomeres associated to the aging process [145]. However, senile neurons that migrate to the AD phenotype suffer an irreversible nuclear transformation that affects not only the neuron itself but complete circuits, and finally, the whole brain, although the details of its propagation are still under study [146]. Tau exit from the nucleus has pathogenic effects that decisively contribute to synaptic dysfunction and neurodegeneration [70]. The first effect is associated with Tau accumulation in the somatodendritic compartment that directly impairs RNA translation [147,148] and inversely correlates with translational output [149,150]. Besides, it drives the transformation of the nucleoskeleton of the AD neuron towards chromatin relaxation, preferentially observed in the LADs and H3K9ac associated domains [71]. As mentioned in the previous section, the spatial chromatin organization, the silencing of heterochromatin blocks, gene expression regulation, and nucleus-cytoplasm transport are modified in the AD neuron (Fig. 2). The decondensation of repetitive DNA sequences implies, among other effects, the disinhibition of brain-specific miR-9 [19], which enables the anomalous expression of Lamin A in more than 50% hippocampal neurons [16,17], influencing at least 2 ongoing processes. First, it arrests DNA replication, which prolongs neuronal life by keeping them in an artificial G1 phase of the initiated cell cycle [151]. Second, it decreases DNA damage through the activation of DNA repair mechanisms such as DNA double-strand break repair (DSB) and DNA excision repair (BER) [152–154]. Despite the genomic stability conferred by Lamin A expression, the excessive ectopic expression of extranuclear kinases will contribute to hyperphosphorylate Tau [122,155]. Similarly, as it takes place in HGPS [156], the perinuclear Lamin A accumulation in AD will be associated to an increased expression of the repressive histone mark H4K20me3 during early and intermediate AD Braak stages [17]. The labile heterochromatin blocks at NADs and LADs will be stabilized through H4K20me3 [57,71,157–159], since they are devoid of nuclear Tau and histone 3 at this stage [70,160].

Pyramidal hippocampal neurons do not express Lamin A, which allows the required nuclear flexibility to deploy their high degree of axonal and dendritic plasticity [23]. The addition of Lamin A to the dimeric network conformed by Lamin B1 and B2 will increase the NL stiffness, resulting in a limited nuclear deformation and reduced chromatin mobility [14,23]. The dynamics of the nucleus-cytoplasm scaffold suffers a decisive modification, since Lamin A regulates the expression of cytoplasmic stress fibers, nuclear actin, and myosin I [23]. This cytoplasmic transformation would finally lead to the production of NFT by cytoplasmic hyperphosphorylated Tau and a disorganized mass of microtubule subunits [161].

It is worth finally mentioning here that the expression of cell cycle markers is not exclusive of AD but has also been reported in other neurodegenerative diseases such as Parkinson [162] amyotrophic lateral sclerosis [163] and Huntington's disease [164] as well as in stressful situations such as stroke [165] and viral encephalitis [166]. Similarly, "mitotic catastrophes" have also been reported in other postmitotic cells such as podocytes [167], cardiomyocytes [168], muscle fibers [169], and retinal pigmental epithelial cells [170].



Fig. 2. Nuclear Tau and neuronal AD transformation. Postmitotic neurons accumulate DNA damage during decades of brain aging. Nuclear Tau expression protects genomic DNA and stabilizes the peripheral and nucleolar heterochromatin blocks in the senile neuron. The phosphorylated AT100 and AT8 sites block the cell cycle while keeping the vulnerable neurons quiescent in the aged hippocampus. After Tau exit from the AD nucleus, the extracellular matrix becomes invaded by protein aggregates, although these changes enable them to survive some years despite synaptic dysfunction.

5. Conclusion

It is very plausible that cell cycle reentry has evolved as a biological mechanism associated with stress in order to restore the nuclear-cellular-tissue homeostasis. Aging may represent an extreme stress situation whereby cell cycle reentry does not allow to recover the equilibrium, resulting in a cascade of finally pathologic events. In the case of replicative cells, cancer may be the outcome, while in the case of postmitotic cells, degeneration and death would be the consequence.

This latter scenario is evidenced in pyramidal hippocampal neurons, whose cell cycle reentry throughout aging is the main cause of neuronal loss. These cells are temporarily rescued from death through the anomalous Lamin A expression and Tau exit from the neuronal nuclei forming NFTs. Nevertheless, research is needed in order to elucidate whether Lamin A expression also triggers a mechanotransduction dysfunction [171], leading hippocampal neurons to neurodegeneration.

Declaration of Competing Interest

The authors declare no conflict of interest.

Acknowledgments

We would like to the acknowledge Maximiliano González-Olazábal, recently deceased, for being the tireless motivator of this research, the project 1.010.924 from the Fundación Alfonso X el Sabio-Banco Santander, Spain and the Biobanco, Hospital Universitario Fundación Alcorcón, Alcorcón, 28922 Madrid, Spain.

References

- C. López-Otín, M.A. Blasco, L. Partridge, M. Serrano, G. Kroemer, The hallmarks of aging, Cell 153 (6) (2013) 1194–1217, doi:10.1016/j.cell.2013.05.039.
- [2] J. Feser, J. Tyler, Chromatin structure as a mediator of aging, FEBS Lett. 585 (13) (2011) 2041–2048, doi:10.1016/j.febslet.2010.11.016.
- [3] L.J. Niedernhofer, A.U. Gurkar, Y. Wang, J. Vijg, J.H.J. Hoeijmakers, P.D. Robbins, Nuclear genomic instability and aging, Annu. Rev. Biochem. 87 (2018) 295–322.
- [4] Y. Hou, X. Dan, M. Babbar, et al., Ageing as a risk factor for neurodegenerative disease, Nat. Rev. Neurol. 15 (10) (2019) 565–581.
- [5] A. Zagórska, A. Jaromin, Perspectives for new and more efficient multifunctional ligands for alzheimer's disease therapy, Molecules 25 (15) (2020) E3337.
- [6] C. Ballard, S. Gauthier, A. Corbett, C. Brayne, D. Aarsland, E. Jones, Alzheimer's disease, Lancet (377) (2011) 1019–1031.
- [7] B. Nmezi, J. Xu, R. Fu, et al., Concentric organization of A- and B-type lamins predicts their distinct roles in the spatial organization and stability of the nuclear lamina, Proc. Natl. Acad. Sci. U S A. 116 (10) (2019) 4307–4315, doi:10.1073/ pnas.1810070116.
- [8] T. Shimi, M. Kittisopikul, J. Tran, et al., Structural organization of nuclear lamins A, C, B1, and B2 revealed by superresolution microscopy, Mol. Biol. Cell 26 (22) (2015) 4075–4086.
- [9] J.L. Broers, B.M. Machiels, H.J. Kuijpers, et al., A- and B-type lamins are differentially expressed in normal human tissues, Histochem. Cell Biol. 107 (6) (1997) 505–517.
- [10] F. Lin, H.J. Worman, Expression of nuclear lamins in human tissues and cancer cell lines and transcription from the promoters of the lamin A/C and B1 genes, Exp. Cell Res. 236 (2) (1997) 378–384, doi:10.1006/excr.1997.3735.
- [11] C.M. Tilli, F.C. Ramaekers, J.L. Broers, C.J. Hutchison, H.A. Neumann, Lamin expression in normal human skin, actinic keratosis, squamous cell carcinoma and basal cell carcinoma, Br. J. Dermatol. 148 (1) (2003) 102–109.
- [12] E.C. Schirmer, L. Gerace, The stability of the nuclear lamina polymer changes with the composition of lamin subtypes according to their individual binding strengths, J. Biol. Chem. 279 (41) (2004) 42811–42817, doi:10.1074/ jbc.M407705200.
- [13] J. Swift, I.L. Ivanovska, A. Buxboim, et al., Nuclear lamin-A scales with tissue stiffness and enhances matrix-directed differentiation, Science 341 (6149) (2013) 1240104.
- [14] O. Wintner, N. Hirsch-Attas, M. Schlossberg, et al., A unified linear viscoelastic model of the cell nucleus defines the mechanical contributions of lamins and chromatin, Adv. Sci. Weinh. (Weinh) 7 (8) (2020) 1901222, doi:10.1002/ advs.201901222.
- [15] F. Martins, J. Sousa, C.D. Pereira, O.A.B. da Cruz E Silva, S. Rebelo, Nuclear envelope dysfunction and its contribution to the aging process, Aging Cell 19 (5) (2020) e13143.
- [16] I. Méndez-López, I. Blanco-Luquin, J. Sánchez-Ruiz de Gordoa, et al., Hippocampal LMNA gene expression is increased in late-stage alzheimer's disease, Int. J. Mol. Sci. 20 (4) (2019) 878.

- [17] L. Gil, S.A. Niño, E. Chi-Ahumada, et al., Perinuclear lamin a and nucleoplasmic lamin B2 characterize two types of hippocampal neurons through alzheimer's disease progression, Int. J. Mol. Sci. 21 (5) (2020) 1841, doi:10.3390/ ijms21051841.
- [18] B. Frost, M. Hemberg, J. Lewis, M.B. Feany, Tau promotes neurodegeneration through global chromatin relaxation, Nat. Neurosci. 17 (3) (2014) 357–366, doi:10.1038/nn.3639.
- [19] B. Frost, Alzheimer's disease: an acquired neurodegenerative laminopathy [published correction appears in extra view to: Frost B., Bardai F.H., Feany M.B. 2016. Lamin disfunction mediates neurodegeneration in taupathies. Current Biology 26(1):129–136. http://dx.doi.org/10.1016/j.cub.2015.11.039], Nucleus 7 (3) (2016) 275–283.
- [20] Y. Takamori, Y. Hirahara, T. Wakabayashi, et al., Differential expression of nuclear lamin subtypes in the neural cells of the adult rat cerebral cortex, IBRO Rep. 5 (2018) 99–109.
- [21] T. Wakabayashi, T. Mori, Y. Hirahara, et al., Nuclear lamins are differentially expressed in retinal neurons of the adult rat retina, Histochem. Cell Biol. 136 (4) (2011) 427–436.
- [22] D.N. Simon, K.L. Wilson, The nucleoskeleton as a genome-associated dynamic network of networks', Nat. Rev. Mol. Cell Biol. 12 (Oct. 11) (2011) 695–708, doi:10.1038/nrm3207.
- [23] S. Cho, M. Vashisth, A. Abbas, et al., Mechanosensing by the Lamina Protects against nuclear rupture, DNA damage, and cell-cycle arrest, Dev. Cell 49 (6) (2019) 920-935.e5.
- [24] J. Lammerding, L.G. Fong, J.Y. Ji, et al., Lamins A and C but not lamin B1 regulate nuclear mechanics, J. Biol. Chem. 281 (35) (2006) 25768–25780, doi:10.1074/jbc.M513511200.
- [25] S. Gonzalo, R. Kreienkamp, P. Askjaer, Hutchinson-Gilford Progeria Syndrome: a premature aging disease caused by LMNA gene mutations, Ageing Res. Rev. 33 (2017) 18–29.
- [26] A. De Sandre-Giovannoli, R. Bernard, P. Cau, et al., Lamin a truncation in Hutchinson-Gilford progeria, Science 300 (5628) (2003) 2055, doi:10.1126/ science.1084125.
- [27] M. Eriksson, W.T. Brown, L.B. Gordon, et al., Recurrent de novo point mutations in lamin A cause Hutchinson-Gilford progeria syndrome, Nature 423 (6937) (2003) 293–298.
- [28] M.W. Glynn, T.W. Glover, Incomplete processing of mutant lamin A in Hutchinson-Gilford progeria leads to nuclear abnormalities, which are reversed by farnesyltransferase inhibition, Hum. Mol. Genet. 14 (20) (2005) 2959–2969, doi:10.1093/hmg/ddi326.
- [29] T. Dechat, T. Shimi, S.A. Adam, et al., Alterations in mitosis and cell cycle progression caused by a mutant lamin A known to accelerate human aging, Proc. Natl. Acad. Sci. U.S.A. 104 (12) (2007) 4955–4960, doi:10.1073/ pnas.0700854104.
- [30] R.D. Goldman, D.K. Shumaker, M.R. Erdos, et al., Accumulation of mutant lamin A causes progressive changes in nuclear architecture in Hutchinson-Gilford progeria syndrome, Proc. Natl. Acad. Sci. U.S.A. 101 (24) (2004) 8963–8968, doi:10.1073/pnas.0402943101.
- [31] I. Solovei, A.S. Wang, K. Thanisch, et al., LBR and lamin A/C sequentially tether peripheral heterochromatin and inversely regulate differentiation, Cell 152 (3) (2013) 584–598.
- [32] K. Gesson, P. Rescheneder, M.P. Skoruppa, A. von Haeseler, T. Dechat, R. Foisner, A-type lamins bind both hetero- and euchromatin, the latter being regulated by lamina-associated polypeptide 2 alpha, Genome Res. 26 (4) (2016) 462–473.
- [33] I. Bronshtein, E. Kepten, I. Kanter, et al., Loss of lamin A function increases chromatin dynamics in the nuclear interior, Nat. Commun. 6 (2015) 8044.
- [34] P. Scaffidi, T. Misteli, Lamin A-dependent nuclear defects in human aging, Science 312 (5776) (2006) 1059–1063, doi:10.1126/science.1127168.
- [35] T. Arendt, M.K. Brückner, H.J. Gertz, L. Marcova, Cortical distribution of neurofibrillary tangles in Alzheimer's disease matches the pattern of neurons that retain their capacity of plastic remodeling in the adult brain, Neuroscience 83 (4) (1998) 991–1002.
- [36] P. Møller, M. Løhr, J.K. Folkmann, L. Mikkelsen, S. Loft, Aging and oxidatively damaged nuclear DNA in animal organs, Free Radic. Biol. Med. 48 (10) (2010) 1275–1285.
- [37] B. Nie, W. Gan, F. Shi, et al., Age-dependent accumulation of 8-oxoguanine in the DNA and RNA in various rat tissues, Oxid. Med. Cell. Longev. 2013 (2013) 303181.
- [38] K.D. Jacob, N. Noren Hooten, A.R. Trzeciak, M.K. Evans, Markers of oxidant stress that are clinically relevant in aging and age-related disease, Mech. Ageing Dev. 134 (3–4) (2013) 139–157.
- [39] J.P. Soares, A. Cortinhas, T. Bento, et al., Aging and DNA damage in humans: a meta-analysis study, Aging (Albany NY). 6 (6) (2014) 432–439, doi:10.18632/ aging.100667.
- [40] R. Sabin, G. Pucci, R.M. Anderson, DNA damage processing is perturbed in both proliferative and non-proliferative cells of increased chronological cellular age, Radiat. Res. 192 (2) (2019) 200–207, doi:10.1667/RR15348.1.
- [41] J. Wang, C.L. Clauson, P.D. Robbins, L.J. Niedernhofer, Y. Wang, The oxidative DNA lesions 8,5'-cyclopurines accumulate with aging in a tissue-specific manner, Aging Cell 11 (4) (2012) 714–716, doi:10.1111/j.1474-9726.2012.00828.x.
- [42] I. Beerman, J. Seita, M.A. Inlay, I.L. Weissman, D.J. Rossi, Quiescent hematopoietic stem cells accumulate DNA damage during aging that is repaired upon entry into cell cycle, Cell Stem Cell 15 (1) (2014) 37–50, doi:10.1016/ j.stem.2014.04.016.
- [43] M.E. Dollé, H. Giese, C.L. Hopkins, H.J. Martus, J.M. Hausdorff, J. Vijg, Rapid accumulation of genome rearrangements in liver but not in brain of old mice, Nat. Genet. 17 (4) (1997) 431–434, doi:10.1038/ng1297-431.
- [44] O.A. Sedelnikova, I. Horikawa, C. Redon, et al., Delayed kinetics of DNA double-strand break processing in normal and pathological aging, Aging Cell 7 (1) (2008) 89–100.

- [45] Z. Li, W. Zhang, Y. Chen, et al., Impaired DNA double-strand break repair contributes to the age-associated rise of genomic instability in humans, Cell Death Differ. 23 (11) (2016) 1765–1777, doi:10.1038/cdd.2016.65.
- [46] Y. Wei, M.H. Qu, X.S. Wang, et al., Binding to the minor groove of the double-strand, tau protein prevents DNA from damage by peroxidation, PLoS One 3 (7) (2008) e2600.
- [47] H. Qi, F.X. Cantrelle, H. Benhelli-Mokrani, et al., Nuclear magnetic resonance spectroscopy characterization of interaction of Tau with DNA and its regulation by phosphorylation, Biochemistry 54 (7) (2015) 1525–1533, doi:10.1021/ bi5014613.
- [48] M.K. Sjöberg, E. Shestakova, Z. Mansuroglu, R.B. Maccioni, E. Bonnefoy, Tau protein binds to pericentromeric DNA: a putative role for nuclear tau in nucleolar organization, J. Cell. Sci. 119 (Pt 10) (2006) 2025–2034, doi:10.1242/jcs.02907.
- [49] P. Vasudevaraju, E. Guerrero, M.L. Hegde, T.B. Collen, G.B. Britton, K.S. Rao, New evidence on α-synuclein and Tau binding to conformation and sequence specific GC* rich DNA: relevance to neurological disorders, J. Pharm. Bioallied Sci. 4 (2) (2012) 112–117.
- [50] M. Bukar Maina, Y.K. Al-Hilaly, L.C. Serpell, Nuclear tau and its potential role in alzheimer's disease, Biomolecules 6 (1) (2016) 9, doi:10.3390/biom6010009.
- [51] M. Violet, L. Delattre, M. Tardivel, et al., A major role for Tau in neuronal DNA and RNA protection in vivo under physiological and hyperthermic conditions, Front. Cell. Neurosci. 8 (2014) 84, doi:10.3389/fncel.2014.00084.
- [52] Q. Hua, R.Q. He, N. Haque, et al., Microtubule associated protein tau binds to double-stranded but not single-stranded DNA, Cell. Mol. Life Sci. 60 (2) (2003) 413–421.
- [53] M.L. Hegde, A.K. Mantha, T.K. Hazra, K.K. Bhakat, S. Mitra, B. Szczesny, Oxidative genome damage and its repair: implications in aging and neurodegenerative diseases, Mech. Ageing Dev. 133 (4) (2012) 157–168, doi:10.1016/j.mad.2012.01.005.
- [54] M.A. Bradley-Whitman, M.D. Timmons, T.L. Beckett, M.P. Murphy, B.C. Lynn, M.A. Lovell, Nucleic acid oxidation: an early feature of Alzheimer's disease, J. Neurochem. 128 (2) (2014) 294–304.
- [55] B.P. Rutten, C. Schmitz, O.H. Gerlach, et al., The aging brain: accumulation of DNA damage or neuron loss?, Neurobiol. Aging 28 (1) (2007) 91–98.
- [56] L. Gil, C. Federico, F. Pinedo, et al., Aging dependent effect of nuclear tau, Brain Res. 1677 (2017) 129–137, doi:10.1016/j.brainres.2017.09.030.
- [57] Z. Mansuroglu, H. Benhelli-Mokrani, V. Marcato, et al., Loss of Tau protein affects the structure, transcription and repair of neuronal pericentromeric heterochromatin, Sci. Rep. 6 (2016) 33047.
- [58] E. Bou Samra, G. Buhagiar-Labarchède, C. Machon, et al., A role for Tau protein in maintaining ribosomal DNA stability and cytidine deaminase-deficient cell survival, Nat. Commun. 8 (1) (2017) 693, doi:10.1038/s41467-017-00633-1.
- [59] G. Rossi, L. Dalprà, F. Crosti, et al., A new function of microtubule-associated protein tau: involvement in chromosome stability, Cell Cycle 7 (12) (2008) 1788–1794.
- [60] Y. Ishimi, M. Kojima, F. Takeuchi, T. Miyamoto, M. Yamada, F. Hanaoka, Changes in chromatin structure during aging of human skin fibroblasts, Exp. Cell Res. 169 (2) (1987) 458–467.
- [61] A. Macieira-Coelho, F. Puvion-Dutilleul, Evaluation of the reorganization in the high-order structure of DNA occurring during cell senescence, Mutat. Res. 219 (3) (1989) 165–170.
- [62] B. Villeponteau, The heterochromatin loss model of aging, Exp. Gerontol. 32 (4–5) (1997) 383–394, doi:10.1016/s0531-5565(96)00155-6.
- [63] D.A. Sinclair, L. Guarente, Extrachromosomal rDNA circles--a cause of aging in yeast, Cell 91 (7) (1997) 1033–1042, doi:10.1016/s0092-8674(00)80493-6.
- [64] D.A. Sinclair, K. Mills, L. Guarente, Molecular mechanisms of yeast aging, Trends Biochem. Sci. 23 (4) (1998) 131–134, doi:10.1016/s0968-0004(98)01188-8.
 [65] J.M. Sedim, C. Baumetha, B.D. Adama Asima have a simular set of the set of
- [65] J.M. Sedivy, G. Banumathy, P.D. Adams, Aging by epigenetics--a consequence of chromatin damage?, Exp. Cell Res. 314 (9) (2008) 1909–1917, doi:10.1016/ j.yexcr.2008.02.023.
- [66] Z. Hu, K. Chen, Z. Xia, et al., Nucleosome loss leads to global transcriptional up-regulation and genomic instability during yeast aging, Genes Dev. 28 (4) (2014) 396–408.
- [67] R.J. O'Sullivan, J. Karlseder, The great unravelling: chromatin as a modulator of the aging process, Trends Biochem. Sci. 37 (11) (2012) 466–476, doi:10.1016/ j.tibs.2012.08.001.
- [68] S. Camero, M.J. Benítez, A. Barrantes, et al., Tau protein provides DNA with thermodynamic and structural features which are similar to those found in histone-DNA complex, J. Alzheimers Dis. 39 (3) (2014) 649–660, doi:10.3233/ JAD-131415.
- [69] A. Sultan, F. Nesslany, M. Violet, et al., Nuclear tau, a key player in neuronal DNA protection, J. Biol. Chem. 286 (6) (2011) 4566–4575, doi:10.1074/ jbc.M110.199976.
- [70] K. Hernández-Ortega, P. Garcia-Esparcia, L. Gil, J.J. Lucas, I. Ferrer, Altered machinery of protein synthesis in alzheimer's: from the nucleolus to the ribosome, Brain Pathol. 26 (5) (2016) 593–605, doi:10.1111/bpa.12335.
- [71] H.U. Klein, C. McCabe, E. Gjoneska, et al., Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimer's human brains, Nat. Neurosci. 22 (1) (2019) 37–46, doi:10.1038/ s41593-018-0291-1.
- [72] V. Khurana, P. Merlo, B. DuBoff, et al., A neuroprotective role for the DNA damage checkpoint in tauopathy, Aging Cell 11 (2) (2012) 360–362.
- [73] P. Tokarz, K. Kaarniranta, J. Blasiak, Role of the cell cycle Re-Initiation in DNA damage response of post-mitotic cells and its implication in the pathogenesis of neurodegenerative diseases, Rejuvenation Res. 19 (2) (2016) 131–139.
- [74] C. Guo, H.H. Jeong, Y.C. Hsieh, et al., Tau activates transposable elements in alzheimer's disease, Cell Rep. 23 (10) (2018) 2874–2880, doi:10.1016/ j.celrep.2018.05.004.
- [75] B. Eftekharzadeh, J.G. Daigle, L.E. Kapinos, et al., Tau protein disrupts nucleocytoplasmic transport in Alzheimer's disease [published correction appears

in Neuron. 2019 Jan 16;101(2):349], Neuron 99 (5) (2018) 925-940.e7, doi:10.1016/j.neuron.2018.07.039.

- [76] P.L. De Jager, Y. Ma, C. McCabe, J. Xu, B.N. Vardarajan, D. Felsky, H.U. Klein, C.C. White, M.A. Peters, B. Lodgson, P. Nejad, A. Tang, L.M. Mangravite, L. Yu, C. Gaiteri, S. Mostafavi, J.A. Schneider, D.A. Bennett, A multi-omic atlas of the human frontal cortex for aging and Alzheimer's disease research, Sci. Data 5 (August) (2018) 180142, doi:10.1038/sdata.2018.142.
- [77] R. Nativio, G. Donahue, A. Berson, et al., Dysregulation of the epigenetic landscape of normal aging in Alzheimer's disease [published correction appears in Nat Neurosci. 2018 Mar 19], Nat. Neurosci. 21 (4) (2018) 497–505, doi:10.1038/ s41593-018-0101-9.
- [78] T. Lu, L. Aron, J. Zullo, et al., REST and stress resistance in ageing and Alzheimer's disease, Nature 507 (7493) (2014) 448–454, doi:10.1038/ nature13163.
- [79] H. Benhelli-Mokrani, Z. Mansuroglu, A. Chauderlier, et al., Genome-wide identification of genic and intergenic neuronal DNA regions bound by Tau protein under physiological and stress conditions, Nucleic Acids Res. 46 (21) (2018) 11405–11422.
- [80] J.M. Zullo, I.A. Demarco, R. Piqué-Regi, et al., DNA sequence-dependent compartmentalization and silencing of chromatin at the nuclear lamina, Cell 149 (7) (2012) 1474–1487.
- [81] M. Magistri, M.A. Faghihi, G. St Laurent 3rd, C. Wahlestedt, Regulation of chromatin structure by long noncoding RNAs: focus on natural antisense transcripts, Trends Genet. 28 (8) (2012) 389–396, doi:10.1016/j.tig.2012.03.013.
- [82] T. Chen, S.Y. Dent, Chromatin modifiers and remodellers: regulators of cellular differentiation, Nat. Rev. Genet. 15 (2) (2014) 93–106, doi:10.1038/nrg3607.
- [83] F. Erdel, K. Müller-Ott, K. Rippe, Establishing epigenetic domains via chromatin-bound histone modifiers, Ann. N. Y. Acad. Sci. 1305 (2013) 29–43, doi:10.1111/nyas.12262.
- [84] J. Signolet, B. Hendrich, The function of chromatin modifiers in lineage commitment and cell fate specification, FEBS J. 282 (9) (2015) 1692–1702, doi:10.1111/febs.13132.
- [85] R.C. Burgess, T. Misteli, P. Oberdoerffer, DNA damage, chromatin, and transcription: the trinity of aging, Curr. Opin. Cell Biol. 24 (6) (2012) 724–730.
- [86] T. Dimauro, G. David, Chromatin modifications: the driving force of senescence and aging?, Aging (Albany NY) 1 (2) (2009) 182–190, doi:10.18632/ aging.100023.
- [87] B. Liu, R.Kh Yip, Z. Zhou, Chromatin remodeling, DNA damage repair and aging, Curr. Genomics 13 (7) (2012) 533–547, doi:10.2174/138920212803251373.
- [88] M. Hokama, S. Oka, J. Leon, et al., Altered expression of diabetes-related genes in Alzheimer's disease brains: the Hisayama study, Cereb. Cortex 24 (9) (2014) 2476–2488.
- [89] A. Miyashita, H. Hatsuta, M. Kikuchi, et al., Genes associated with the progression of neurofibrillary tangles in Alzheimer's disease, Transl. Psychiatry 4 (6) (2014) e396.
- [90] E. Castillo, J. Leon, G. Mazzei, et al., Comparative profiling of cortical gene expression in Alzheimer's disease patients and mouse models demonstrates a link between amyloidosis and neuroinflammation, Sci. Rep. 7 (1) (2017) 17762.
- [91] Q. Luo, Y. Chen, Long noncoding RNAs and Alzheimer's disease, Clin. Interv. Aging 11 (2016) 867–872, doi:10.2147/CIA.S107037.
- [92] P. Riva, A. Ratti, M. Venturin, The long non-coding RNAs in neurodegenerative diseases: novel mechanisms of pathogenesis, Curr. Alzheimer Res. 13 (11) (2016) 1219–1231.
- [93] M. Hetman, M. Pietrzak, Emerging roles of the neuronal nucleolus, Trends Neurosci. 35 (5) (2012) 305–314, doi:10.1016/j.tins.2012.01.002.
- [94] R. Parlato, G. Kreiner, Nucleolar activity in neurodegenerative diseases: a missing piece of the puzzle?, J. Mol. Med. 91 (5) (2013) 541–547.
- [95] V.C. Thurston, R.P. Zinkowski, L.I. Binder, Tau as a nucleolar protein in human nonneural cells in vitro and in vivo, Chromosoma 105 (1) (1996) 20–30, doi:10.1007/BF02510035.
- [96] C. Federico, L. Gil, F. Bruno, A.G. D'Amico, V. D'Agata, S. Saccone, Phosphorylated nucleolar Tau protein is related to the neuronal in vitro differentiation, Gene 664 (2018) 1–11.
- [97] I. Sotiropoulos, M.C. Galas, J.M. Silva, E. Skoulakis, S. Wegmann, M.B. Maina, D. Blum, C.L. Sayas, E.M. Mandelkow, E.M. Mandelkow, M.G. Spillantini, N. Sousa, J. Avila, M. Medina, A. Mudher, L. Buee, Atypical, non-standard functions of the microtubule associated Tau protein, Acta Neuropathol. Commun. 5 (Nov. 1) (2017) 91, doi:10.1186/s40478-017-0489-6.
- [98] V. Jaber, Y. Zhao, W.J. Lukiw, Alterations in micro RNA-messenger RNA (miRNA-mRNA) coupled signaling networks in sporadic alzheimer's disease (AD) hippocampal CA1, J. Alzheimers Dis. Parkinsonism 7 (2) (2017) 312, doi:10.4172/2161-0460.1000312.
- [99] Y.C. Hsieh, C. Guo, H.K. Yalamanchili, et al., Tau-mediated disruption of the spliceosome triggers cryptic RNA splicing and neurodegeneration in alzheimer's disease, Cell Rep. 29 (2) (2019) 301-316.e10, doi:10.1016/j.celrep.2019.08.104.
- [100] M.L. Fishel, M.R. Vasko, M.R. Kelley, DNA repair in neurons: so if they don't divide what's to repair?, Mutat. Res. 614 (1–2) (2007) 24–36.
- [101] A.R. Silva, A.C. Santos, J.M. Farfel, et al., Repair of oxidative DNA damage, cell-cycle regulation and neuronal death may influence the clinical manifestation of Alzheimer's disease, PLoS One 9 (6) (2014) e99897, doi:10.1371/ journal.pone.0099897.
- [102] T. Lu, Y. Pan, S.Y. Kao, et al., Gene regulation and DNA damage in the ageing human brain, Nature 429 (6994) (2004) 883–891, doi:10.1038/nature02661.
- [103] E. Jacobsen, T. Beach, Y. Shen, R. Li, Y. Chang, Deficiency of the Mre11 DNA repair complex in Alzheimer's disease brains, Brain Res. Mol. Brain Res. 128 (1) (2004) 1–7.
- [104] E.I. Schwartz, L.B. Smilenov, M.A. Price, et al., Cell cycle activation in postmitotic neurons is essential for DNA repair, Cell Cycle 6 (3) (2007) 318–329.
- [105] C. Joseph, A.S. Mangani, V. Gupta, N. Chitranshi, T. Shen, Y. Dheer, D. Kb, M. Mirzaei, Y. You, S.L. Graham, V. Gupta, Cell cycle deficits in neurodegenerative

disorders: uncovering molecular mechanisms to drive innovative therapeutic development, Aging Dis. 11 (4) (2020) 946–966.

- [106] S. Ren, B.J. Rollins, Cyclin C/cdk3 promotes Rb-dependent G0 exit, Cell 117 (2) (2004) 239–251, doi:10.1016/s0092-8674(04)00300-9.
- [107] A. Tomashevski, D.R. Webster, P. Grammas, M. Gorospe, I.I. Kruman, Cyclin-C-dependent cell-cycle entry is required for activation of non-homologous end joining DNA repair in postmitotic neurons, Cell Death Differ. 17 (7) (2010) 1189–1198.
- [108] Z. Nagy, M.M. Esiri, A.D. Smith, The cell division cycle and the pathophysiology of Alzheimer's disease, Neuroscience 87 (4) (1998) 731–739.
- [109] T. Arendt, M.K. Brückner, B. Mosch, A. Lösche, Selective cell death of hyperploid neurons in Alzheimer's disease, Am. J. Pathol. 177 (1) (2010) 15–20.
- [110] E. Barrio-Alonso, A. Hernández-Vivanco, C.C. Walton, G. Perea, J.M. Frade, Cell cycle reentry triggers hyperploidization and synaptic dysfunction followed by delayed cell death in differentiated cortical neurons, Sci. Rep. 8 (1) (2018) 14316 Published 2018 Sep 25, doi:10.1038/s41598-018-32708-4.
- [111] K. Herrup, R. Neve, S.L. Ackerman, A. Copani, Divide and die: cell cycle events as triggers of nerve cell death, J. Neurosci. 24 (42) (2004) 9232–9239.
- [112] A. McShea, H.G. Lee, R.B. Petersen, et al., Neuronal cell cycle re-entry mediates Alzheimer disease-type changes, Biochim. Biophys. Acta 1772 (4) (2007) 467–472.
- [113] M.E. Seward, E. Swanson, A. Norambuena, et al., Amyloid-β signals through tau to drive ectopic neuronal cell cycle re-entry in Alzheimer's disease, J. Cell. Sci. 126 (Pt 5) (2013) 1278–1286, doi:10.1242/jcs.1125880.
- [114] C. Andorfer, C.M. Acker, Y. Kress, P.R. Hof, K. Duff, P. Davies, Cell-cycle reentry and cell death in transgenic mice expressing nonmutant human tau isoforms, J. Neurosci. 25 (22) (2005) 5446–5454, doi:10.1523/JNEUROSCI.4637-04.2005.
- [115] T. Hayashi, N. Shishido, K. Nakayama, et al., Lipid peroxidation and 4-hydroxy-2-nonenal formation by copper ion bound to amyloid-beta peptide, Free Radic. Biol. Med. 43 (11) (2007) 1552–1559, doi:10.1016/ j.freeradbiomed.2007.08.013.
- [116] M. Nakamura, N. Shishido, A. Nunomura, et al., Three histidine residues of amyloid-beta peptide control the redox activity of copper and iron, Biochemistry 46 (44) (2007) 12737–12743.
- [117] E. Tamagno, P. Bardini, A. Obbili, et al., Oxidative stress increases expression and activity of BACE in NT2 neurons, Neurobiol. Dis. 10 (3) (2002) 279–288.
- [118] E. Tamagno, M. Guglielmotto, M. Aragno, et al., Oxidative stress activates a positive feedback between the gamma- and beta-secretase cleavages of the beta-amyloid precursor protein, J. Neurochem. 104 (3) (2008) 683–695.
- [119] R.D. Moir, M. Montag-Lowy, R.D. Goldman, Dynamic properties of nuclear lamins: lamin B is associated with sites of DNA replication, J. Cell Biol. 125 (6) (1994) 1201–1212.
- [120] I.R. Kill, C.J. Hutchison, S-phase phosphorylation of lamin B2, FEBS Lett. 377 (1) (1995) 26–30.
- [121] J.M. Frade, N. López-Sánchez, Neuronal tetraploidy in Alzheimer and aging,
- Aging (Albany NY) 9 (10) (2017) 2014–2015, doi:10.18632/aging.101312. [122] Y. Yang, E.J. Mufson, K. Herrup, Neuronal cell death is preceded by cell cycle
- events at all stages of Alzheimer's disease, J. Neurosci. 23 (7) (2003) 2557–2563.
 [123] E. Barrio-Alonso, B. Fontana, M. Valero, J.M. Frade, Pathological aspects of neuronal hyperploidization in alzheimer's disease evidenced by computer
- simulation, Front. Genet. 11 (287) (2020) Published 2020 Mar 27.
 [124] D.X. Liu, L.A. Greene, Neuronal apoptosis at the G1/S cell cycle checkpoint, Cell Tissue Res. 305 (2) (2001) 217–228, doi:10.1007/s004410100396.
- [125] E.B. Becker, A. Bonni, Cell cycle regulation of neuronal apoptosis in development and disease, Prog. Neurobiol. 72 (1) (2004) 1–25.
- [126] A. Giovanni, F. Wirtz-Brugger, E. Keramaris, R. Slack, D.S. Park, Involvement of cell cycle elements, cyclin-dependent kinases, pRb, and E2F x DP, in B-amyloid-induced neuronal death, J. Biol. Chem. 274 (27) (1999) 19011–19016, doi:10.1074/jbc.274.27.19011.
- [127] Y. Yang, N.H. Varvel, B.T. Lamb, K. Herrup, Ectopic cell cycle events link human Alzheimer's disease and amyloid precursor protein transgenic mouse models, J. Neurosci. 26 (3) (2006) 775–784, doi:10.1523/JNEUROSCI.3707-05.2006.
- [128] J.P. Lopes, M. Blurton-Jones, T.R. Yamasaki, P. Agostinho, F.M. LaFerla, Activation of cell cycle proteins in transgenic mice in response to neuronal loss but not amyloid-beta and tau pathology, J. Alzheimers Dis. 16 (3) (2009) 541–549, doi:10.3233/JAD-2009-0993.
- [129] A. Saul, F. Sprenger, T.A. Bayer, O. Wirths, Accelerated tau pathology with synaptic and neuronal loss in a novel triple transgenic mouse model of Alzheimer's disease, Neurobiol. Aging 34 (11) (2013) 2564–2573, doi:10.1016/ j.neurobiolaging.2013.05.003.
- [130] A. Arner, E. Rockenstein, M. Mante, et al., Increased vulnerability of the Hippocampus in transgenic mice overexpressing APP and triple repeat tau, J. Alzheimers Dis. 61 (3) (2018) 1201–1219, doi:10.3233/JAD-170388.
- [131] F.A. Schmitt, D.G. Davis, D.R. Wekstein, C.D. Smith, J.W. Ashford, W.R. Markesbery, "Preclinical" AD revisited: neuropathology of cognitively normal older adults, Neurology 55 (3) (2000) 370–376, doi:10.1212/wnl.55.3.370.
- [132] C.F. Lippa, J.E. Hamos, D. Pulaski-Salo, L.J. DeGennaro, D.A. Drachman, Alzheimer's disease and aging: effects on perforant pathway perikarya and synapses, Neurobiol. Aging 13 (3) (1992) 405–411, doi:10.1016/ 0197-4580(92)90115-e.
- [133] Y. Fukutani, K. Kobayashi, I. Nakamura, K. Watanabe, K. Isaki, N.J. Cairns, Neurons, intracellular and extracellular neurofibrillary tangles in subdivisions of the hippocampal cortex in normal ageing and Alzheimer's disease, Neurosci. Lett. 200 (1) (1995) 57–60.
- [134] H.G. Lee, G. Perry, P.I. Moreira, et al., Tau phosphorylation in Alzheimer's disease: pathogen or protector?, Trends Mol. Med. 11 (4) (2005) 164–169.
- [135] T. Gómez-Isla, R. Hollister, H. West, et al., Neuronal loss correlates with but exceeds neurofibrillary tangles in Alzheimer's disease, Ann. Neurol. 41 (1) (1997) 17–24.
- [136] S. Jeganathan, A. Hascher, S. Chinnathambi, J. Biernat, E.M. Mandelkow, E.M.

induces a compaction of the paperclip folding of Tau and generates a pathological (MC-1) conformation, J. Biol. Chem. 283 (46) (2008) 32066–32076, doi:10.1074/jbc.M805300200.

- Y. Wang, E. Mandelkow, Tau in physiology and pathology, Nat. Rev. Neurosci. 17 (1) (2016) 5–21, doi:10.1038/nrn.2015.1.
- [138] W. Li, X.S. Wang, M.H. Qu, Y. Liu, R.Q. He, Human protein tau represses DNA replication in vitro, Biochim, Biophys. Acta 1726 (3) (2005) 280–286.
- [139] M. Regalado-Reyes, D. Furcila, F. Hernández, J. Ávila, J. DeFelipe, G. León-Espinosa, Phospho-tau changes in the human CA1 during alzheimer's disease progression, J. Alzheimers Dis. 69 (1) (2019) 277–288, doi:10.3233/JAD-181263.
- [140] K. Okamoto, M. Amari, T. Fukuda, K. Suzuki, M. Takatama, Comparison of AT8 immunoreactivity in the locus ceruleus and hippocampus of 154 brains from routine autopsies, Neuropathology 37 (4) (2017) 306–310, doi:10.1111/ neup.12367.
- [141] P.A. Loomis, T.H. Howard, R.P. Castleberry, L.I. Binder, Identification of nuclear tau isoforms in human neuroblastoma cells, Proc. Natl. Acad. Sci. U S A 87 (21) (1990) 8422–8426.
- [142] R.M. Brady, R.P. Zinkowski, L.I. Binder, Presence of tau in isolated nuclei from human brain, Neurobiol. Aging 16 (3) (1995) 479–486.
- [143] M.B. Maina, L.J. Bailey, S. Wagih, et al., The involvement of tau in nucleolar transcription and the stress response, Acta Neuropathol. Commun. 6 (1) (2018) 70, doi:10.1186/s40478-018-0565-6.
- [144] M.H. Qu, H. Li, R. Tian, et al., Neuronal tau induces DNA conformational changes observed by atomic force microscopy, Neuroreport 15 (18) (2004) 2723–2727.
- [145] Q. Ain, C. Schmeer, D. Penndorf, et al., Cell cycle-dependent and -independent telomere shortening accompanies murine brain aging, Aging (Albany NY) 10 (11) (2018) 3397–3420.
- [146] M.C. Hoenig, G.N. Bischof, J. Seemiller, et al., Networks of tau distribution in Alzheimer's disease, Brain 141 (2) (2018) 568–581, doi:10.1093/brain/awx353.
- [147] S. Meier, M. Bell, D.N. Lyons, et al., Pathological tau promotes neuronal damage by impairing ribosomal function and decreasing protein synthesis, J. Neurosci. 36 (3) (2016) 1001–1007.
- [148] S.A. Koren, S. Galvis-Escobar, J.F. Abisambra, Tau-mediated dysregulation of RNA: evidence for a common molecular mechanism of toxicity in frontotemporal dementia and other tauopathies, Neurobiol. Dis. 141 (2020) 104939.
- [149] J.F. Abisambra, U.K. Jinwal, L.J. Blair, et al., Tau accumulation activates the unfolded protein response by impairing endoplasmic reticulum-associated degradation, J. Neurosci. 33 (22) (2013) 9498–9507.
- [150] H.T. Evans, J. Benetatos, M. van Roijen, L.G. Bodea, J. Götz, Decreased synthesis of ribosomal proteins in tauopathy revealed by non-canonical amino acid labelling, EMBO J. 38 (13) (2019) e101174, doi:10.15252/embj.2018101174.
- [151] D. Ranade, R. Pradhan, M. Jayakrishnan, S. Hegde, K. Sengupta, Lamin A/C and Emerin depletion impacts chromatin organization and dynamics in the interphase nucleus, BMC Mol Cell Biol. 20 (1) (2019) 11, doi:10.1186/s12860-019-0192-5.
- [152] S. Gonzalo, DNA damage and lamins, Adv. Exp. Med. Biol. 773 (2014) 377-399.
 - [153] S. Ghosh, B. Liu, Y. Wang, Q. Hao, Z. Zhou, Lamin a is an endogenous SIRT6 activator and promotes SIRT6-Mediated DNA repair, Cell Rep. 13 (7) (2015) 1396–1406.
 - [154] S. Maynard, G. Keijzers, M. Akbari, et al., Lamin A/C promotes DNA base excision repair, Nucleic Acids Res. 47 (22) (2019) 11709–11728, doi:10.1093/nar/gkz912.
 - [155] A. Currais, T. Hortobágyi, S. Soriano, The neuronal cell cycle as a mechanism of pathogenesis in Alzheimer's disease, Aging (Albany NY). 1 (4) (2009) 363–371.
 - [156] P. Sabatelli, G. Lattanzi, A. Ognibene, et al., Nuclear alterations in autosomal-dominant Emery-Dreifuss muscular dystrophy, Muscle Nerve 24 (6) (2001) 826–829.
 - [157] I. Gonzalez-Suarez, S. Gonzalo, Nurturing the genome: A-type lamins preserve genomic stability, Nucleus 1 (2) (2010) 129–135, doi:10.4161/nucl.1.2.10797.
 - [158] M. Pietrzak, G. Rempala, P.T. Nelson, J.J. Zheng, M. Hetman, Epigenetic silencing of nucleolar rRNA genes in Alzheimer's disease, PLoS One 6 (7) (2011) e22585.
 - [159] J. Hallgren, M. Pietrzak, G. Rempala, P.T. Nelson, M. Hetman, Neurodegeneration-associated instability of ribosomal DNA, Biochim. Biophys. Acta 1842 (6) (2014) 860–868.
 - [160] O. Ogawa, X. Zhu, H.G. Lee, et al., Ectopic localization of phosphorylated histone H3 in Alzheimer's disease: a mitotic catastrophe?, Acta Neuropathol. 105 (5) (2003) 524–528.
 - [161] D.J. Bonda, V.P. Bajić, B. Spremo-Potparevic, et al., Review: cell cycle aberrations and neurodegeneration, Neuropathol. Appl. Neurobiol. 36 (2) (2010) 157–163.
 - [162] G.U. Höglinger, J.J. Breunig, C. Depboylu, et al., The pRb/E2F cell-cycle pathway mediates cell death in Parkinson's disease, Proc. Natl. Acad. Sci. U S A. 104 (9) (2007) 3585–3590.
 - [163] M.D. Nguyen, J.P. Julien, Cyclin-dependent kinase 5 in amyotrophic lateral sclerosis, Neurosignals 12 (4–5) (2003) 215–220, doi:10.1159/000074623.
 - [164] C. Pelegrí, J. Duran-Vilaregut, J. del Valle, et al., Cell cycle activation in striatal neurons from Huntington's disease patients and rats treated with 3-nitropropionic acid, Int. J. Dev. Neurosci. 26 (7) (2008) 665–671, doi:10.1016/ j.ijdevneu.2008.07.016.
 - [165] S. Love, Apoptosis and brain ischaemia, Prog. Neuropsychopharmacol. Biol. Psychiatry 27 (2) (2003) 267–282, doi:10.1016/S0278-5846(03)00022-8.
 - [166] K.L. Jordan-Sciutto, L.M. Malaiyandi, R. Bowser, Altered distribution of cell cycle transcriptional regulators during Alzheimer disease, J. Neuropathol. Exp. Neurol. 61 (4) (2002) 358–367, doi:10.1093/jnen/61.4.358.
 - [167] L. Lasagni, E. Lazzeri, S.J. Shankland, H.J. Anders, P. Romagnani, Podocyte mitosis - a catastrophe, Curr. Mol. Med. 13 (1) (2013) 13–23, doi:10.2174/ 1566524011307010013.
 - [168] J. Zhou, F. Ahmad, S. Parikh, et al., Loss of adult cardiac myocyte GSK-3 leads to mitotic catastrophe resulting in fatal dilated cardiomyopathy, Circ. Res. 118 (8) (2016) 1208–1222.
 - [169] S. Nakano, A.G. Engel, I. Akiguchi, J. Kimura, Myofibrillar myopathy. III. Abnormal expression of cyclin-dependent kinases and nuclear proteins, J.

Neuropathol. Exp. Neurol. 56 (8) (1997) 850–856, doi:10.1097/00005072-199708000-00002.

- [170] S.Y. Lee, J.S. Oh, J.H. Rho, et al., Retinal pigment epithelial cells undergoing mitotic catastrophe are vulnerable to autophagy inhibition, Cell Death Dis. 5 (6) (2014) e1303.
 [171] L. Wang, J. Xia, J. Li, et al., Tissue and cellular rigidity and mechanosensitive signaling activation in Alexander disease, Nat. Commun. 9 (1) (2018) 1899.