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# Modulation and detection of tau aggregation with smallmolecule ligands

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#### Abstract

Recent results from high-throughput and other screening approaches reveal that small molecules can directly interact with recombinant full-length tau monomers and fibrillar tau aggregates in three distinct modes. First, in the high concentration regime (>10 micromolar), certain anionic molecules such as Congo red efficiently promote tau filament formation through a nucleation-elongation mechanism involving a dimeric nucleus and monomer-mediated elongation. These compounds are useful for modeling tau aggregation *in vitro* and in biological models. Second, in the low concentration regime (<1 micromolar), other ligands, including cyanine dyes, display aggregation antagonist activity. Compounds that can prevent or reverse fibrillization are candidate modifiers of disease pathology. Finally, certain compounds bind mature tau fibrils with varying affinities at multiple binding sites without modulating the aggregation reaction. For some ligands, >10-fold selectivity for tau aggregates relative to filaments composed of beta-amyloid or alpha-synuclein can be demonstrated at the level of binding affinity. Together these observations suggest that small-molecules have utility for interrogating the tau aggregation pathway, for inhibiting neuritic lesion formation, and for selective pre-mortem detection of neurofibrillary lesions through whole brain imaging.

#### Keywords

Alzheimer's disease; frontotemporal lobar degeneration; tau; neurofibrillary tangle; paired helical filaments; aggregation

## INTRODUCTION

Alzheimer's disease (AD) is definitively diagnosed on the basis of pathology. Characteristic neuritic brain lesions include neurofibrillary tangles (corresponding to affected nerve cell bodies), neuropil threads (affected neuronal processes), and dystrophic neurites (swollen and misshapen nerve cell processes associated with A $\beta$  plaques). All neuritic morphologies involve intracellular deposition of aggregated forms of tau, a microtubule-associated protein that normally functions as a monomer in conjunction with its physiological binding partner, tubulin. Because the transformation of tau from monomer to aggregate along with changes in its state of post-translational modification correlates with neurodegeneration and cognitive decline, neuritic lesion formation can serve as a marker of AD neurodegeneration. In fact, the hierarchical appearance of neuritic lesions is commonly used to stage AD progression (1). Alzheimer's like changes in tau structure occur in certain frontotemporal

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lobar degeneration (FTLD) diseases as well, where they can involve glial cells in addition to neurons, and also in inclusion body myositis, where they accumulate in muscle cells. In some familial cases of FTLD, disease is conferred by mutations in the tau gene, suggesting a closer link between tau misfunction and neurodegeneration than implied solely by histological correlation studies, and raising the possibility that tau structural transitions contribute to pathogenesis through gain-of-function or loss-of-function effects. Because of tau's established role as a marker of AD progression, and its putative role as a mediator of neurodegeneration, small molecules that directly interact with tau protein are being investigated in three contexts: as a means of leveraging an established marker of neurodegeneration for premortem diagnosis of AD and other tauopathic neurodegenerative diseases, as a means of modeling the biological effects of intracellular tau aggregation in biological models, and as a potential avenue to therapeutics that attack a root cause of neurodegeneration. Recent progress in these areas is summarized below.

#### NEUROFIBRILLARY LABELS

Filamentous tau adopts cross- $\beta$ -sheet conformation, consisting of parallel, in-register  $\beta$ sheets oriented perpendicular to the filament axis, with two molecules of tau per  $\beta$ -sheet spacing (2). Mature tau filaments having this architecture are termed paired helical filaments when isolated from AD brain, but other morphologies have been observed in AD and certain FTLD diseases (3). The cross- $\beta$ -sheet folding pattern, which is shared with A $\beta$ protofilaments, generates channels along the filaments (4) to which heterocyclic small molecules can bind (5) (Fig. 1). However, molecular dynamics simulations have identified other potential binding modes, suggesting that  $cross-\beta$ -sheet conformations harbor multiple non- or partially overlapping binding sites for small molecules (6,7). These sites have been directly observed through ligand binding experiments carried out in three distinct formats. Radiometric methods involve direct incorporation of a radionuclide into a candidate ligand, followed by direct measurement of specific binding stoichiometry and affinity in filter trap assays. In contrast, fluorescent ligands that change fluorescence intensity or undergo a Stokes shift in excitation and/or emission optima when bound to filamentous aggregates are assayed by measurement of intrinsic fluorescence. Finally, either of these approaches can be used in competition format with unlabeled compounds to assess binding affinity and relative occupancy of binding sites. The competition strategy frequently involves thioflavine dyes as intrinsic fluorescent probes (8), in part because these agents label authentic lesions in brain sections (9). Together, these assays have identified at least three distinct sites on synthetic  $A\beta_{(1-40)}$  fibrils that are capable of binding diverse scaffold classes with varying stoichiometries and affinities (10,11). Certain derivatives of these molecules, including <sup>11</sup>C-PIB, <sup>11</sup>C-SB-13, <sup>18</sup>F-AV-45, and <sup>18</sup>F-BAY94-9172, are under development as contrast agents for  $\beta$ -amyloid plaques in whole-brain PET imaging (12). This approach is especially attractive for assessing the activity of investigational therapies designed to clear brain  $A\beta$ deposits (13). However, contrast agents capable of selectively binding tau lesions may better reflect AD stage and progression than those based on A $\beta$  plaque formation. This is because total plaque density in neocortical regions correlates poorly with cognitive decline, whereas the appearance of neuritic lesions correlates well with neurodegeneration and cognitive decline (1,14,15).

Pursuit of this strategy will require molecules with selectivity for aggregates composed of tau protein relative to those composed of A $\beta$  or other proteins. But because of the folding commonalities among filamentous aggregates composed of different proteins, it is likely that binding sites are shared among different lesions. Indeed, both  $\beta$ -amyloid plaques and taubearing neuritic lesions can be detected *in situ* by <sup>18</sup>F-FDDNP (16), <sup>18</sup>F-FENE (17), <sup>18</sup>F-BF-108 (18), non-radiolabeled X-34 (19,20), and a family of iodinated flavones (21). Therefore, these agents may be suboptimal for selective detection of neuritic lesions. In the

absence of a selective ligand for neuritic lesions, Shin and colleagues suggest both PIB and FDDNP be employed in the same subject for visualization of total AD pathology, with the net difference between them used to selectively assess the neuritic component (16).

Two *in vitro* studies have identified compounds that selectively bind tau aggregates. The first by Kudo and colleagues demonstrated that the benzimidazole BF-126 and quinolines BF-158 and BF-170 exhibited 2- to 3-fold selectivity for synthetic 1N4R tau aggregates compared to those composed of A $\beta_{(1-42)}$  (22). Despite modest selectivity, neurofibrillary lesions were preferentially stained compared to  $\beta$ -amyloid plaques in AD hippocampal brain sections. Because these measurements were carried out at nominally saturating concentrations of ligand, the observations may reflect higher binding stoichiometry on tau filaments, or the higher concentration of tau protomers (120 pmol/mg frontal cortex protein (23)) relative to protomeric A $\beta$  (3–4 pmol/mg midfrontal, parietal, or temporal cortex protein (24,25)) reported in other areas of late-stage AD brain. Interestingly, these compounds did not detect neuropathological lesions in brain sections prepared from Pick's disease or progressive supranuclear palsy brains, suggesting that these compounds favor the tau isoform composition and post-translational modification signature associated with AD. The second selectivity study identified small molecules that preferentially bound synthetic tau aggregates (composed of 2N4R human tau) over aggregates composed of A $\beta_{(1-42)}$  or asynuclein (8). A library of 70,000 compounds was screened in competition binding format to identify compounds with submicromolar binding affinity. A secondary screen revealed that Thiazine Red R bound tau aggregates with greater than 10-fold selectivity compared to the other two substrate proteins tested. These data suggest that at least one order of magnitude selectivity can be generated at the major Thioflavine S binding site. The presence of multiple binding sites suggests that additional scaffold classes potentially capable of supporting selective binding await discovery.

Still, the approach faces additional challenges beyond binding selectivity. First, early stage tau aggregates appear within cells, as opposed to A $\beta$  plaques which appear in the extracellular space. Thus, tau proteins are exposed to an extensive array of post-translational modifications and immersed in a crowded molecular environment. Indeed, authentic Lewy bodies (composed of α-synuclein as the aggregating protein) fail to bind <sup>3</sup>H-PIB, although high affinity binding sites for this compound reside on synthetic a-synuclein filaments prepared *in vitro* (26). It will be essential to confirm the activity of all ligands discovered on the basis of *in vitro* binding assays against authentic tissue since binding sites may differ in protein protomers associated with lesions (27,28). Second, the rate of uptake into cells will influence the pharmacokinetic profile of each ligand, and hence the apparent selectivity for neuritic lesions versus other types of lesions. In silico pharmacokinetic modeling may clarify the kinetic properties that favor detection of intracellular tau aggregates. Finally, tau consists of multiple isoforms that may differentially interact with certain ligands. For example, aggregates composed of human A $\beta_{(1-40)}$  doped with small amounts of rodent A $\beta_{(1-40)}$ displayed fewer high affinity binding sites, suggesting that filament microheterogeneity arising from protein isoform mixtures influences binding site structure (29). This issue may be especially important for tau aggregates, which are composed of up to six distinct isoforms, each of which contributes different sequences to the cross- $\beta$ -sheet structure at the core of each filament (30). Different isoform ratios predominate in other tauopathies (31), and this may change binding site characteristics in ways that are difficult to predict.

#### AGGREGATION AGONISTS

Unlike A $\beta$  or  $\alpha$ -synuclein, full-length tau proteins resist spontaneous aggregation *in vitro* under physiological conditions of protein concentration, temperature, pH, and ionic strength over tractable time periods (32). In biological models, this limitation has been overcome by

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high level tau overexpression (33–36), incorporation of aggregation-promoting missense mutations or deletions (37–43), or through aggressive post-translational modification (41,44). *In vitro*, resistance to aggregation can be overcome in the presence of polyanions (*e.g.*, heparin (45,46)) or anionic surfactants (arachidonic acid or alkyl sulfate detergents). Although surfactants are small monomers in dilute solution, they readily aggregate to form micelles above a critical concentration. The presence of protein depresses surfactant critical micelle concentration and leads to formation of tau-surfactant complexes (47). These are predicted to vary in size depending on the surfactant employed and its concentration, ranging from small micelles arranged along the natively unfolded tau polypeptide chain (48) to larger protein-bound bodies visible in the electron microscope (47). Thus, despite their much smaller monomeric size relative to heparin, surfactants may share a limited ability to achieve aggregation-inducing concentrations in intact cells.

Recent studies show that the kinetic barrier to fibrillization also can be overcome by addition of agonist dyes such as Congo red, Thiazine red, and Thioflavine S (32). The resultant tau filaments display a twisted-ribbon morphology and a mass-per-unit-length similar to that of authentic tissue-derived filaments (49). Congo red can populate partiallyfolded amyloidogenic conformations of proteins (50), suggesting that agonists may function through thermodynamic linkage of binding with the aggregation reaction. Regardless of mechanism, the performance of small-molecule aggregation agonists differs substantially from macromolecular and micelle-based inducers. For example, the extent of the aggregation reaction does not depend on dye/tau ratios, thereby simplifying kinetic analysis (32). In addition, agonists facilitate fibrillization of full-length 4-repeat tau isoforms at submicromolar concentrations (49), which is well within physiological levels. These properties make small-molecule based tau aggregation inducers ideal for kinetic characterization of tau aggregation. In vitro, Thiazine red-induced aggregation follows a nucleation-elongation mechanism consistent with a dimeric nucleus, a monomeric extension reaction, and a submicromolar critical concentration (Fig. 1). Preliminary estimates of elementary rate constants derived from this model were consistent with the time dependent evolution of total filament length and also filament length distribution (49). These data suggest that tau fibrillization at physiological tau concentrations need not involve small soluble aggregates as intermediate species.

Wild-type tau aggregation provides a baseline for comparing the mechanism of action of FTLD-causing missense mutations, which act at different points in the aggregation pathway to promote fibril formation. Mutations that affect the Pro-Gly-Gly-Gly segments of microtubule binding repeats (e.g., G272V and P301L) lower the minimal concentration of tau necessary to support the aggregation reaction, while speeding reaction rate at the level of nucleation (51). In contrast, other mutations, such as R5L and V337M, accelerate the rate of filament formation at the level of nucleation without significantly altering the minimal tau concentration necessary to support the reaction. The differential activity of missense mutations on individual steps in the pathway may influence how tau misfunction leads to clinically and histopathologically distinct diseases.

Self association mechanism is but one constraint on the ability of tau to form filaments *in vivo*. Within cells, normal and misfolded tau interacts with chaperones and protein quality control circuitry as well. The complex interplay of these pathways, and whether tau aggregation is associated with toxicity, is best approached in biological models. Certain agonists, such as Congo red, are capable of passively crossing cell membranes (but not the blood brain barrier) so as to contact cytoplasmic tau, drive *in situ* aggregation, and create novel biological models of aggregation (52). The approach complements the strategy of expressing aggregation-promoting mutations/truncations in three ways. First, agonists drive robust aggregation, with up to 40% of bulk tau becoming insoluble at reaction plateau (52).

Second, agonists offer superior control over aggregation initiation, which ensues once agonist is added to culture media. Aggregation is reversible after removal of agonist from media, and can be further modulated by changes in bulk tau expression afforded by use of inducible promoters (52). Finally, agonists are amenable to use with microfluidic strategies for isolating cell bodies from cell processes (53), and so may offer a route to spatial control over aggregation initiation. Together these characteristics may be advantageous for assessing tau aggregate toxicity and accumulation, and its temporal relationship with post-translational modifications.

### **AGGREGATION ANTAGONISTS**

The association of aggregation-promoting missense tau mutations with neurodegenerative disease (31), combined with toxicity associated with tau aggregation in model systems (54), suggests that the accumulation of tau aggregates may contribute to neurodegeneration. If so, then direct interference with aggregation may halt disease progression in affected individuals. The strategy is attractive because tau aggregation is associated with diseased neurons but not normal biology. Early screens for tau aggregation antagonists focused on the ability of aggregation-prone tau fragments to recruit full-length tau into aggregates. These assays identified methylene blue (tetramethylthionine chloride) and other phenothiazine derivatives as inhibitors of this reaction at low or even sub-micromolar concentrations (55). Treatment of mild-to-moderate AD sufferers with methylene blue (30 – 60 mg twice daily) has been reported to halt cognitive decline, improve cerebral blood flow, and improve fluorodeoxyglucose uptake relative to placebo over a  $\sim 1$  year treatment period (55). Thus at least one tau aggregation antagonist may have therapeutic utility for AD. Nonetheless, methylene blue also is a redox-active agent with affinity for the heme moieties of several proteins. In fact, this activity has been leveraged to treat methemoglobinemia in humans (*i.e.*, to reduce heme-associated iron from the abnormal ferric state to the oxygen-carrying ferrous state) (56). Moreover, it has antioxidant activity owing to effects on the electron transport chains of mitochondria (57). Currently, it is not clear whether the therapeutic benefits of methylene blue stem from its aggregation antagonist activity, its antioxidant effects on mitochrondria, or its direct binding to and modulation of heme-containing proteins.

Additional non-phenothiazine aggregation inhibitors will help clarify this issue. Toward this end, the ability of heparin and anionic surfactants to induce the aggregation of recombinant tau or tau fragments *in vitro* has been leveraged to screen for novel aggregation antagonists. High throughput screening has identified over 400 candidate inhibitors composed of diverse heterocycle scaffolds (58–60). Many of these are polyalcohols, which when incubated under nonreducing conditions generate Michael acceptors capable of covalently reacting with tau protomer. For example 5,6,7-trihydroxyflavone (baicelein) oxidizes at pH 7.5 to form protein-reactive baicelein quinone with  $t_{1/2} \sim 15$  h (61). Covalent modification effectively sequesters tau, thereby raising the apparent minimal concentration required to support the aggregation as well, suggesting that the mechanism can be widely generalized to different aggregating proteins. Inhibition of protein aggregation through covalent modification has been shown for other scaffold classes as well (62). Further studies will be required to determine whether this mechanism can modulate tau aggregation *in vivo*.

Other antagonist scaffolds include phenylthiazolyl-hydrides (63), N-phenylamines (64), rhodanines (65), and thiacarbocyanines (66). The first two classes are reportedly active down to the micromolar range, whereas some rhodanines and cyanines are active at submicromolar concentrations. The mechanism of action of these compounds on tau is not established, but they may act to stabilize off-pathway aggregates, thereby depleting tau

available to support the nucleation and extension reactions (Fig. 1). In fact, whether a compound acts as aggregation agonist or antagonist may depend on its ability to stabilize on- or off-aggregation pathway species (67,68). For tau, the former is generally favored by anionic compounds, whereas the latter appears to be favored by cationic compounds. Closer inspection of phenothiazine and thiacarbocyanine antagonists, representing two of the most potent antagonist scaffolds, reveals that both not only are cationic, but share push-pull electronic character (*i.e.*, they contain an electron donating substituent separated from an electron accepting substituent by a conjugated ring system). As a result, both scaffolds are highly polarizable (*i.e.*, charge can be localized to specific parts of the extended  $\pi$  system). This may facilitate  $\pi$ - $\pi$  interactions with a complimentary set of one or more residue side chains present on tau. If so, then additional scaffolds with drug-like properties will be capable of supporting tau aggregation antagonist activity.

#### CONCLUSION

Tau aggregation is an established marker and potential mediator of neurodegeneration. Further development of small molecules capable of modulating tau biology will clarify the mechanisms underlying neuritic lesion formation, the feasibility of selectively detecting their presence, and the utility of antagonists for arresting their development. However, only clinical studies can validate the activity of molecules selected on the basis of biochemical or biological models. The recently demonstrated efficacy of methylene blue for treatment of Alzheimer's disease supports further inquiry into tau-based diagnostic and therapeutic approaches.

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### ABBREVIATIONS USED

AD	Alzheimer's disease	

**FTLD** Frontotermporal lobar degeneration

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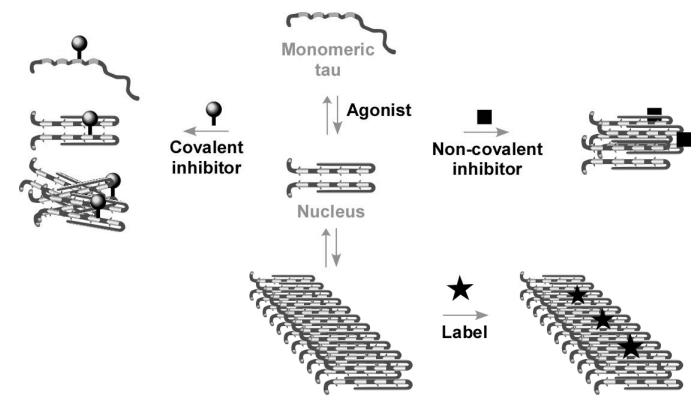
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Filamentous tau

#### Fig. (1).

Hypothetical model of the tau aggregation pathway. Soluble full-length tau isoforms exist as natively disordered monomers that aggregate poorly at physiological concentrations. Agonists allow the aggregation reaction to proceed through a dimeric nucleus under physiological conditions over a period of hours. Antagonists inhibit fibrillization through covalent modification of nucleophilic tau residues or through non-covalent stabilization of off-fibrillization pathway species, both of which act to decrease free tau available to support filament formation. Labels bind mature tau filaments with high affinity but do not necessarily modulate the aggregation reaction.