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The role of tau kinases in Alzheimer's disease

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Abstract

A principal feature of the progression of Alzheimer's disease (AD) is the appearance of aberrant phosphorylation of the microtubule-associated protein tau in the brains of affected individuals. Significant research efforts have been directed at identifying the kinases involved in this process, as well as developing pharmacological agents to inhibit these molecules. This review focuses on recent developments in both the physiological and pathological effects of tau phosphorylation, and the contribution of phosphorylation to tau toxicity and pathological progression in AD. The evolving concepts of the roles tau plays in cellular biology, and the mechanisms by which phosphorylation regulates tau function, is reshaping the framework for the development of therapeutics targeting tau to treat AD.

Keywords

Alzheimer's disease; axonal transport; β-amyloid; kinase; microtubule; phosphatase; phosphorylation; tau

Introduction

Tau is an alternatively spliced microtubule-binding protein that is predominantly expressed in neurons [1–3]. The abnormal accumulation of tau and the formation of neurofibrillary tangles (NFTs) composed primarily of this protein, as well as the formation of β -amyloid (A β) plaques, have been implicated in the progression of Alzheimer's disease (AD) [4–6]. The exact pathways and precipitating events leading to the abnormal accumulation of tau remain unclear, but phosphorylation has been postulated to be an important contributor [7].

In the human brain, tau exists primarily as six different isoforms, which vary in the presence or absence of one or two N-terminal acidic repeats, and in the presence or absence of the second of four microtubule-binding repeats [8], although other splice variants have been reported [9, 10]. The expression of tau is regulated developmentally, and the specific ratios of the tau isoforms differ in fetal and adult animals [11]. In 1984, Lindwall and Cole demonstrated that the dephosphorylation of tau isolated from bovine brains increases the ability of the protein to bind microtubules and to promote microtubule assembly, clearly demonstrating a functional

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outcome of phosphorylation, although the kinases involved were unknown [12]. Since this initial report, various studies have focused on delineating the kinases involved in tau phosphorylation, as well as identifying the specific sites on tau that are phosphorylated and their contribution to physiological, as well as pathological, processes.

Because aberrant phosphorylation and aggregation are a defining hallmark of tau in AD brains, and because the prominent belief is that abnormal phosphorylation results in tau dysfunction and pathological properties, significant research efforts have been focused on developing effective kinase inhibitor therapies (for a comprehensive review, see reference [13]). These potential therapeutics are directed at a wide variety of kinases, including glycogen synthase kinase 3β (GSK3 β), cyclin-dependent kinase 5 (Cdk5), JNK and microtubule-associated regulatory kinase (MARK).

In this review, some of the processes that may contribute to alterations in tau phosphorylation in the context of AD, the effect that these phosphorylation events may have on neuronal physiology, and the possible contribution of different protein kinases, as well as protein phosphatases, are discussed.

Tau kinases and disease processes

Activation of tau kinases by β -amyloid

The exposure of cells or neurons to $A\beta$ in situ leads to increases in tau phosphorylation at various sites as a result of the activation of different kinases. Early studies demonstrated that the treatment of neurons with A β fibrils increased the immunoreactivity of phosphorylated tau [14,15], and that this increase was lithium-sensitive, implicating GSK3 β as the responsible kinase [16]. Moreover, studies focusing on the immediate downstream effects of $A\beta$ in vivo demonstrated that the generation of $A\beta$ leads to an increase in intraneuronal calcium levels [17], which can result in calpain activation and increased Cdk5 activity because of the cleavage of p35 to p25 [18,19]. This calcium increase is NMDA-dependent, and can be blocked by NMDA antagonists, such as MK-801 or memantine [20,21]. Correspondingly, treatment with memantine reduces the amount of phosphorylated tau in the CSF of humans with AD, as well as in rats [22–24]. However, the contribution of Cdk5 to tau phosphorylation is unclear, as p35-null mice exhibit a decrease in Cdk5 activity, but significant increases in tau phosphorylation, as well as GSK3 β activity [25]. A more recent study also demonstrated that Cdk5 activity was not required for the pathological phosphorylation of tau in a mouse model of Niemann-Pick Type C disease; in fact, genetic ablation of p35 resulted in an increase in tau phosphorylation, as indicated by increases in AT8 (Ser¹⁹⁹/Ser²⁰²/Thr²⁰⁵) and PHF1 (Ser³⁹⁶/ Ser⁴⁰⁴) immunoreactivity [26] (antibody epitopes are provided in Table 1). Therefore, the role of Cdk5 in the direct modulation of tau phosphorylation remains to be clarified, and this enzyme may have indirect effects.

In addition to its effects on calcium homeostasis, $A\beta$ may modulate tau phosphorylation through other mechanisms. $A\beta$ treatment can increase reactive oxygen species generation, leading to JNK activation and to an increase in tau phosphorylation [27,28]. Recent research has demonstrated that the $A\beta$ -induced increase in JNK activation and tau phosphorylation in neurons can be blocked by treatment with the omega-3 fatty acid docosahexaenoic acid (DHA) and, also, that JNK activation and tau phosphorylation in AD mouse models, as well as correlated behavioral deficits, can be abrogated with a DHA/curcumin diet [29]. In addition, $A\beta$ -catalyzed disruptions in phosphocholine metabolism have been suggested to cause Cdk5 upregulation and AT8 phosphorylation [30].

Aβ also activates tyrosine kinases [31,32]. For example, recent evidence indicated that c-Abl activity was increased in mutant amyloid-precursor protein (APP) mouse models [33]. In this

particular study [33], elevated c-Abl activity correlated with downstream Cdk5 activation and phosphorylation of tau at PHF1/AT8, although other studies have revealed that c-Abl, as well as the Abl-related gene (Arg) tyrosine kinase, can phosphorylate tau directly at Tyr³⁹⁴ [34, 35]. Tau phosphorylated at Tyr³⁹⁴ has been detected in paired helical filaments isolated from AD brains, suggesting a role in AD pathogenesis [35]. Tau is also phosphorylated at Tyr¹⁸ by Fyn, and it has been postulated that tau and Fyn function together to regulate microtubule structure [36].

A correlation between increased A β levels and the activation of tau kinases is also evident in some AD mouse models. Several transgenic models expressing APP or APP and presenilin with familial AD mutations displayed increases in tau phosphorylation [37,38] or the mislocalization of phosphorylated tau species [39], although NFTs did not develop. However, other mouse models expressing mutated APP/presenilin did not exhibit tau pathology, despite aggressive amyloid pathology, Cdk5 activation and cell loss [40]. A transgenic mouse model with five familial AD mutations has also provided an association between increased tau phosphorylation and the expression of the C-terminus of APP [41]. In addition, in another mouse model expressing an APP construct mutated to enhance A β oligomerization, an increase in phosphorylated tau (ie, PHF1 immunoreactivity) without fibrillization was demonstrated [42]. Combining a tau (P301L) transgene, a frontotemporal dementia and Parkinsonism linked to chromosome 17 (FTDP-17) mutation in tau (FTDP-17 tau) and the APP (Swe)/PS1 (M146V) transgenes resulted in a substantial increase in the extent of tau phosphorylation and pathology [43,44]. However, overexpression of FTDP-17 tau alone resulted in increased phosphorylation and neurofibrillary pathology [45,46]. Combined, these and other studies indicate that there may not necessarily be direct associations between A β , kinase activation and tau phosphorylation in AD, although Aβ likely plays an indirect or modulatory role.

Insights into tau phosphorylation from insulin-resistant models

The existence of a correlation between type 2 diabetes and an increased risk for AD is still being debated [47]; however, this possible association has led to studies examining the relationships between tau phosphorylation, kinase activation and insulin dysfunction. An early hypothesis of the possible role of insulin resistance in aberrant tau phosphorylation stated that downregulation of the insulin receptor/PI3K/Akt pathway led to reduced inhibition of GSK3 β and increased tau phosphorylation [48]. However, recent studies have provided data that suggest this may not be the primary mechanism by which insulin dysfunction contributes to increased tau phosphorylation, as described in the following paragraphs.

Systemic administration of streptozotocin (STZ), a compound that is selectively toxic toward insulin-producing β -cells in the islets of Langerhans, is often used to induce diabetes in rodent models of disease [49]. In wild-type mice, peripheral administration of STZ led to increased tau phosphorylation at various sites, but did not lead to the formation of insoluble aggregates [50]. In a mouse model expressing FTDP-17 tau, a similar treatment paradigm exacerbated tau pathology, including increasing the levels of AT8 immunoreactivity, dystrophic neurites and NFTs [51]. The mechanism responsible for the increase in tau phosphorylation in response to insulin deficiency is unlikely to be elevated GSK3 β activity (in fact, a decrease in the active form of the kinase was observed); instead, the specific inactivation of protein phosphatase 2A (PP2A) may be responsible [50]. One potential mechanism for STZ-induced reduction of PP2A activity is through the induction of hypothermia [52]. Interestingly, anesthesia-induced hypothermia also results in increases in tau phosphorylation through the inhibition of phosphatase activity [53].

Central administration of STZ has been proposed to induce AD, as this agent induces behavioral and neuropathological changes that recapitulate the disease phenotype [54]. Although the mechanism of action of centrally administered STZ differs from that observed when the

compound is administered systemically, central administration of STZ results in reduced levels of both the insulin receptor and insulin in the brain [55]. In a recent study, STZ injected directly into the cerebral ventricles resulted in acute increases in tau phosphorylation at AD-related epitopes, as well as the expected increase in the levels of activated GSK3 β [56]. Interestingly, a decrease in the levels of GluT1 was also observed, as well as a decrease in the levels of *O*-*N*-acetylglucosamine (*O*-GlcNAc) and *O*-GlcNAc transferase ([OGT], which catalyzes *O*-GlcNAcylation). A reciprocal relationship between phosphorylation and *O*-GlcNAcylation has been reported previously, and inhibition of phosphatase activity (resulting in increased tau phosphorylation) leads to decreased levels of *O*-GlcNAcylation of tau [57]. Therefore, this mechanistic link between impaired *O*-GlcNAcylation and impaired glucose metabolism presents an interesting pathway, resulting in tau hyperphosphorylation that is independent of increased tau kinase function. Indeed, compounds that inhibit O-GlcNAcase prevent tau hyperphosphorylation by inhibiting the removal of *O*-GlcNAc modifications [58].

Tau phosphorylation and Alzheimer's disease pathophysiology

Tau kinases and microtubule stability

Although increasing evidence suggests that tau has roles in the cell beyond its ability to regulate microtubule dynamics, the phosphorylation-regulated function of tau remains of primary interest in studies assessing the potential pathophysiological role of the protein in AD and other tauopathies (for a review, see reference [8]). Studies have clearly demonstrated that tau phosphorylation at various sites, by many different kinases, regulates the microtubule affinity of the protein, as well as its ability to regulate microtubule dynamics ([59], and reviewed in reference [60]). Phosphorylation of tau by GSK3β and Cdk5 [61] affects tau-microtubule interactions by reducing the microtubule affinity of tau; phosphorylation of Ser²¹⁴ by PKA has also been demonstrated to have a similar effect [62]. Most notably, phosphorylation of the serines within the Lys-Xaa-Gly-Ser (KXGS) motifs (and particularly at the 12E8 [Ser²⁶²/ Ser³⁵⁶] site) of the microtubule-binding domains (MTBDs) of tau consistently exerted a strong negative effect on tau-microtubule interactions; a prominent kinase that phosphorylates the KXGS motif is MARK [63]. A recent structural study of pseudo-phosphorylated tau indicated that phosphorylation at the KXGS motif introduces a destabilizing rigid turn to three residues adjacent to Ser²⁶² that decouples tau from microtubules [64]. Given these and other findings, it is reasonable to speculate that the hyperphosphorylation of tau may contribute to the reported defects of microtubule integrity in AD brains [65].

The prevailing model of microtubule-related tau toxicity suggests that phosphorylation of tau precedes the dissociation of the protein from microtubules, and this event is followed by the aggregation of phosphorylated tau, leading to NFT formation in AD brains [66]. This model is supported by a study in which 12E8 phosphorylation promoted further phosphorylation at the possible GSK3β-phosphorylated epitopes AT8 and PHF1 [67]. This increased phosphorylation could be the result of a structural change induced by Ser²⁶² phosphorylation that either renders tau more amenable to further phosphorylation or, potentially, less amenable to dephosphorylation by phosphatases. Notably, the tau binding site for PP2A has been localized to the MTBDs [68]. A crystallization study confirmed this localization, and also determined that a negatively charged pocket of PP2A interacted with tau, allowing dephosphorylation of Ser³⁹⁶ [69]. Therefore, the addition of an electronegative phosphate group to the binding tract of tau may interfere with the binding of PP2A to tau, allowing aberrant increases in tau phosphorylation because of decreased phosphatase activity.

However, separating the normal flux of tau phosphorylation and dephosphorylation, both of which are required for microtubule stability and neuronal health, from aberrant phosphorylation that leads to a pathogenic cascade is challenging. Complicating the phosphorylation/dephosphorylation model, an early study determined that, *in vitro*, tau

phosphorylated at Ser²⁶², which decreases the affinity of tau for microtubules, also prevented it from assembling into paired helical filaments (PHFs) [62]. More recently, in a *Drosophila* tauopathy model, tau that could not be phosphorylated at either two of the KXGS motifs, or at the 11 GSK3β-targeted sites, was expressed [70]. Unexpectedly, tau that could not be phosphorylated at the GSK3β-targeted sites, but could be phosphorylated at the KXGS motifs, was completely bound to the microtubules and, nevertheless, was the most toxic form of tau studied. In contrast, tau that could not be phosphorylated at the KXGS motifs, but could be phosphorylaed at all other sites, was present in the soluble fractions and was almost completely non-toxic. This study indicates that the relationship between phosphorylation and taumicrotubule interactions extends beyond the microtubule-binding regions, and that the relationship between microtubule binding and toxicity is likely to be more subtly complex than usually presumed.

Tau kinases and axonal transport

Defective axonal transport has long been considered to have a role in neurodegenerative diseases [71], including AD [72,73]. Tau's identity as a microtubule-associated protein has made it an attractive candidate in AD-associated axonal transport defects. Different mechanisms and protein complexes have been observed for the transport of various cargoes, and tau itself can be described as a substrate for axonal transport [74]. The binding of tau to the anterograde transport protein kinesin, as well as its rate of transport in the axons, is dependent on the degree of phosphorylation; suppression of GSK3 β activity by lithium results in the suppression of kinesin-tau binding [75].

Similar to microtubule dynamics, phosphorylation of different tau sites can have opposing effects on axonal transport. A recent study demonstrated that increased GSK3β (and Cdk5) activity decreased the frequency of mitochondrial movement in neurons, and was accompanied by increases in PHF1 and AT270 (Thr¹⁸¹) immunoreactivity [76]. A separate study demonstrated that tau overexpression decreased the quantity of moving mitochondria in the axons, and that this effect was reversed by the co-expression of MARK, implicating microtubule affinity in the regulation of mitochondrial movement by tau [77]. The relative expression of tau in these models should be considered carefully, as a study of fast axonal transport in which various low monomeric tau:tubulin ratios were investigated in a squid axoplasm model displayed no effect following the introduction of phosphorylated tau, although transport impediment was achieved at high tau:tubulin ratios [78]. In a more recent study using the same methodology, monomeric tau did not affect transport, but filamentous tau inhibited anterograde transport – an effect that was relieved by inhibiting GSK3 β [79]. However, consideration of this latter finding needs to be tempered by results from an earlier study, which also used the squid axoplasm as well as other models, indicating that addition of active GSK3 β (in the absence of tau) inhibited fast anterograde transport by phosphorylating kinesin [80].

An attractive alternative role for tau phosphorylation in the regulation of axonal transport has recently emerged. JNK-interacting protein 1 (JIP1) has been described as a regulator of axonal development and transport [81]. A promoter variant of this protein has also been associated with AD [82]. Tau phosphorylated at pathogenic residues (ie, AT8, AT180 [Thr²³¹/Ser²³⁵] and PHF1) has recently been demonstrated to compete with the kinesin-1 complex for binding to JIP1, resulting in mislocalization of JIP1 from neurites to neuronal somata [83]. This interaction of abnormally phosphorylated tau with JIP1 may impair the axonal transport of specific cargoes in a tauopathy mouse model (in the absence of amyloid toxicity) [84], and could be a contributing factor to the documented axonal transport deficits observed in AD [71,83].

Although tau has been implicated as a causative agent in axonal transport deficits, recent data have alluded to a reverse sequence, whereby microtubular transport deficits cause tau

pathology. Falzone and colleagues described a kinesin light chain 1 (KLC-1)-null mouse model with predicted deficits in cargo transport [85]. The null mutation resulted in axonal structural defects and significant accumulation of tau that was phosphorylated at AD-associated epitopes (Ser²⁰²/Thr²⁰⁵) along the axonal tracts, and this accumulation correlated with aberrant activation of JNK [85]. The potential dual role of JNK in both tau-JIP1-mediated regulation of transport, as well as in the initiation of aberrant tau pathology by deficits in axonal transport, is intriguing and warrants further study.

Tau kinases and protein aggregation

The correlation between insoluble NFT formation and memory impairment in AD originally led to the hypothesis that insoluble tau is the pathogenic form of this protein [86]. Since the discovery that the tau present in NFTs is hyperphosphorylated [6,7,87], the kinases responsible for this hyperphosphorylation have been the focus of various studies. However, the results of recent studies have led to an emerging conceptual framework in which pre-aggregate, soluble tau species may be causative elements in tau pathology [88], and even that expression of potentially abnormally processed soluble tau, independent of its fibrillar state, may drive tau pathology. The key findings of several of the studies that have led to this developing hypothesis are described in this section.

In 2005, a doxycycline-repressible mouse model of tauopathy was used to demonstrate that suppressing the expression of tau, while leaving insoluble tau aggregates intact, led to improved memory function [89]. This result was confirmed in a more recent study in which soluble phosphorylated tau species were demonstrated to contribute to neurodegeneration in a *Drosophila* model of human tauopathies [90]. Soluble, non-PHF tau was also responsible for inhibiting microtubule dynamics [91]. Interestingly, studies on tau-tubulin kinase (TTBK), a serine/threonine kinase belonging to the casein kinase 1 family [92], also support these findings. For example, the TTBK2 isoform has been associated with spinocerebellar ataxia [93]. In addition, TTBK1 has been linked to tau phosphorylation at multiple AD-relevant sites [94], and, in a tauopathy mouse model, this phosphorylation occurred without the appearance of phosphorylated sarkosyl-insoluble aggregates, but with the emergence of proto-fibrillar tau oligomers [95]. The presence of activated GSK3 β and Cdk5 was noted, highlighting the possibility that TTBK1 does not phosphorylate tau directly, but may mediate tau phosphorylation indirectly by the GSK3 β and Cdk5 putative tau kinases.

These and other data are supportive of the hypothesis that insoluble tau may be protective by acting as a 'sink' for soluble pathological species. The concept that aggregates of pathological proteins may be protective has also been proposed for other neurodegenerative diseases. For example, data suggest that soluble mutant huntingtin (mhtt) may be more toxic than aggregated mhtt, as cells in which mhtt aggregates form survive significantly longer than cells in which the mhtt does not aggregate [96]. Although the hypothesis that 'pre-aggregated' tau is the toxic form is attractive, it still remains to be substantiated, as visualization methods for specifically detecting oligomeric or pre-aggregates of tau have not been developed, and analysis presently relies on time-consuming biochemical assays. The strongest evidence supporting the 'soluble-tau' hypothesis remains the presence of toxicity and hyperphosphorylation in the absence of microscopically visible aggregates.

Conclusion

There is still much to learn regarding the role of tau kinases in AD, and hypotheses and perspectives continue to evolve as new data arise. As an understanding of the role of tau phosphorylation in AD pathogenesis is gained, the field is becoming better equipped to develop therapeutic strategies to treat the disease. Although it is important to consider tau kinases in the AD pathological processes, identifying pathogeneic events that occur prior to the onset of

memory deficits is of crucial importance and will undoubtedly be an ever-increasing area of investigation as effective therapeutic strategies are sought.

In addition, the possibility that inhibiting kinases in models of AD pathogenesis is having beneficial effects that are not related directly to a reduction in tau phosphorylation should not be discounted. For example, lithium inhibits GSK3 β , reduces APP processing [97], acts as a neurotrophin [98] and lowers inflammatory activity [99]; the Cdk5 inhibitor seliciclib (Cyclacel Pharmaceuticals Inc) prevents A β -induced Golgi fragmentation [100]; and, in an unrelated model, the JNK inhibitor SP-600125 (Celgene Corp) reduces proinflammatory microglial activity [101]. The kinases targeted are all considered to be tau kinases, but the beneficial effects of the kinase inhibitors in *in vitro* and *in vivo* models could be the result of their effects on other pathways. Changes that occur in tau phosphorylation following treatment with these inhibitors may only represent a marker of kinase activity, and may not be related directly to the attenuation of pathogenic outcomes. An indicator of this possibility is the observation that the expression of an extensively pseudophosphorylated tau construct in a mouse model did not result in any obvious pathology, memory loss, changes in tau localization or alterations in dendritic spine density [102].

In addition to the search for tau kinase modifiers, there is a focus on developing strategies to reduce the levels of phosphorylated tau using immunotherapy. This approach has yielded promising results in a tangle mouse model [103], resulting in a reduction in the amounts of phosphorylated and total tau in neurons, as well as improvements in cognitive defects. A promising therapeutic strategy may be immunotherapy combined with modifiers of tau kinases.

More recent studies have focused on post-translational modifications other than tau phosphorylation that may be early facilitators of tau pathology. For example, a recent imaging study conducted in the brains of mice in a tauopathy model indicated that non-terminal caspase activation in neurons can result in tau cleavage at the C-terminus, and that this event may be one of the primary drivers of pathogenicity that is independent of phosphorylation, although the two events (phosphorylation and cleavage) may function together [104]. Overall, it is clear that site-specific phosphorylation of tau plays a crucial role in regulating the physiological functions of tau, and that dysregulation of tau phosphorylation, be it as a primary or a secondary event, is a hallmark of AD pathology. Therefore, further studies that increase the knowledge of kinases that phosphorylate tau are of crucial importance. The abundance of information regarding the role of inappropriate kinase activation and tau phosphorylation (as well as other important post-translational modifications of tau, such as cleavage and O-GlcNAcylation) in neuronal dysfunction and death has certainly helped determine the pathogenic processes involved in AD. It is also exciting to consider that as new data emerge, paradigm shifts regarding the relative contribution of tau phosphorylation and aggregates to AD pathogenesis are likely to occur.

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