Heparan Sulfate Proteoglycans in Tauopathy

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Contributor: Yanan Zhu, Lauren Gandy, Fuming Zhang, Jian Liu, Chunyu Wang, Laura J. Blair, Robert J.

Linhardt, Lianchun Wang

Tauopathies are a class of neurodegenerative diseases, including Alzheimer's disease, and are characterized by intraneuronal tau inclusion in the brain and the patient's cognitive decline with obscure pathogenesis. Heparan sulfate proteoglycans, a major type of extracellular matrix, have been believed to involve in tauopathies. The heparan sulfate proteoglycans co-deposit with tau in Alzheimer's patient brain, directly bind to tau and modulate tau secretion, internalization, and aggregation.

tauopathy heparan sulfate proteoglycan

tau

Alzheimer's disease

1. Introduction

Tauopathies are a heterogenous family of progressive neurodegenerative diseases featured with the deposition of abnormally folded species of the microtubule-associated protein tau (tau) mainly in neurons, glia, and extracellular space [1]. There are 26 tauopathies identified, including Alzheimer's disease (AD), frontotemporal dementia with parkinsonism-17 (FTDP-17), corticobasal degeneration (CBD), progressive supranuclear palsy (PSP), argyrophilic grain disease (AGD), Pick's disease (PiD), and other diseases where tau plays a major role. Based on the major tau isoforms contained in the tau deposits, tauopathies are classified into 3 repeat (R) tauopathies, 4R tauopathies, and 3R+4R tauopathies (with approximately an equal ratio of 3R tau and 4R tau) [1][2][3]. The diseases are also classified into primary and secondary tauopathies [1]3. The primary tauopathies are a group of neurodegenerative diseases in which tau is believed to be the major contributing factor of the neurodegenerative process, such as PiD, PSP, CBD, and AGD. The secondary tauopathies are featured with tau aggregation as a response to other pathological proteins or events, like amyloid beta (AB) in AD and repetitive brain injury in the chronic traumatic encephalopathy $^{[1]}$.

2. The Tau Protein

Tau protein belongs to the microtubule-associated proteins family [4]. Tau is found predominantly in the axon of the adult neurons and at low levels in the cell body, dendritic spines, and axonal presynaptic terminal [4]. The subcellular distribution of the tau is developmentally and environmentally regulated and isoform-dependent [5][6][7] 8. In addition, tau is detected at low levels in glial cells and outside cells [2][7][9]. The various subcellular, extracellular, and cell-type expressions indicate that tau may play various functions under different circumstances. Human tau is encoded by a single gene, microtubule-associated protein tau (Mapt), located on chromosome 17g21. Mapt gene comprises 16 exons (Figure 1. By alternative splicing of exon 2 (E2), exon 3 (E3), and exon 10

(E10), six isoforms of tau are expressed in the normal adult human brain ^[2]. The largest isoform contains 441 amino acid residues, including an N-terminus projection domain with two inserts (N1 and N2), a proline-rich domain, and a microtubule-binding repeat domain composed of four repeat motifs (R1–R4) that mediate microtubule-binding and tau aggregation ^[2]. The isoforms differ in the absence or presence of N1, N2, and R2 domains leading to the following 6 isoforms: 2N4R, 1N4R, 0N4R, 2N3R, 1N3R, and 0N3R (**Figure 1**) ^{[1][3][10]}. The N1 and N2 are encoded by E2 and E3, respectively, and R2 is encoded by E10. Besides the six tau isoforms, researchers also widely use another two truncated tau proteins, the K18 and K19, which contain only the four and three microtubule-binding domains, respectively (**Figure 1**). Given the differential distribution of tau in different cell compartments and presence of various tau isoforms, tau likely plays different functions in different environments.

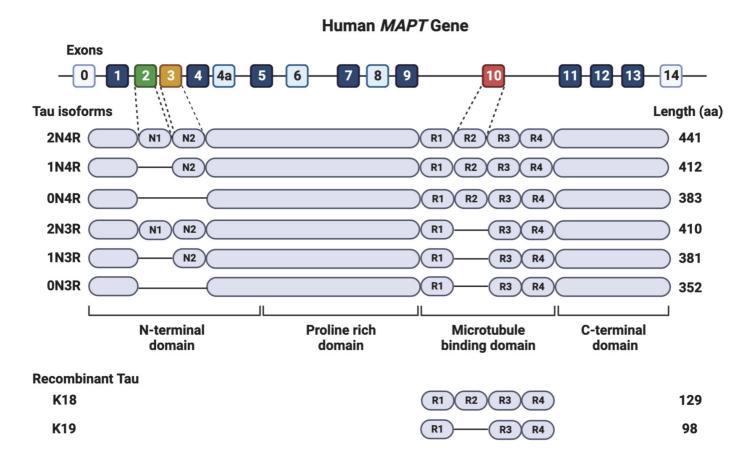
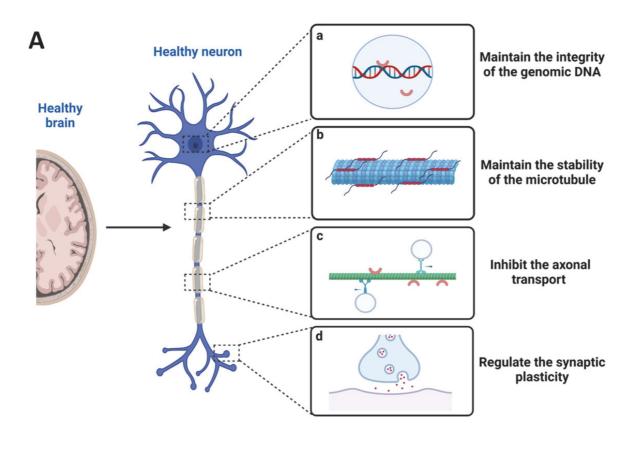


Figure 1. Human *MAPT* gene. The *MAPT* gene encodes human tau and contains 16 exons. E0 and E14 are transcribed but not translated. E1, E4, E5, E7, E9, E11, E12, and E13 are constitutive, and E4a, E6, and E8 are transcribed only in peripheral tissue. The alternative splicing of E2, E3, and E10 generates six tau isoforms seen in normal human brains. The recombinant tau proteins K18 and K19 contain four (R1–R4) and three repeats (R1, R3, R4) of the microtubule-associated domain, respectively.

3. Tau in Physiological States

As a microtubule-associated protein, Tau promotes axonal outgrowth through stabilizing neuronal microtubules [2]. Early studies indeed showed that tau stabilizes the axonal microtubules, promotes the assembly of microtubules,

and regulates the dynamic instability of the microtubules (Figure 2A) [11][12][13], suggesting that tau is critical for developing a healthy neuron. However, knockout of mouse Mapt, the gene encoding tau protein, does not lead to a severe developmental defect or overt abnormalities at young ages [14][15][16]. Additionally, in neuronal cell line studies, tau was shown to inhibit axonal transport through multiple mechanisms, including competing with kinesin or dynein for binding to microtubules [17], competing with other cargos for binding to kinesin [18][19], reducing the number of cargo-associated kinesin motors [20], and releasing cargos from the kinesin chains [21] (Figure 2A). However, knockout or overexpression of tau does not alter axonal transport in cultured primary neurons [22][23][24]. These observations suggest that tau might be dispensable for microtubule assembly, stability, and axonal transport. The lack of the expected microtubule and axonal transport defects in the Mapt^{-/-} mice is likely due to redundancy in function among tau and compensatory effect from other microtubule-associated proteins for the loss of tau [15][25]. Tau has been suggested to regulate synaptic physiology and plasticity, although it is expressed at a low level in the dendrites (Figure 2A) [26][27][28]. Tetsuya et al. observed a selective deficit in long-term depression (LTD) but not long-term potential (LTP) in $Mapt^{-/-}$ mice [27]. A study reported by Ahmed et al. observed a severe deficit in LTP, but no change in LTD, in another $Mapt^{-/-}$ mouse line [28]. Tau is also expressed in the nuclei and is thought to maintain the integrity of the genomic DNA (Figure 2A) [29]. Recent studies have emerged that tau may act generally as a scaffolding protein interacting with various kinases and phosphatases to regulate phosphorylation-based signaling pathways, functioning as a signaling hub protein within cells [30].



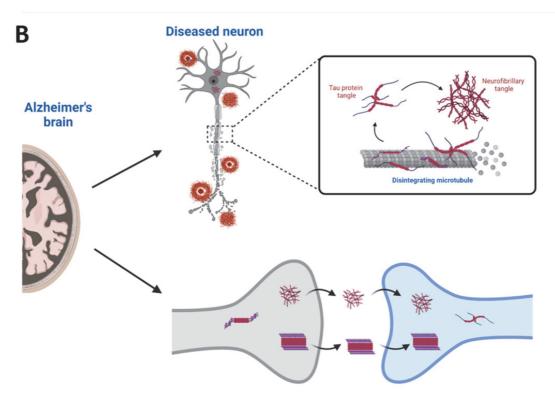


Figure 2. Biological functions of tau in the CNS. (**A**). In the physiological state. Tau protein plays different roles according to its subcellular localization in normal, healthy neurons. In nuclei, tau may function to maintain the integrity of the genomic DNA (a). In the axon, tau maintains the microtubule's stability and inhibits axonal transport (b and c). In the dendrite, tau functions to regulate synaptic plasticity (d). (**B**). In the pathological state. Under

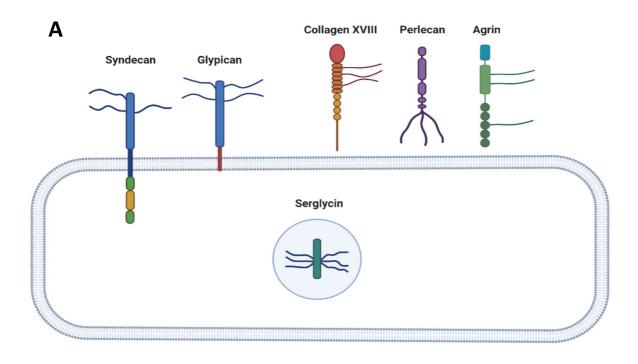
certain stress conditions, the normal tau undergoes hyperphosphorylation and is detached from the microtubule to form tau fibrils and, eventually, the NFTs, leading to neurodegeneration. Meanwhile, NFTs are released from the diseased neurons and uptaken by the neighbor healthy neuron, spreading the disease through prion-like propagation in the CNS.

4. Tau in Pathological States

Physiological tau is a natively unfolded and highly soluble protein with little tendency for aggregation $^{[Q]}$. Under pathogenic conditions, the dynamics and equilibrium of tau-microtubule binding are disrupted, leading to tau aggregation and oligomerization into paired helical filaments (PHFs) and, further, the neurofibrillary tangles (NFTs) which accumulate in neurons, glia, and extracellular space (**Figure 2**B) $^{[Q]}$. The formation of tau aggregates is more strongly correlated with cognitive decline than the distribution of senile plaques formed by amyloid beta (A β) protein deposits, another pathological hallmark of AD $^{[31]}$.

5. Heparan Sulfate Proteoglycans

Heparan sulfate proteoglycans (HSPGs) are macromolecules ubiquitously expressed in mammalian tissues. They are comprised of a core protein to which one or more HS glycosaminoglycan (GAG) chains are covalently attached [32][33]. The HSPGs are classified based on the location of their core proteins (Figure 3A). Syndecans (SDCs) and glypicans are the two major membrane-bound PGs that are linked to the plasma membrane by a transmembrane domain or a glycosylphosphatidylinositol (GPI) linker, respectively. In addition, there are three "part-time" cell-surface PGs, betaglycans, neuropilins, and CD44v3, which do not always have an HS chain moiety and are located on the cell surface through their transmembrane domains. Other HSPGs include agrin, perlecan, type XVIII collagen in the extracellular matrix (ECM), and serglycin in the intracellular secretory vesicles (Figure 3A) [32][33].



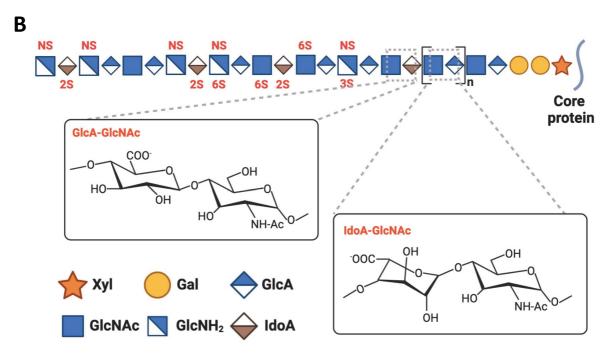


Figure 3. HSPG and HS structure. **(A)**. HSPG classification. Mian HSPGs include membrane-bound syndecans and glypicans, extracellular matrix collagen XVIII, perlecan and agrin, and serglycin expressed in the intracellular secretory vesicles. **(B)** HS structure. HS is a linear polysaccharide composed of 20–150 GlcA-GlcNAc/IdoA-GlcNAc repeats with sulfation modifications at NH-Ac, C6, and C3 positions of GlcNAc and C2 position of IdoA and GlcA (lower frequency). The modifications tend to occur in clusters (sulfated domain). The modification pattern and the sulfated domain arrangement form specific ligand binding sites.

Most of the biological functions of HSPGs are mediated by their HS chains [32]. The HS chain is a linear polysaccharide containing 50–200 disaccharide repeats composed of uronic acid (either glucuronic acid (GlcA) or

iduronic acid (IdoA)) and N-acetylglucosamine (GlcNAc) (**Figure 3**B). The biosynthesis of HS occurs in the endoplasmic reticulum and the Golgi apparatus and involves various enzymes. HS biosynthesis occurs in three major steps: chain initiation, elongation, and modification [33].

Due to substrate specificity and incompletion of the modification by the enzymes, the modifications tend to occur in clusters and generate tremendous structural heterogeneity. The modification patterns form binding sites for many protein ligands, including growth factors, growth factor receptors, and tauopathy-related proteins such as tau, A β , and α -syn [34][35][36][37]. In addition, the HS structures are cell-type/tissue/developmental stage-specific, indicating that HS may interact selectively with a fraction of protein ligands to play unique spatiotemporal regulatory roles under different biological conditions [32][38].

6. Heparan Sulfate-Tau Interaction: The Related Structures

HS and heparin, a highly sulfated form of HS, directly bind to tau protein [39][40]. Snow et al. and Su et al. observed by ultrastructural immunolocalization that HS co-localizes with NFTs in neurons in the brains of AD patients [41][42], suggesting that HS interacts with tau in the AD brain. Like other heparin-protein interactions [43][44], the tau binds HS and the binding is mediated by electrostatic interaction through the highly positively charged residues/domain within the tau protein and the highly negatively charged sulfate residues within HS. Further studies determined that the hexapeptides ²⁷⁵VQIINK²⁸⁰ in R2 and ³⁰⁶VQIVYK³¹¹ in R3 of tau bind to HS [45][46][47][48][49]. In NMR titration of heparin to K18, L282 displayed the most chemical shift perturbation, suggesting that the two lysines near ²⁷⁵VQIINK²⁸⁰ in R2, K280 and K281, are likely crucial to heparin and HS binding. A recent study further showed that Arixtra, a sulfated pentamer analog of heparin, bound proline-rich region II (PRR2) with 4 times stronger binding affinity than R2 [50]. These studies indicate that the major HS binding sites within tau protein are in the R2 and PRR2 domains (Figure 4A).

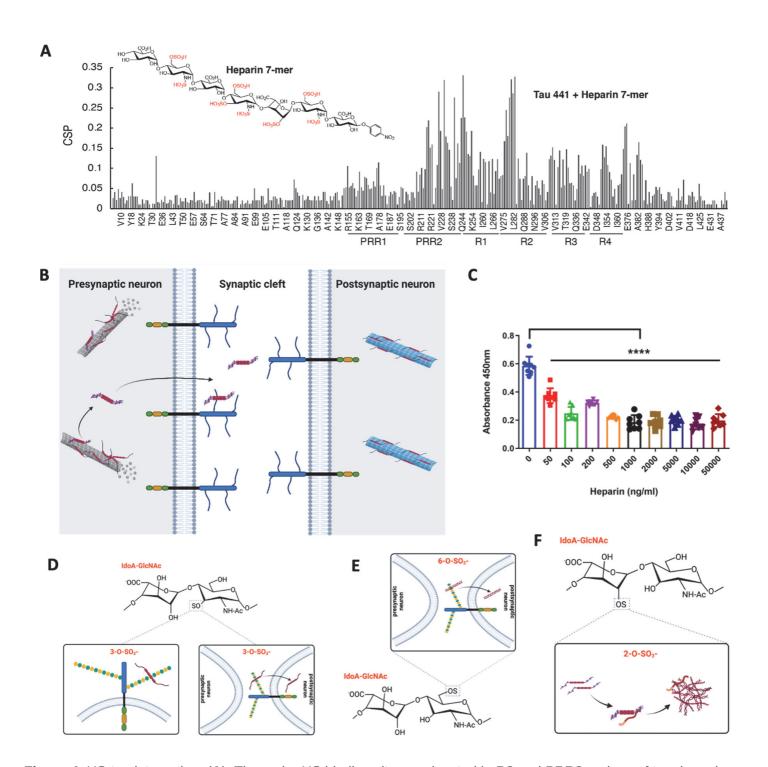


Figure 4. HS-tau interaction. **(A)**. The major HS binding sites are located in R2 and PRR2 regions of tau, based on chemical shift perturbation (CS) caused by a heparin 7mer ^[50]. **(B)**. Tau secretion from the presynaptic neuron through an unconventional pathway is facilitated by cell surface HSPGs. **(C)**. Tau at 50 ng/mL binds to the mouse lung endothelial cell surface. Heparin inhibits tau protein binding to the cell surface dose-dependently and reaches a plateau at 500 ng/mL. ****, *p* value < 0.0001 in ANOVA multiple group analysis **(D)**. 3-*O*-sulfation of HS enhances tau protein cell surface binding and cellular uptake. **(E)**. 6-*O*-sulfation of HS enhances tau protein cellular uptake. **(F)**. 2-*O*-sulfation of HS enhances the tau aggregation.

7. The Role of Heparan Sulfate in the Tau-Mediated Pathological Process

HS has been suggested to play an essential role in each stage of the prion-like propagation of tau pathology, including Tau secretion, cell surface binding, internalization, and aggregation [51].

7.1. HS in Tau Secretion

Tau is predominately an intracellular protein and has also been found in the extracellular space under both physiological and pathological conditions [52]. Tau is continuously secreted under physiological conditions without cell death, indicating some functional roles of the extracellular tau [53][54][55]. Several studies have demonstrated that tau does not follow the conventional secretory pathway but uses multiple unconventional secretory pathways [56][57]. Merezhko et al. showed that phosphorylated, oligomeric tau clusters on the plasma membrane in neuronal cells and is secreted in the vesicle-free form in an unconventional process, and the secretion was supported by cell surface HSPGs, possibly by facilitating its release after membrane penetration [58]. Katsinelos et al. further delineated that in the cytosol, free tau interacts with phosphatidylinositol 4,5-bisphosphate enriched at the inner leaflet of the plasma membrane, leading to its translocation across the plasma membrane via HSPGs (**Figure 4**B) [59].

7.2. HS in Tau Cell Surface Binding

The association between tau and the cell surface implicates tau protein uptake and related intracellular signaling. Tau was observed to bind to endothelial cell surface and the cell surface binding was inhibited by externally added heparin (**Figure 4**C), suggesting that HS mediates the cell surface binding of tau, which is consistent with other groups' findings in which HSPGs mediated the binding of tau to C17.2 cells [51][60]. In addition, knockout of HS 3-O-sulfotransferase-1 (*Hs3st1*) reduces 3-O-sulfation of HS and attenuated endothelial cell surface HS-mediated tau protein binding, supporting the high-affinity tau binding site within HS containing 3-O-sulfate (**Figure 4**D) [35][61].

7.3. HS in Tau Internalization

In 2013, Holmes et al. first demonstrated that HSPGs is a critical mediator for tau uptake in mouse neural progenitor cell line [51]. Using differently sized and chemically modified heparins, the same group further determined that tau aggregates required a somewhat specific HS architecture with defined sulfate moieties containing *N*- and 6-*O*-sulfations, confirmed by reduced tau cellular uptake upon knockout of *Ndst1* or *Hs6st2*, the genes responsible for N-sulfation and 6-*O*-sulfation modification in HS biosynthesis, respectively [37]. Rauch et al. also reported that tau protein internalization depends on 6-*O*-sulfation of HS (**Figure 4**E) [62].

The 3-*O*-sulfation has been proven to enhance HS-mediated tau internalization. Sepulveda-Diaz et al. reported that 3-*O*-sulfated HS could be internalized into cells where HS interacts with tau and promotes tau phosphorylation ^[61]. In the recent study, the researchers showed that introducing a 3-*O*-sulfate significantly increased the binding of an HS dodecasaccharide to tau and knockout of *Hs3st1*, which reduces about 50% 3-*O*-sulfation of HS in mouse lung

endothelial cells ^[63], significantly decreased tau uptake by the cells (**Figure 4**D) ^[35]. Knockout of *Hs3st1* in HEK293T cells appeared not to affect tau uptake ^[37], which might be due to the low expression of *Hs3st1* in this cell line (https://www.proteinatlas.org/ENSG00000002587-HS3ST1/cell+line (accessed on 20 November 2022)). These studies demonstrated that HS facilitates tau protein internalization and further support that the tau-binding HS structure contains *N*-, 6-*O*-, and 3-*O*-sulfations, in agreement with previous biochemical binding studies ^[37]. In contrast, HSPGs were dispensable for tau protein uptake by primary astrocytes, revealing that HS's function in facilitating tau internalization is cell-type dependent ^[37]64].

7.4. HS in Tau Aggregation

HS was found to accumulate with NFTs in the AD brain, suggesting that HS may promote tau aggregation in the brain 42. Arrasate et al. incubated the isolated PHFs from AD patients with heparinase and found that the PHF morphology was changed after digestion [65]. These observations suggested that HS may facilitate tau protein aggregation to exacerbate tauopathy. This hypothesis has been supported by the regular in vitro tau aggregation experimental setting, which requires the addition of polyanionic cofactors such as RNA or heparin to initiate the aggregation [66][67][68][69][70][71]. This facilitation depends on the direct binding of heparin to soluble tau monomers, which is thought to neutralize the positive, repulsive charges on tau and allow more contact between monomers [66] [67][71]. Townsend et al. examined truncated tau (\Delta\tau187, residue 255-441) aggregation induced with chemically modified heparins [68]. Removal of 6-O-sulfation, not 2-O-sulfation, reduces heparin's binding affinity for Δtau187, which in agreement with other study findings, showing 6-O-sulfation is required for HS to bind tau protein [37][48]. However, tau aggregation is considerably slower in the presence of 2-O-desulfated heparin than with N- or 6-Odesulfated heparin, indicating that 2-O-sulfation contributes more than 6-O and N-sulfation in facilitating tau aggregation (Figure 4F), apparently due to 2-O-sulfation promoting tau primary and secondary nucleation and filament elongation [68]. However, the sulfation pattern dependence has not been determined in the aggregation of full-length tau and phosphorylated tau. It may be different, especially considering the importance of PRR2 in tau binding. In addition, Sepulveda-Diaz, J.E. et al. reported that Hs3st2 increases tau phosphorylation in a cell model and a zebrafish model of tauopathy, showing that HS promotes tau phosphorylation to facilitate tau aggregation indirectly. This is supported by Huynh et al. reporting that Hs3st2 expression induces the cell-autonomous oligomerization of tau and the phosphorylation of tau in an *in vitro* cell model $\frac{72}{2}$.

8. Aberrant HSPG Expression in AD and Other Tauopathies

The proteoglycan cores of HSPGs are differentially expressed in AD compared with normal human brains, which has been shown to impact tau internalization [73]. The impact of Alzheimer's disease on membrane-bound HSPG agrin distribution has been documented since 1999; in normal brains, agrin is in the soluble fraction of detergent extracted samples, while in AD brains, agrin shifts to the insoluble fraction [74]. One study found that genes associated with syndecan-4 (*SDC4*), followed by *SDC3*, *SDC2*, *agrin*, and *serglycin* (the dominant intracellular PG in immune cells) [75] were consistently overexpressed in AD brains compared with controls [76]. SDC3 has the highest affinity for tau monomer, but interestingly, overexpression of *SDC3* and -4 in K562 cells (lymphoblast cells with low endogenous HS) did not lead to a greater internalization of tau, but increased fibrillation and accumulation

of fibrils on the cell surface [73]. These studies emphasize the impact of tauopathies on the specific core proteins of HSPGs.

Several studies have documented altered HS expression in AD patients (**Table 1**). Su et al. examined 7 AD patients and 4 age-matched controls and observed that the number and intensity of the HS co-staining with PHFs were denser in AD than in control brains [41]. Shimizu et al. examined 25 AD patients with 10 non-demented elderly patient controls. They detected a 9.3-fold HS increase in the hippocampus and a 6.6-fold HS increase in gyrus frontalis superior in the AD patients. They also observed that HS is most abundantly expressed in the basement membrane of capillary endothelial cells [77]. Other groups' studies confirmed the abnormal HS expression in the AD brain [34][78].

Table 1. Altered HS expression and function in AD patients. -, No change; ↑, increase; N/A, not available.

Clinical Diagnosis	Predominant Tau Isoforms	Human Brain Samples	GAGs/Gene Expression in Disease	GAGs Function in Disease	Reference
AD	3R + 4R Tau	7 AD vs. 4 control	HS↑	N/A	[<u>41</u>]
AD	3R + 4R Tau	N/A	N/A	Helicity of PHFs changed (potential)	[<u>65]</u>
AD	3R + 4R Tau	25 AD vs. 10 control	HS↑	N/A	[<u>77</u>]
AD	3R + 4R Tau	20 AD vs. 20 control	Sulf1 -; Sulf2 ↓	N/A	[<u>79</u>]
AD	3R + 4R Tau	5 AD vs. 5 control	HS ↑; Ndst2 ↑; Hs3st2 ↑; Hs3st4 ↑; Glce ↑; HPSE ↑	HS-tau binding capacity ↑	[<u>34</u>]
AD	3R + 4R Tau	18 AD vs. 6 control	Altered expression of multiple HS biosynthesis/remodeling genes	N/A	[80]

Clinical Diagnosis	Predominant Tau Isoforms	Human Brain Samples	GAGs/Gene Expression in Disease	GAGs Function in Disease	Reference	
AD	3R + 4R Tau	5 AD vs. 5 control	HS ↑; 3-o-sulfation ↑	N/A	[<u>78</u>]	
						lenges.

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