

Alzheimer's Disease-Related Phospho-Tau181 Signals Are Localized to Demyelinated Axons of Parvalbumin-Positive GABAergic Interneurons in an *App* Knock-In Mouse Model of Amyloid- β Pathology

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Abstract.

Background: The tau protein phosphorylated at Thr181 (p-tau181) in cerebrospinal fluid and blood is a sensitive biomarker for Alzheimer's disease (AD). Increased p-tau181 levels correlate well with amyloid- β (A β) pathology and precede neurofibrillary tangle formation in the early stage of AD; however, the relationship between p-tau181 and A β -mediated pathology is less well understood. We recently reported that p-tau181 represents axonal abnormalities in mice with A β pathology (*App*^{NLGF}). However, from which neuronal subtype(s) these p-tau181-positive axons originate remains elusive.

Objective: The main purpose of this study is to differentiate neuronal subtype(s) and elucidate damage associated with p-tau181-positive axons by immunohistochemical analysis of *App*^{NLGF} mice brains.

Methods: Colocalization between p-tau181 and (1) unmyelinated axons positive for vesicular acetylcholine transporter or norepinephrine transporter and (2) myelinated axons positive for vesicular glutamate transporter, vesicular GABA transporter, or parvalbumin in the brains of 24-month-old *App*^{NLGF} and control mice without A β pathology were analyzed. The density of these axons was also compared.

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Results: Unmyelinated axons of cholinergic or noradrenergic neurons did not overlap with p-tau181. By contrast, p-tau181 signals colocalized with myelinated axons of parvalbumin-positive GABAergic interneurons but not of glutamatergic neurons. Interestingly, the density of unmyelinated axons was significantly decreased in *App^{NLGF}* mice, whereas that of glutamatergic, GABAergic, or p-tau181-positive axons was less affected. Instead, myelin sheaths surrounding p-tau181-positive axons were significantly reduced in *App^{NLGF}* mice.

Conclusion: This study demonstrates that p-tau181 signals colocalize with axons of parvalbumin-positive GABAergic interneurons with disrupted myelin sheaths in the brains of a mouse model of A β pathology.

Keywords: Alzheimer's disease, amyloid- β , biomarker, GABAergic interneuron, myelin, parvalbumin, phospho-tau

INTRODUCTION

Phospho-tau proteins have been reported as promising fluid biomarkers for Alzheimer's disease (AD). Increases in the levels of tau phosphorylated at Thr181 (p-tau181), Thr217 (p-tau217), and Thr231 (p-tau231) in cerebrospinal fluid (CSF) and plasma correlate well with amyloid-positron emission tomography (PET) positivity [1, 2] and detect AD during the preclinical period with high accuracy [3–8]. Moreover, a study in a mouse model of familial AD has shown that extracellular amyloid- β (A β) pathology is sufficient to increase p-tau181 and p-tau217 levels in CSF in the absence of tau tangles [9]. However, relationships between these p-tau proteins and A β -mediated brain pathology are less well understood.

By utilizing the *App* knock-in mouse model of A β pathology (*App^{NLGF}* mice), we recently reported that p-tau217 and p-tau231 signals were specifically detected around A β plaques in the brains of *App^{NLGF}* mice and colocalized with the postsynaptic marker, postsynaptic density protein 95 (PSD-95). This suggests that the appearance of p-tau217 and p-tau231 may represent postsynaptic pathology of glutamatergic neurons associated with A β plaques [10]. By contrast, most p-tau181 signals did not colocalize with p-tau217 or p-tau231; rather, they were readily detectable in the axons of wild-type (WT) mouse brains, and these axonal structures were disrupted in *App^{NLGF}* mice [10]. Interestingly, although tau proteins are ubiquitously expressed in neuronal axons, p-tau181 signals are localized to only certain axons. Whether a specific neuronal subtype(s) is responsible for p-tau181-positive axons, and the type of axonal damage caused by A β pathology, remains elusive.

Widespread brain regions and several neurotransmitter systems are affected in AD brains. For example, aberrant neurotransmission and neurode-

generation in the cholinergic system are observed in the early stage of AD [11, 12] and have been a therapeutic target for improving clinical symptoms [13, 14]. The nucleus basalis of Meynert (NBM) is a major source of cortical cholinergic innervation with long and thin unmyelinated axons [15]. In the prodromal stage of AD, reduced cholinergic projections and tau pathology have been observed [16–20]. Monoaminergic neurons, including the noradrenergic system, are also affected in the early stage of AD, which is thought to cause cognitive deficits. Noradrenergic neurons in the locus coeruleus extend their unmyelinated axons throughout the cortex [21–24] and are reported to degenerate and develop tau pathology in the early stage of AD [25–29]. These reports suggest that p-tau181 signals might be localized to unmyelinated axons.

In addition to unmyelinated neurons in subcortical and brainstem regions, excitatory-inhibitory imbalance in myelinated neurons in the cortex has been linked to cognitive decline in early AD [30]. During AD progression, neuronal hyperactivity is hypothesized to be induced by A β pathology, followed by neuronal loss. And altered GABAergic transmission [31], especially fast-spiking parvalbumin-expressing interneurons, is suggested to play a role in this network dysfunction [32, 33]. Several studies have also shown that glutamatergic and GABAergic synapses are damaged by A β accumulation in the brains of AD patients [34–37]. These reports suggest that p-tau181 signals might localize to myelinated glutamatergic and/or GABAergic axons.

To elucidate from which neuronal subtype(s) p-tau181-positive axons originate, and the type of axonal damage induced by A β pathology, we utilized an *App* knock-in mouse model of A β pathology [38]. *App^{NLGF}* mice harbor three familial AD mutations (Swedish [NL], Arctic [G], and Beyreuther/Iberian [F]) and show progressive A β pathology in the brain parenchyma along with severe neuroinflamma-

tion and cognitive deficits [38, 39]. Our systematic immunohistochemical analyses revealed that p-tau181 signals overlapped with myelinated axons of parvalbumin-expressing GABAergic interneurons but not those of glutamatergic, cholinergic, or noradrenergic neurons, and that myelin sheaths of p-tau181-positive axons were disrupted in *App^{NLGF}* mice. These results suggest that p-tau181 may reflect demyelination of parvalbumin-expressing GABAergic interneurons upon A β accumulation in the early stage of AD.

MATERIALS AND METHODS

Animals

Experiments were performed using 6- or 24-month-old male C57BL/6J and *App* knock-in (*App^{NL}*, *App^{NLGF}*) mice [38]. All handling and experimental procedures were previously described [10] and performed in accordance with the NIH Guide for the Care and Use of Laboratory Animals and other national regulations and policies with the approval of the Animal Care and Use Committee at National Center for Geriatrics and Gerontology, Japan (Approval number: 2–45).

Tissue preparation

All animals were deeply anesthetized by intraperitoneal administration of a combination of medetomidine (0.3 mg/kg), midazolam (4.0 mg/kg), and butorphanol (5.0 mg/kg), and whole brains were collected and processed for cryosectioning, as previously described [10].

Immunohistochemistry

Immunohistochemical staining was performed as described previously [10]. The primary and secondary antibodies used in this study were listed in Supplementary Table 1. For nuclear staining, 4',6-diamidino-2-phenylindole (DAPI) or propidium iodide (PI) were used in an appropriate combination. For detection of A β amyloidosis, 1-fluoro-2,5-bis (3-carboxy-4-hydroxystyryl) benzene (FSB) was used.

Image acquisition and analysis

As described previously [10, 40], images were acquired using either a LSM700 or LSM780 confocal laser-scanning microscope (Carl Zeiss, Germany)

fitted with 20 \times or 63 \times objectives. All image processing and analyses were performed with Fiji software using appropriate plugin.

Measurement of coverage with vesicular acetylcholine transporter (VACHT)- and myelin basic protein (MBP)-positive fibers

Procedures for measuring coverage with the fibers from the acquired images were described previously [10, 40]. We captured images using a LSM700 confocal microscopy with a 20 \times objective, and 10 μ m Z-stacks (0.85 μ m interval between images) were reconstructed with a maximum intensity projection. Immunoreactivities for VACHT or MBP were defined as numbers of signal-positive pixels within an entire image, which were determined by thresholding with an automated method (Li's method for VACHT and Otsu's method for MBP).

Counting of choline acetyltransferase (ChAT)-positive cell in the NBM

For counting number of ChAT-positive cells in the NBM, we captured images using a LSM780 confocal microscopy with a 20 \times objective and reconstructed 25 μ m Z-stacks (2.88 μ m interval between images) with a maximum intensity projection. We chose the coronal sections including the NBM evenly through rostral to caudal portions (–0.34 to –0.94 mm from bregma) and counted ChAT-positive cell number according to the procedure previously described [10, 40].

Measurement of immunoreactivity for p-tau181, vesicular glutamate transporter 1 (VGLUT1) and vesicular GABA transporter (VGAT)

Procedures for measuring immunoreactivity from the acquired images were described previously [10, 40]. For acquisition of immunofluorescence for p-tau181, VGLUT1, and VGAT, we captured images using a LSM700 confocal microscopy with a 20 \times objective, and reconstructed 10 μ m Z-stacks (0.85 μ m interval between images) with a maximum intensity projection. Fluorescent intensity from each signal was evaluated and expressed as relative percentage to WT mice.

Statistical analysis

All statistical analyses were conducted using GraphPad Prism 9 (GraphPad software) as previously described [10]. One-way ANOVA followed by the Tukey's *post hoc* tests or Student's *t*-test was used. Data are presented as mean \pm SEM. All alpha levels were set at 0.05. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

RESULTS

p-tau181-positive axons do not overlap with unmyelinated cholinergic or noradrenergic axons in mouse brains

We recently reported that p-tau181 signals were localized to neuronal axons in WT mice [10], and that these structures were disrupted in *App*^{NLGF} mice, which develop massive A β plaques but not neurofibrillary tangles [38, 41]. However, whether a specific neuronal subtype(s) is associated with p-tau181 signals was unclear. Here, we first examined whether p-tau181 signals overlap with unmyelinated axons of cholinergic and noradrenergic neurons in *App*^{NLGF} mice and control mice without A β pathology.

The *App*^{NLGF} mice exhibit age-dependent A β deposits in the cortex and hippocampus, but do not show tau pathology such as neurofibrillary tangles [41, 42]. Thus, *App*^{NLGF} mice are thought to recapitulate A β pathology at the preclinical and early stages of AD. In addition to WT mice with the same C57BL/6J background, we also included *App*^{NL} mice, which harbor a familial AD-related Swedish [NL] mutation and produce human A β and A β PP fragments but do not develop A β pathology as controls [39, 43]. We costained brain sections from 24-month-old *App*^{NLGF}, *App*^{NL}, and WT mice with antibodies against p-tau181 and vesicular acetylcholine transporter (VAcHT), a marker of cholinergic axon terminals (Fig. 1A1–A5, B1–B4, and C1–C5), or norepinephrine transporter (NET), a marker of noradrenergic axon terminals (Fig. 1D1–D5, E1–E4, and F1–F5) in the cortex. High-magnification images revealed that these signals did not overlap (Fig. 1A5, C5, D5, and F5). To further confirm these results, we used 3D reconstruction imaging techniques and found that there was no overlap between p-tau181-positive signals and VAcHT or NET signals (Supplementary Movies 1 and 2).

Taken together, these results indicate that p-tau181 signals are not localized to unmyelinated cholinergic or noradrenergic axons in mouse brains.

The density of cholinergic axons, but not p-tau181 signals, is significantly reduced in the cortex of App^{NLGF} mice

We next analyzed and compared how cholinergic axons and p-tau181-positive axons were affected in the brains of *App*^{NLGF} mice. Brain sections from 24-month-old *App*^{NLGF}, *App*^{NL}, and WT mice were stained with an antibody against VAcHT, and the area of VAcHT immunoreactivity was quantified. The density of VAcHT-positive fibers was significantly reduced in *App*^{NLGF} mice compared with the density of those in *App*^{NL} or WT mice, both in the cortex (Fig. 2A, B) and hippocampus (Supplementary Figure 1A, B). In addition, cholinergic axons showed axonal dystrophy around A β plaques in *App*^{NLGF} mice (Fig. 2C, higher magnification of framed region in 2A). By contrast, the density of VAcHT-positive fibers was similar between *App*^{NL} and WT mice (Fig. 2A, B). To determine whether a reduction in cholinergic afferents in the cortex reflects neuron loss in the NBM, we immunostained brain sections containing the NBM from *App*^{NLGF}, *App*^{NL}, and WT mice with an antibody against choline acetyltransferase (ChAT), a marker of cholinergic neurons (Fig. 2D). Quantitative analysis revealed similar numbers of ChAT-positive neurons in the NBM regions of all genotypes (Fig. 2E), indicating that the reduced density of cholinergic afferents in *App*^{NLGF} mice is not due to NBM neuron loss. These results are similar to those of our previous study showing that the density of unmyelinated noradrenergic afferents is significantly reduced without neuron loss in the locus coeruleus in *App*^{NLGF} mice [40].

We next stained brain sections with an antibody against p-tau181, and the signal intensity was quantified (Fig. 3A, B). Although p-tau181-positive axons showed axonal dystrophy around A β plaques (Fig. 3C, higher magnification of framed region in 3A), the density of p-tau181-positive axons was not significantly reduced in the cortex of *App*^{NLGF} mice compared to that in *App*^{NL} or WT mice (Fig. 3A, B).

Myelin sheaths of p-tau181-positive axons are disrupted in App^{NLGF} mice

As p-tau181 signals did not overlap with unmyelinated axons, we next examined whether p-tau181

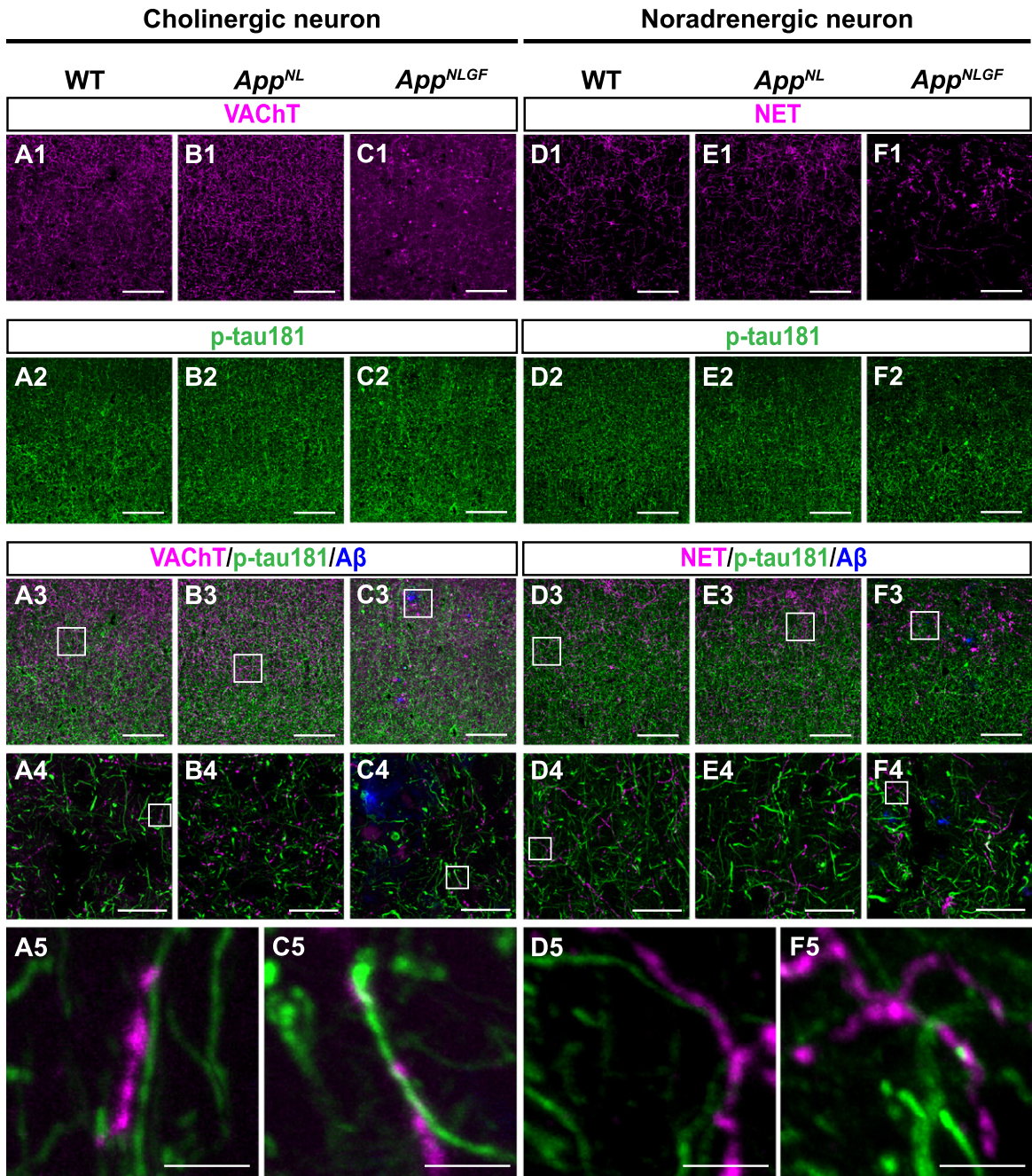


Fig. 1. p-tau181-positive axons do not overlap with unmyelinated cholinergic or noradrenergic axons in mouse brains. Representative images of the cortex from frozen coronal brain sections immunostained with antibodies against VAcHT (A1–C1; magenta in A3–C3), NET (D1–F1; magenta in D3–F3), and p-tau181 (A2–F2; green in A3–F3). FSB was used for detecting A β plaques (blue in A3–F3). Scale bars, 100 μ m. (A4–F4) Higher magnification of framed regions indicated in A3–F3. Scale bars, 20 μ m. (A5–F5) Higher magnification of framed regions indicated in A4–F4. Scale bars, 2.5 μ m.

signals are localized to myelinated axons. Brain sections from 24-month-old *App^{NLGF}*, *App^{NL}*, and WT mice were costained with antibodies against p-tau181 and myelin basic protein (MBP), a major

component of myelin sheaths (Fig. 4A1–A5, B1–B4, and C1–C5). High-magnification images revealed that these signals overlapped well in the cortex of WT and *App^{NLGF}* mice (Fig. 4A5 and C5, white arrows).

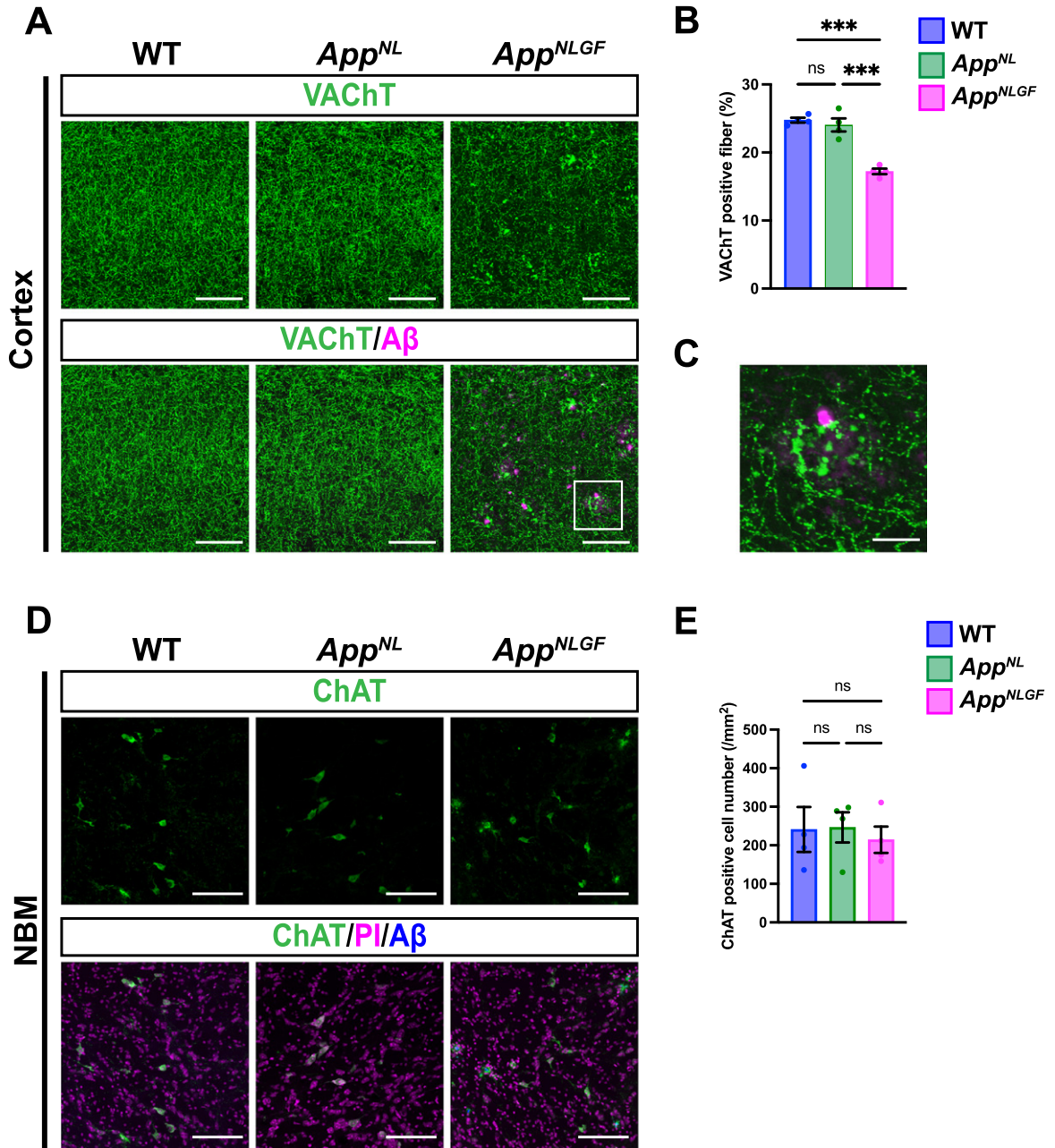


Fig. 2. The density of cholinergic axons is significantly reduced in the cortex of *App^{NLGF}* mice. (A) Representative images of the cortex from frozen coronal brain sections immunostained with antibodies against VAcHT (green). FSB was used for detecting A β plaques (magenta). Scale bars, 100 μ m. (B) VAcHT immunoreactivity was quantified and expressed as positive area (%). *n* = 4/group. ****p* < 0.001. (C) A higher magnification of framed region indicated in A. Scale bar, 20 μ m. (D) Representative images of the NBM from frozen coronal brain sections immunostained with antibodies against ChAT (green) were shown (magenta indicated PI staining). FSB was used for detecting A β plaques (blue). (E) The number of ChAT-positive cells was counted and expressed as cell number per area (/mm²). Scale bar, 100 μ m. *n* = 4/group. ns, not significant.

Further 3D reconstruction confirmed that p-tau181-positive axons were located close to MBP-positive myelin sheaths in the cortex of WT and *App^{NLGF}* mice (Supplementary Movie 3).

Of particular interest, coverage with MBP-positive myelin sheaths was significantly reduced in the cortex of *App^{NLGF}* mice compared to that in WT and *App^{NL}* mice (Fig. 4A1, B1, C1, and G). Myelin

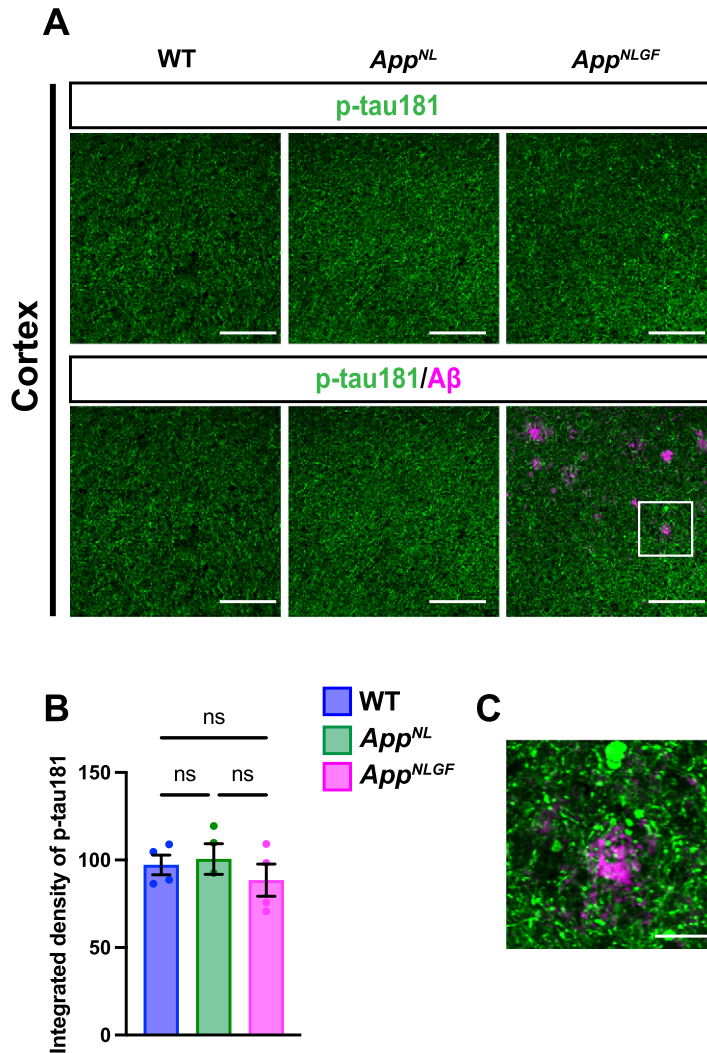


Fig. 3. The density of p-tau181 signals is not significantly reduced in the cortex of *App*^{NLGF} mice. (A) Representative images of the cortex from frozen coronal brain sections immunostained with antibodies against p-tau181 (green) and Aβ (magenta). Scale bars, 100 μm. (B) P-tau181 immunoreactivity was quantified and expressed as relative percentage to WT. *n* = 4 /group. ns; not significant. (C) A higher magnification of framed region indicated in A. Scale bars, 20 μm.

sheaths were disrupted in *App*^{NLGF} mice with massive Aβ pathology (Fig. 4C1), but not in *App*^{NL} mice (Fig. 4B1), which overproduce soluble Aβ but do not exhibit Aβ plaques, suggesting that the disruption of myelin sheaths was correlated with insoluble Aβ deposits. We also noticed that reductions in myelin sheaths were not limited to areas near Aβ plaques but also were evident in areas distant from Aβ plaques, suggesting that disruption of myelin sheaths was not only due to physical damages caused by Aβ plaques but also due to altered brain homeostasis induced by Aβ pathology, such as neuroinflammation. To ask whether the disruption of myelin sheaths

is due to developmental defects, we stained brain sections from 6-month-old *App*^{NLGF} and WT mice with antibodies against MBP and p-tau181. Again, these two signals were well colocalized (Supplementary Figure 2A), however, unlike 24-month-old mice, MBP-positive myelin sheaths enwrapping p-tau181-positive axons were not significantly reduced in the brains of 6-month-old *App*^{NLGF} mice (Supplementary Figure 2B). These results indicate that disruption of myelin sheaths in 24-month-old *App*^{NLGF} mice is not due to developmental defects but is a progressive event in response to accumulation of Aβ pathology.

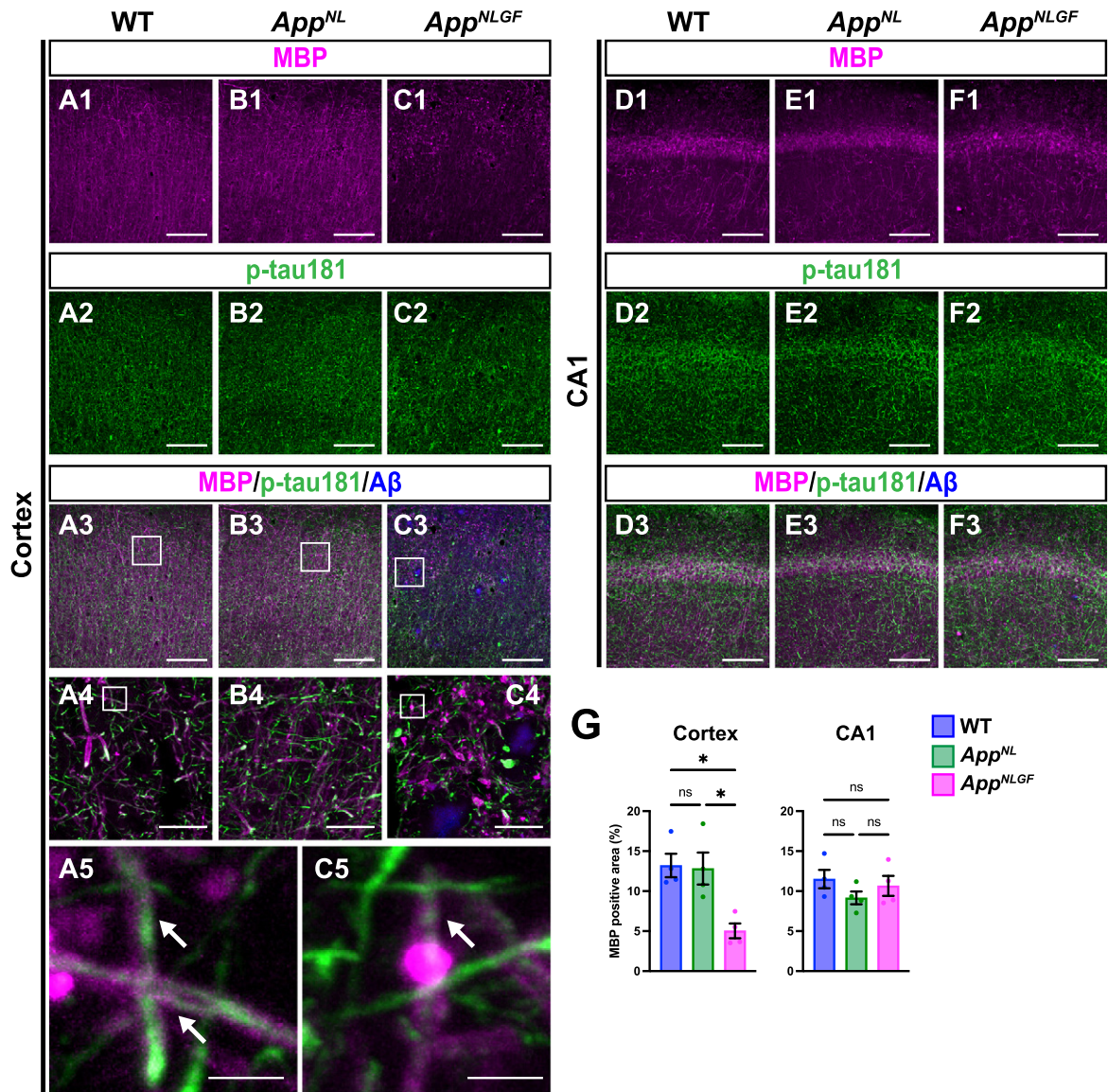


Fig. 4. Myelin sheaths of p-tau181-positive axons are disrupted in *App^{NLGF}* mice. Representative images of the cortex (A1–C3) and hippocampal CA1 subfield (D1–F3) from frozen coronal brain sections immunostained with antibodies against MBP (magenta) and p-tau181 (green). FSB was used for detecting A β plaques (blue). Scale bars, 100 μ m. (A4–C4) Higher magnification of framed regions indicated in A3–C3. Scale bars, 20 μ m. (A5 and C5) Higher magnification of framed regions indicated in A4 and C4. White arrows indicate p-tau181-positive axons overlapped with MBP-positive myelin sheaths. Scale bars, 2.5 μ m. (G) MBP immunoreactivity in the cortex or hippocampal CA1 subfield was quantified and expressed as positive area (%). $n = 4$ /group. * $p < 0.05$, ns, not significant.

In contrast to the cortex, myelin sheaths were not significantly affected in the hippocampus of *App^{NLGF}* mice compared to that in WT and *App^{NL}* mice (Fig. 4D1, E1, F1, and G), which is presumably due to that A β pathology in the hippocampus is less severe than that in the cortex in *App^{NLGF}* mice as previously reported [38].

Taken together, these results indicate that p-tau181 signals are localized to cortical myelinated axons

whose myelin sheaths are significantly disrupted by A β pathology.

p-tau181-positive axons do not overlap with glutamatergic axons in mouse brains

As axons of glutamatergic excitatory neurons and GABAergic interneurons are both highly myelinated by oligodendrocytes [44], we first examined whether

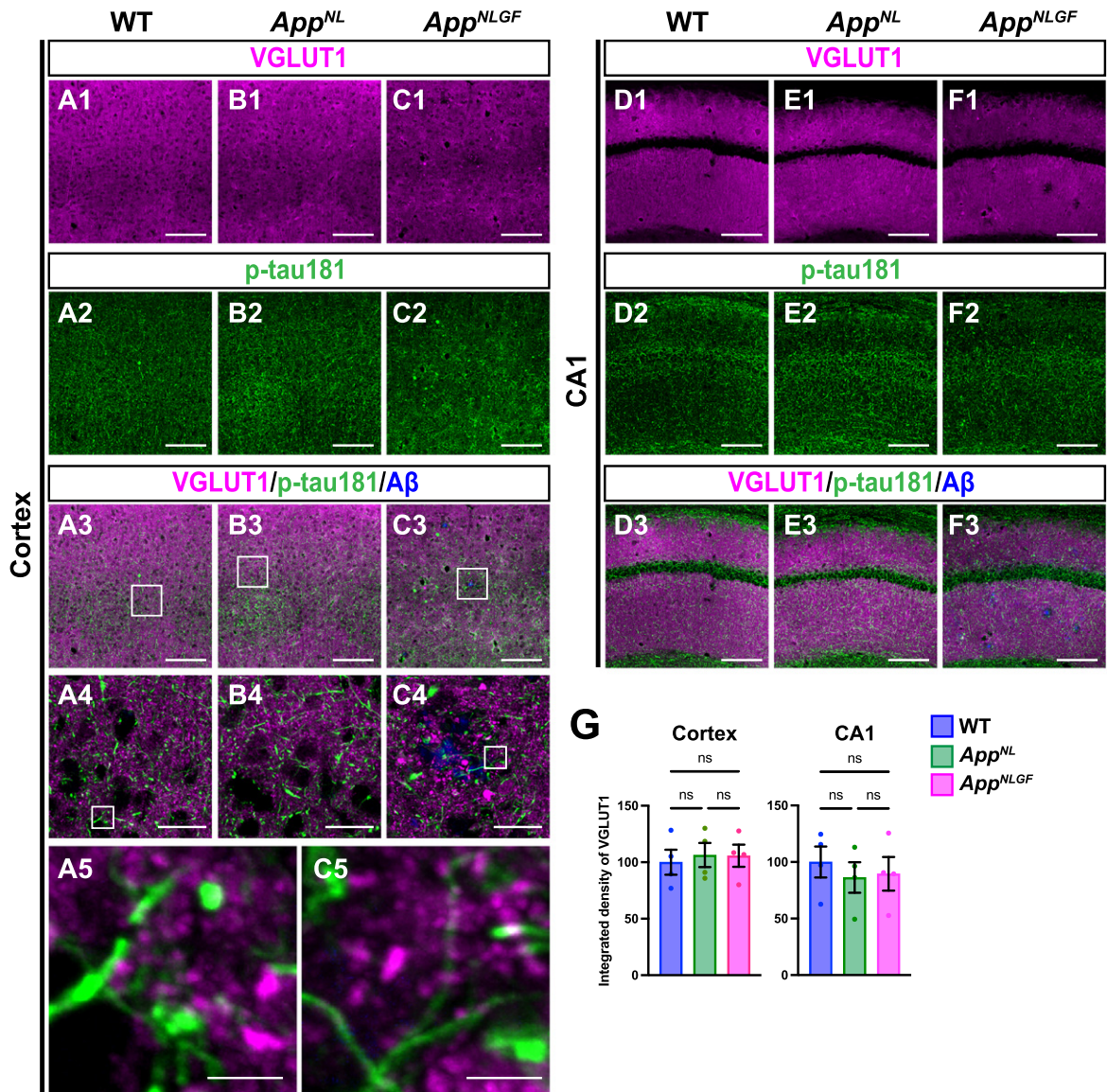


Fig. 5. p-tau181-positive axons do not overlap with glutamatergic axons in mouse brains. Representative images of the cortex (A1–C3) and hippocampal CA1 subfield (D1–F3) from frozen coronal brain sections immunostained with antibodies against VGLUT1 (magenta) and p-tau181 (green). FSB was used for detecting A β plaques (blue). Scale bars, 100 μ m. (A4–C4) Higher magnification of framed regions indicated in A3–C3. Scale bars, 20 μ m. (A5 and C5) Higher magnification of framed regions indicated in A4 and C4. Scale bars, 2.5 μ m. (G) VGLUT1 immunoreactivity in the cortex or hippocampal CA1 subfield was quantified and expressed as relative percentage to WT. $n = 4$ /group. ns, not significant.

p-tau181 signals overlapped with axons of glutamatergic neurons. Brain sections of the cortices of 24-month-old *App^{NLGF}*, *App^{NL}*, and WT mice were costained with antibodies against p-tau181 and the glutamatergic terminal marker vesicular glutamate transporter 1 (VGLUT1) (Fig. 5A1–A5, B1–B4, and C1–C5). High-magnification images revealed that these signals did not overlap (Fig. 5A5 and C5), and 3D reconstruction imaging confirmed this result

(Supplementary Movie 4). We also analyzed the distribution pattern of VGLUT1 and p-tau181 signals in the CA1 subfield of the hippocampus and found that their staining patterns were dissimilar (Fig. 5D1–D3, E1–E3, and F1–F3). Consistent with previous reports [45–47], VGLUT1 signals were widely distributed through the synaptic laminae (*stratum oriens* and *stratum radiatum*) with low immunoreactivity in the somatic layers (*stratum pyramidale*) (Fig. 5D1, E1,

and F1). By contrast, p-tau181-positive axons were distributed more densely in the somatic layers than in the synaptic laminae (Fig. 5D2, E2, and F2). Together, these results indicate that p-tau181-positive signals are not localized to glutamatergic axons in mouse brains.

We also analyzed the density of glutamatergic axons in *App^{NLGF}* and control mice. Unlike unmyelinated cholinergic axons (Fig. 2A, B), the overall density of VGLUT1-positive axon terminals was not significantly reduced in the cortex or hippocampus in *App^{NLGF}* mice compared to those in WT or *App^{NL}* mice (Fig. 5G).

p-tau181-positive axons overlap with GABAergic axons in mouse brains

We next examined whether p-tau181-positive axons overlap with GABAergic interneurons. Brain sections of the cortices of 24-month-old *App^{NLGF}*, *App^{NL}*, and WT mice were costained with antibodies against p-tau181 and the GABAergic terminal marker vesicular GABA transporter (VGAT) (Fig. 6A1–A5, B1–B4, and C1–C5). High-magnification images revealed that these two signals strongly overlapped in the cortex (Fig. 6A5 and C5, white arrows), and 3D reconstruction imaging confirmed this result (Supplementary Movie 5). We also analyzed the overlap between VGAT and p-tau181 signals in the CA1 subfield of the hippocampus in *App^{NLGF}*, *App^{NL}*, and WT mice. The distribution pattern of VGAT-positive axon terminals was similar to that of p-tau181-positive axons (Fig. 6D1–D5, E1–E4, and F1–F5). Both VGAT-positive axons (Fig. 6D1, E1, and F1) and p-tau181-positive axons (Fig. 6D2, E2, and F2) were evident in the somatic layers (*stratum pyramidale*) with less immunoreactivity in the synaptic laminae (*stratum oriens* and *stratum radiatum*). High-magnification imaging (Fig. 6D5 and F5, white arrows) and 3D reconstruction (Supplementary Movie 6) demonstrated clear colocalization of VGAT and p-tau181 signals. These results indicate that p-tau181 signals are localized to GABAergic axons in mouse brains.

We also analyzed the density of GABAergic axons in *App^{NLGF}*, *App^{NL}*, and WT mice. Compared to those in WT or *App^{NL}* mice, the overall density of VGAT-positive axon terminals was significantly reduced in the cortex but not in the hippocampus of *App^{NLGF}* mice (Fig. 6G). Unlike in the cortex, the immunoreactivity of MBP in the hippocampus was not significantly reduced in *App^{NLGF}* mice

(Fig. 4D1, E1, F1, and G), so that GABAergic axons might be injured in the cortex, but not in the hippocampus.

Taken altogether, these results suggest that axons of GABAergic interneurons may be more affected than those from glutamatergic excitatory neurons in the brains with A β pathology.

p-tau181-positive axons overlap with parvalbumin-expressing axons in mouse brains

To further validate the above results, we examined whether p-tau181-positive axons overlap with axons of parvalbumin-expressing interneurons, which comprise nearly half of the interneuron population in the cortex [48, 49]. Brain sections of the cortices of 24-month-old *App^{NLGF}*, *App^{NL}*, and WT mice were costained with antibodies against p-tau181, parvalbumin and MBP (Fig. 7A1–A6, B1–B5, and C1–C6). High-magnification images revealed that these three signals strongly overlapped in the cortex (Fig. 7A6 and C6, white arrows), and 3D reconstruction imaging confirmed this result (Supplementary Movie 7).

Taken together, these results indicate that p-tau181-positive signals are localized to parvalbumin-expressing GABAergic interneurons in mouse brains, and that the myelin sheaths of these interneurons are significantly disrupted in the *App^{NLGF}* mouse model of A β pathology.

DISCUSSION

p-tau181 in CSF is an established biomarker for AD [6, 50, 51], and recent studies demonstrate that increased levels of p-tau181 in plasma as well as CSF correlate with A β pathology in the preclinical and early stages of AD [1, 2]. Using *App^{NLGF}* mice, which represent a model of A β pathology, we previously reported that p-tau181 localizes to axons and may reflect axonal abnormalities caused by A β accumulation [10]. However, whether these p-tau181-positive axons originate from specific neuronal subtype(s) remains elusive. In this study, we demonstrated that p-tau181 signals colocalized with myelinated, parvalbumin-expressing, GABAergic interneurons (Fig. 7) but not with cholinergic, noradrenergic, or glutamatergic neurons (Figs. 1 and 5). Moreover, their myelin sheaths were significantly disrupted upon A β accumulation (Fig. 4), suggesting that increased p-tau181 levels in fluids may reflect demyelinated axons

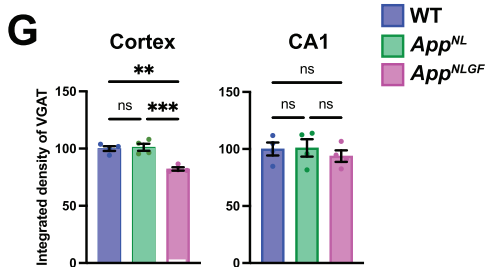
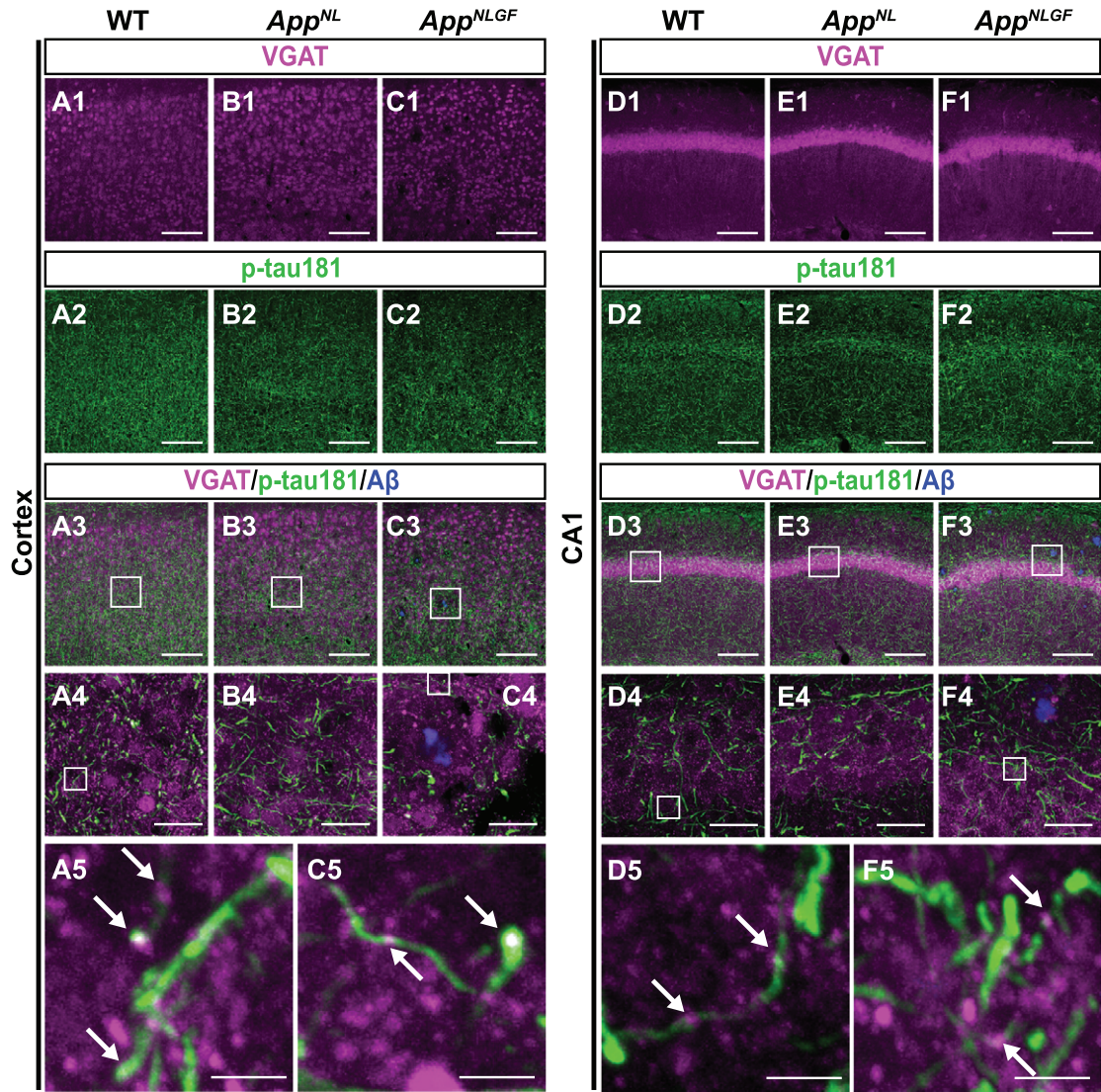


Fig. 6. p-tau181-positive axons overlap with GABAergic axons in mouse brains. Representative images of the cortex (A1–C3) and hippocampal CA1 subfield (D1–F3) from frozen coronal brain sections immunostained with antibodies against VGAT (magenta) and p-tau181 (green). FSB was used for detecting A β plaques (blue). Scale bars, 100 μ m. (A4–C4 and D4–F4) Higher magnification of framed regions indicated in A3–C3 and D3–F3, respectively. Scale bars, 20 μ m. (A5, C5, D5, F5) Higher magnification of framed regions indicated in A4, C4, D4, and F4, respectively. White arrows indicate colocalization of VGAT and p-tau181 signals. Scale bars, 2.5 μ m. (G) VGAT immunoreactivity in the cortex or hippocampal CA1 subfield was quantified and expressed as relative percentage to WT. $n = 4$ /group. ** $p < 0.01$, *** $p < 0.001$, ns, not significant.

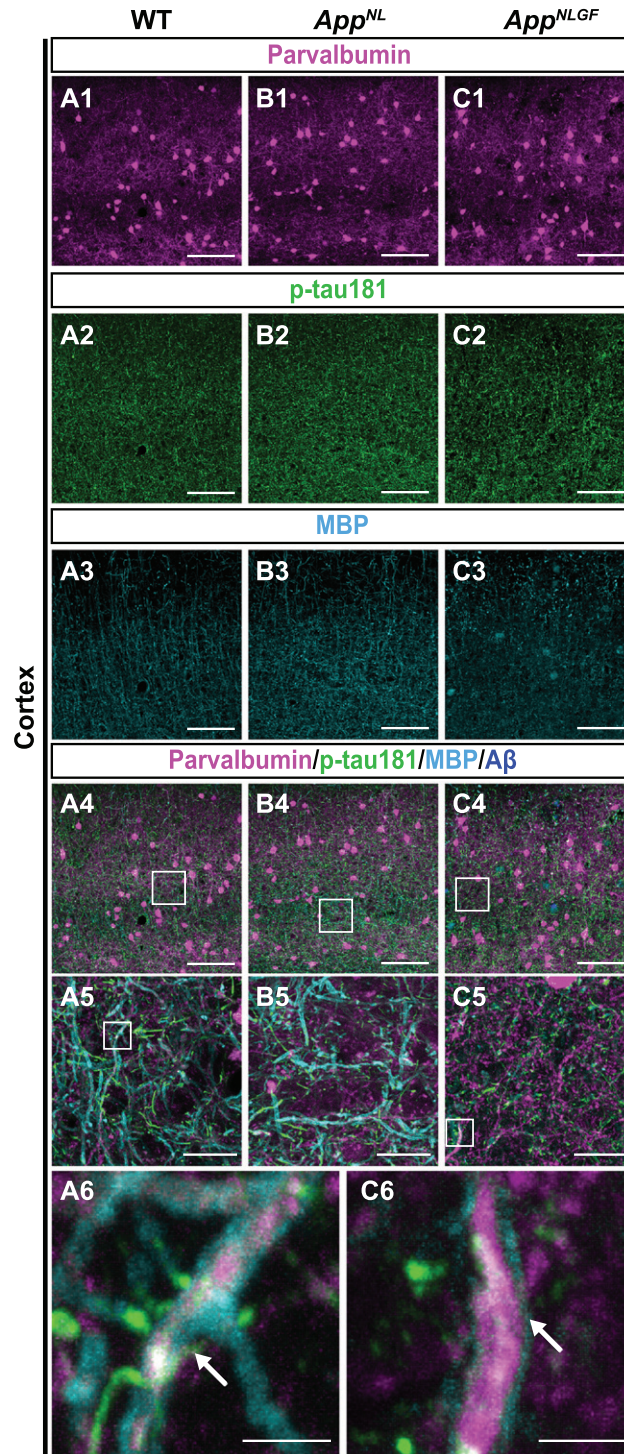


Fig. 7. p-tau181-positive axons overlap with parvalbumin-expressing axons in mouse brains. (A1–C4) Representative images of the cortex from frozen coronal brain sections immunostained with antibodies against parvalbumin (magenta), p-tau181 (green), and MBP (cyan). FSB was used for detecting A β plaques (blue). Scale bars, 100 μ m. (A5–C5) Higher magnification of framed regions indicated in A4–C4. Scale bars, 20 μ m. (A6, C6) Higher magnification of framed regions indicated in A5 and C5. White arrows indicate MBP signals wrapped with the p-tau181-positive axons of parvalbumin-expressing interneurons. Scale bars, 2.5 μ m.

of parvalbumin-expressing GABAergic interneurons under A β pathology.

Excitatory-inhibitory imbalance may cause abnormal network activity and influence neuronal oscillations important for cognitive functions in early AD [52–54]. Neurophysiological studies in humans have shown that neuronal hyperactivity is associated with amyloid-PET positivity [55], suggesting that aberrant excitatory responses are induced by A β accumulation [56]. Several studies indicate that functional impairments of inhibitory GABAergic interneurons, especially fast-spiking parvalbumin-expressing neurons, underlie network hyperactivity in early AD [57] as inhibitory interneurons play critical roles in synchronizing neuronal activity and generating neuronal oscillations [58, 59]. Of particular interest, studies using resting-state magnetoencephalography and electroencephalography showed that lower A β ₄₂ levels and higher p-tau181 levels in CSF were associated with cortical network disruption in early AD [60, 61]. Our data demonstrate that p-tau181 is associated with axonal abnormalities in parvalbumin-expressing GABAergic interneurons in A β pathology in mouse brains (Fig. 7). This suggests links among p-tau181, impaired inhibitory neurotransmission, and A β pathology in early AD.

Evidence from neuroimaging studies demonstrates that A β pathology correlates well with myelin damage in the early stage of AD [62, 63]. A previous study has reported a relationship between myelin water fraction (MWF), a surrogate of myelin content, and p-tau181/A β ₄₂ ratio in the CSF from preclinical AD patients, in which higher levels of p-tau181/A β ₄₂ resulted in an increased decline in MWF with age [63]. Also, elevated plasma p-tau181 has been associated with lower axonal density quantified by MWF in the occipital lobe [64]. These reports suggest that increased levels of fluid p-tau181 correlate with reduced myelin content in human brains.

Single-cell transcriptomic analyses have also revealed that oligodendrocytes show AD pathology-responsive transcriptional signatures, suggesting that disruption of myelination plays a key role in AD pathogenesis [65]. A recent study demonstrated that myelin on parvalbumin-expressing inhibitory interneurons is critical for feedforward inhibition of cortical circuits [66], and that myelin loss reduces the number of presynaptic terminals from these interneurons and alters neural oscillations [67]. Interestingly, a large fraction of the myelin present in the cortex enwraps mainly the axons of parvalbumin-expressing GABAergic interneurons in mouse brains [44, 68,

69]. Our results showed that myelin sheaths are significantly disrupted (Fig. 4), and that, interestingly, axons of GABAergic interneurons (Fig. 6), but not of glutamatergic neurons (Fig. 5), are significantly reduced in the cortex of *App*^{NLGF} mice. These results suggest that GABAergic interneurons are more vulnerable in early AD due to myelin disruption caused by A β pathology. A preclinical study using a mouse model of AD showed that enhancing myelination reversed cognitive impairment [70]. This suggests that myelin repair may be a therapeutic approach to prevent inhibitory dysfunction in early AD [71], and that p-tau181 may be a useful biomarker to monitor therapeutic efficacy.

Another interesting finding from this study is that p-tau181 signals colocalize well with axons of myelinated interneurons (Fig. 6) but not those of unmyelinated cholinergic or noradrenergic neurons (Fig. 1). We recently reported that signals of p-tau217 and p-tau231, other fluid biomarkers for A β pathology in the preclinical stage of AD, colocalized with the postsynaptic marker of myelinated glutamatergic neurons but not of unmyelinated cholinergic or noradrenergic neurons [10]. These results suggest that currently used p-tau biomarkers may reflect synaptic and axonal abnormalities of myelinated neurons but not of unmyelinated neurons. Dysfunction and degeneration of unmyelinated cholinergic and monoaminergic neurons are associated with cognitive decline and psychological symptoms in the early stage of AD [72–75] and have been important therapeutic targets to improve clinical symptoms [11, 76, 77]. Thus, developing biomarkers that reflect abnormalities in unmyelinated subcortical neurons will be important for AD diagnosis and drug development.

This study has several limitations. For example, this study did not address whether p-tau181 was released from demyelinated axons of parvalbumin-positive GABAergic interneurons into the CSF or plasma in mouse models. Further study is required to investigate the correlation among p-tau181 levels in the CSF/plasma/interstitial fluid, A β pathology and disruption of myelinated structures of parvalbumin-positive GABAergic axons in the brains of *App*^{NLGF} mice. Another limitation is that this study focused on the analysis of p-tau181 localization in mouse brains. In human brain, six tau isoforms with three or four microtubule-binding domain repeats (3R or 4R tau, respectively) are expressed [78], whereas only three tau isoforms with 4R tau are expressed in mouse brain [79–81]. In addition, although the primary structures of human and mouse tau proteins are

highly conserved, they differ in several amino acids. These differences might influence tau aggregation, phosphorylation profile, and metabolism in neurons. Thus, key findings from this study must be validated in human brains in the preclinical stage of AD in future studies.

In conclusion, this study demonstrates that AD-related p-tau181 is localized to myelinated axons of parvalbumin-expressing GABAergic interneurons in mouse brains. This study also suggests that increased p-tau181 levels in the CSF and plasma may reflect loss of myelin sheaths and dysfunction of GABAergic interneurons upon A β accumulation. This is thought to underlie cognitive deficits in the preclinical and early stages of AD.

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CONFLICT OF INTEREST

The authors have no conflict of interest to report.

DATA AVAILABILITY

All data generated or analyzed during this study are included in this published article.

SUPPLEMENTARY MATERIAL

The supplementary material is available in the electronic version of this article: <https://dx.doi.org/10.3233/JAD-230121>.

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