The inhibition of LSD1 via sequestration contributes to tau-mediated neurodegeneration

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ABSTRACT

Tauopathies are a class of neurodegenerative diseases associated with pathological tau. However, the mechanism through which tau contributes to neurodegeneration remains unknown. Previously, our lab implicated the histone demethylase LSD1 in tau-induced neurodegeneration by showing that LSD1 localizes to pathological tau aggregates in Alzheimer's disease cases, and that it is continuously required for the survival of hippocampal and cortical neurons in mice. Here, we utilize the P301S tauopathy mouse model to demonstrate that pathological tau can exclude LSD1 from the nucleus in neurons. In addition, we show that reducing LSD1 in these mice is sufficient to highly exacerbate tau-mediated neurodegeneration. Finally, we find that overexpressing LSD1 in the hippocampus of tauopathy mice, even after pathology has formed, is sufficient to significantly delay neurodegeneration. These results suggest that inhibiting LSD1 via sequestration contributes to tau-mediated neurodegeneration. Thus, LSD1 is a promising therapeutic target for tauopathies such as Alzheimer's disease.

INTRODUCTION

Tauopathies such as corticobasal degeneration, progressive supranuclear palsy, and frontotemporal lobar degeneration with tau inclusions are neurodegenerative diseases pathologically defined by different forms of tau positive intraneuronal deposits (*1-5*). In addition to these primary tauopathies, neuropathological observations of postmortem Alzheimer's disease (AD) brains show the presence neurofibrillary tangles (NFTs) of hyperphosphorylated tau protein, as well as plaques containing β-amyloid (Aβ) peptide (*6-9*). AD is the leading cause of age-related dementia, resulting from neuronal cell death in the frontal and temporal cortices, as well as the hippocampus (*7*). As dementia progresses, the spatial pattern of tau pathology highly correlates with the level of cognitive impairment (*10-13*). In addition, Aβ oligomers and/or plaques can enhance tau pathology in various mouse models (*24, 25*), and there is increasing evidence that accumulation of Aβ plaques can contribute to tau pathology (*3, 26, 27*). The most well-defined physiological role of tau is in stabilizing microtubules, particularly in neuronal axons (*2*). However, in the pathological state, tau becomes aberrantly phosphorylated (*2, 14, 15*), truncated (*1, 4*), and aggregates into oligomers and larger insoluble filaments (*16, 17*). This pathology is thought to trigger synaptic loss, dramatic genome-wide expression changes, increased inflammatory response, and neuronal cell death (*18-21*). These data suggest that pathological tau may be a downstream mediator of the neurotoxic effects leading to neuronal degeneration in AD.

Previously, our lab demonstrated that deleting the histone demethylase *Lsd1* in adult mice leads to significant neuronal cell death in the hippocampus and cortex with associated learning and memory defects (*28*). In this mouse model, loss of *Lsd1* induces genome-wide expression changes that significantly overlap with those observed in the brains of postmortem human AD

cases, but not other neurodegenerative diseases, such as Parkinson's disease or amyotrophic

lateral sclerosis (ALS) cases. Consistent with this overlap, we observed LSD1 protein

mislocalized to cytoplasmic NFTs, but not associated with Aβ plaques in AD cases or Lewy

bodies of α-synuclein in Parkinson's disease cases (*28*). These data highlight the requirement for

LSD1 in neuronal survival and suggest that the nuclear function of the histone demethylase

LSD1 could be disrupted by mislocalization to pathological tau.

To investigate how LSD1 may contribute to tau-mediated neurodegeneration, we utilized

the PS19 P301S tauopathy mouse model (hereafter referred to as PS19 Tau). PS19 Tau mice

express a P301S mutated form of the human tau protein, originally identified in a frontotemporal

dementia with parkinsonism (FTDP-17) patient, driven by the prion promoter throughout the

nervous system (*29*). When expressed in mice, the P301S tau protein is prone to

hyperphosphorylation and somatodendritic aggregation, without the presence of Aβ plaques.

PS19 Tau mice develop a heavy pathological tau burden and have been well characterized for the

temporal progression of tau pathology and disease-related phenotypes (*30, 31*). However, the

mechanism of neuronal cell death caused by pathological tau is still unknown.

Here, we provide functional data that the inhibition of LSD1 function contributes to tau

induced neurodegeneration. We demonstrate in PS19 Tau mice that pathological tau sequesters

LSD1 in the cytoplasm of neurons throughout the brain. This results in depletion of LSD1 from

the nucleus. Additionally, we provide genetic and molecular evidence that pathological tau

contributes to neurodegeneration by disrupting LSD1. Finally, we show that overexpressing

LSD1 in hippocampal neurons is sufficient to suppress neuronal cell death even after

pathological tau has formed. We propose that pathological tau contributes to neuronal cell death

by sequestering LSD1 in the cytoplasm, depleting the nuclear pool of LSD1 that is required for

neuronal survival.

RESULTS

Tau pathology depletes LSD1 from the nucleus in the PS19 Tau mouse model

Previously, we showed in human AD cases that LSD1 protein inappropriately colocalizes with

NFTs in the cell body of hippocampal and cortical neurons, while in unaffected controls LSD1

was properly localized exclusively to the nucleus (*28*). However, because neurons in AD cases

with intracellular NFTs presumably die and are cleared, it was difficult to determine whether tau

prevents LSD1 from localizing to the nucleus in a dying neuron. To address this possibility, we

performed LSD1 immunofluorescence on 12 month old PS19 Tau mice, which have significant

tau pathology (*29*). Because PS19 Tau mice undergo neurodegeneration over a shortened period,

there are more neurons undergoing neurodegeneration at any given time point. Thus, we

reasoned that it may be possible to observe LSD1 depletion from the nucleus. Similar to what we

observe in humans, LSD1 protein in 12 month old Wild Type mice was localized to the nucleus

of neurons in the cerebral cortex (Fig. 1A-C) and the hippocampus (Fig. S1 A-C). However, in

12 month old PS19 Tau mice, LSD1 protein was sequestered in the cytoplasm and depleted from

the nucleus both in the cerebral cortex (Fig. 1D-F) and the hippocampus (Fig. S1 D-F). These are

both regions where we observe substantial cytoplasmic tau pathology (Fig. 1G-I; Fig. S1 G-I).

Similarly, in other brain regions that accumulate tau pathology, such as the thalamus and

amygdala, LSD1 was localized to the nucleus in 12 month old Wild Type control mice (Fig. S1

J-O), but abnormally localized to the cytoplasm in PS19 Tau mouse littermates (Fig. S1 P-U).

Overall, we observed sequestration of LSD1 in 6 out of 7 mice analyzed. In each of the 6 mice,

there were varying levels of sequestration ranging from LSD1 found in both the nucleus and

cytoplasm (Fig. S1 V-X), to depletion from the nucleus (Fig. S1 Y-DD).

Reduction of LSD1 increases the mouse tauopathy phenotype

If the presence of pathological tau in the cytoplasm is leading to neuronal cell death through the

sequestration and nuclear depletion of LSD1, we would expect that lowering the overall levels of

LSD1 would accelerate depletion and exacerbate the progression of disease. To test this, we

made PS19 Tau mice heterozygous for *Lsd1* (hereafter referred to as PS19;*Lsd1*$^{\Delta/+}$, Fig. S2 A).

Lsd1 heterozygotes (hereafter referred to as *Lsd1*$^{\Delta/+}$) have a functioning copy of *Lsd1* and don't

have phenotypes associated with LSD1 loss of function (*32-34*). Thus, *Lsd1* heterozygosity does

not completely compromise LSD1 function. Instead mice that are heterozygous for *Lsd1* are

sensitized to mechanisms affecting LSD1 localization and function. Consistent with this, we

observed a 30% reduction in transcript levels (Fig. S2 B) and a 35% reduction in protein levels

(Fig. S2 C,D) in *Lsd1*$^{\Delta/+}$ mice compared to their *Lsd1*$^{+/+}$ littermates. Surprisingly, PS19 Tau mice

have a 20% increase in LSD1 protein levels compared to *Lsd1*$^{+/+}$ littermates. Nevertheless,

consistent with the reduction in LSD1 that we observe in *Lsd1*$^{\Delta/+}$ mice, PS19;*Lsd1*$^{\Delta/+}$ mice have

a similar 26% reduction in transcript levels (Fig. S2 B) and a 31% reduction in protein levels

(Fig. S2 C,D) compared to PS19 Tau littermates. In addition, all genotypes were born at normal

Mendelian ratios with equal male/female ratios.

As expected, *Lsd1*$^{\Delta/+}$ mice had normal survival (Fig. 2A). In contrast, PS19 Tau mice had

a reduced overall survival (Fig. 2A) (*29*). When one copy of *Lsd1* was removed from PS19 Tau

mice, their reduced survival was significantly exacerbated (P-value = 0.0017, Fig. 2A). As

expected, there was little effect on the onset of reduced viability. The initial decline in the

survival of PS19;*Lsd1*$^{\Delta/+}$ mice started only slightly earlier than PS19 Tau mice, but after the

appearance of pathological tau in neurons (Fig. S6 K-M) (*29*). This suggests that pathological tau

may have to be present before *Lsd1* heterozygosity has deleterious effects. Subsequently,

PS19;*Lsd1*$^{\Delta/+}$ mice had a 14% reduction in median lifespan compared to PS19 Tau mice and

reached median survival 44 days earlier then PS19 Tau mice. In addition, there was a further

exacerbation of reduced lifespan as pathology became more severe. PS19;*Lsd1*$^{\Delta/+}$ mice reached

the point when there was only 10% of the population remaining 83 days earlier than PS19 Tau

mice, and all but one of the last 25% of PS19;*Lsd1*$^{\Delta/+}$ mice died between 11.5-13.5 months,

compared to 13.5-19 months in PS19 Tau mice. As a result, 28% of PS19 Tau mice were still

alive after all but one of the PS19;*Lsd1*$^{\Delta/+}$ mice had died (Fig. 2A).

PS19 Tau mice develop paralysis starting with hind limb clasping which progresses until

they are unable to feed (*29*). In our hands*,* PS19 Tau mice displayed intermittent hind limb

clasping starting at approximately 6 months of age. At 12 months, these mice had a severe clasp,

but were still mobile. This is delayed compared to what was originally reported by Yoshiyama

and colleagues (*29*). PS19;*Lsd1*$^{\Delta/+}$ mice also displayed intermittent hind limb clasping beginning

at approximately 6 months of age. However PS19;*Lsd1*$^{\Delta/+}$ mice became terminally paralyzed at a

faster rate compared to PS19 Tau mouse littermates. At 12 months, when PS19 Tau mice were

still mobile, PS19;*Lsd1*$^{\Delta/+}$ mice were severely paralyzed and typically terminal (Movie S1). To

quantitatively assess paralysis we performed rotarod and grid performance tests. In the rotarod,

we assessed the ability of the mice to stay on the rotating rod (latency to fall) (Fig. 2B), the speed

of the rod at which they fall off the rotarod (rotations per minute) (Fig. 2C), and the total distance

traveled (Fig. 2D). All genotypes performed the same at 6 months and 8 months (Fig. 2B-D).

However, at 10 months, when PS19 Tau mice still performed normally, PS19;*Lsd1*$^{\Delta/+}$ mice had a

significant deficit in mobility (P-value < 0.01, Fig. 2B,C). A deficit in PS19;*Lsd1*$^{\Delta/+}$ mice was

also observed at 10 months in the total distance traveled (Fig. 2D) and in grid performance

testing (Fig. S3 A), though neither were statistically significant.

To further investigate the exacerbation of paralysis we examined the spinal cord motor

neurons. Healthy motor neurons from *Lsd1*$^{+/+}$ control mice express LSD1 (Fig. S3 B-D) and are

classically identified by circular nuclei at the center of a large cell body. In contrast to the

healthy motor neurons we observed in 12 month old PS19 Tau mice (Fig. S3 E), many of the

motor neurons in PS19;*Lsd1*$^{\Delta/+}$ mice at 12 months had abnormal morphology, with the nucleus

skewed to the edge of the cell body (Fig. S3 E vs. S3 F) and a ballooned cell body (Fig. S3 F).

Within the cell body we found aberrant hyperphosphorylated NFH (heavy chain neurofilament),

which is a sign of activated neuronal stress pathways (Fig S3 G vs. S3 H) (*35, 36*). This

abnormal morphology is highly reminiscent of a well-established process known as

chromatolysis, which is characterized by swelling of the neuronal cell body, disruption of Nissl

granules, and pyknotic or shrunken nuclei abnormally skewed to the edge of the cell body (*37,*

38). Chromatolysis, which is linked to neuronal stress and often leads to apoptosis (*38*), has been

observed in AD and other neurodegenerative diseases (*37, 39-41*).

Reduction of LSD1 exacerbates PS19 Tau neurodegeneration

In addition to accelerating the paralysis phenotype, reducing the level of *Lsd1* in PS19 Tau mice

exacerbated neuronal cell death in the brain. At 6 months and 8 months, we observed no

difference between genotypes in the overall morphology in the hippocampus (Fig. S4 A-H)

based on histological analysis. There was also no difference between *Lsd1*$^{+/+}$ and *Lsd1*$^{\Delta/+}$ mice at

10 months or 12 months (Fig. 3A,B; Fig. S4 I,J,M,N; Fig. S5 A,B,E,F,I,J,M,N). At 10 months,

PS19 Tau mice had very little cell loss in the hippocampus compared to $Lsd1^{+/+}$ and $Lsd1^{\Delta/+}$

control mice (Fig. S4 I-K, M-O). In contrast, at 10 months, PS19;$Lsd1^{\Delta/+}$ mice had dramatic cell

loss both in the CA1 region of the hippocampus and throughout the posterior hippocampus (Fig.

S4 L,P). At 12 months, the PS19 Tau mice had a slight decrease in CA1 and CA3 neurons

spanning the hippocampal pyramidal cell layer compared to $Lsd1^{+/+}$ control mice (17% and

19.4% respectively, Fig. 3A,B; Fig. S5 A-C, E-G). In comparison, PS19;$Lsd1^{\Delta/+}$ mice had a 52%

and 54% decrease in the CA1 and CA3 respectively (Fig. 3A,B; Fig. S5 D,H) compared to

$Lsd1^{+/+}$ control mice. This resulted in decreased overall brain size (Fig. 3C) and brain weight

(Fig. 3D) in PS19;$Lsd1^{\Delta/+}$ mice compared to PS19 Tau and $Lsd1^{\Delta/+}$ mouse littermates.

Additionally, at 12 months there were increased levels of cell loss in the Dentate Gyrus (Fig. S5

I-L), and throughout the posterior hippocampus (Fig. S5 M-P).

Along with the histology, we monitored the progression of neuronal cell death in the

same individual over time by performing magnetic resonance imaging (MRI) at 6 months and

again at 10 months (Movie S2). At 6 months, there was no sign of cell loss or ventricular

dilatation in $Lsd1^{\Delta/+}$, PS19 Tau, or PS19;$Lsd1^{\Delta/+}$ mice (Fig. 3E-G). However, at 10 months the

MRI showed that there was dramatic ventricular dilatation in PS19;$Lsd1^{\Delta/+}$ mice, as evidenced by

high-intensity areas in T2- weighted imaging, with substantial hippocampal and neocortical

atrophy (Fig. 3J vs. 3H, Movie S2). At this timepoint, PS19 Tau mice had some ventricular

dilatation and hippocampal atrophy throughout the hippocampus (Fig. 3I), but much less than

PS19;$Lsd1^{\Delta/+}$ mice (Fig. 3J, Movie S2. 0:51sec vs. 1:00sec).

Tau pathology is not affected by change in LSD1 levels

Since LSD1 is a chromatin regulator, it is possible that reducing LSD1 protein levels affects the

PS19 Tau transgene. However, we confirmed that there was no difference between PS19 Tau

mice and PS19;*Lsd1*$^{Δ/+}$ mice in the endogenous mouse *Mapt* RNA expression, nor in the human

P301S MAPT transgene expression (Fig. S6 A). It is also possible that LSD1 affects tau

pathology. To test this, we performed immunohistochemistry staining for a hyperphosphorylated

form of tau (AT8). As expected, we did not observe any AT8 positive staining in *Lsd1*$^{Δ/+}$ at 6, 8,

or 10 months (Fig. S6 B,E,H). Additionally, we observed very little AT8 positive

immunoreactivity at 6 months in both PS19 Tau or PS19;*Lsd1*$^{Δ/+}$ mice (Fig. S6 C,D). At 8

months both PS19 Tau and PS19;*Lsd1*$^{Δ/+}$ mice had low but consistent levels of AT8 positive

immunoreactivity (Fig. S6 F,G), and by 10 months both PS19 Tau and PS19;*Lsd1*$^{Δ/+}$ mice

developed the same high level of AT8 positive tau immunoreactivity (Fig. S6 I,J). This was

consistent throughout both the CA1 and CA3 regions of the hippocampus and the cerebral cortex

(Fig. S6 K-M). We also did not observe any difference between PS19 Tau mice and

PS19;*Lsd1*$^{Δ/+}$ mice when assaying PHF1 (an alternative phospho-tau antibody) immunoreactivity

in the CA1 region of the hippocampus at 8 months (Fig. S7 A-C, G) and 10 months (Fig. S7 D-F,

G), nor in the CA3 region of the hippocampus or the cerebral cortex at 8 and 10 months (Fig. S7

H,I).

The functional interaction between tau pathology and LSD1 inhibition is specific

To test the specificity of the functional interaction between tau pathology and LSD1, we

investigated the overlap in the effected molecular pathways associated with both pathological tau

and *Lsd1* heterozygosity. To address this, we performed RNA sequencing on the hippocampus of

9 month *Lsd1*$^{+/+}$, *Lsd1*$^{Δ/+}$, PS19 Tau, and PS19;*Lsd1*$^{Δ/+}$ littermates. As opposed to analyzing

transcriptional changes at the terminal stage of disease, this time point allows us to assess

molecular changes prior to the onset of neuronal cell death. This is also the time point that we

observed the earliest signs of exacerbation of paralysis in PS19;$Lsd1^{\Delta/+}$ mice. Because of this

early stage in the progression of the disease, we would not expect dramatic changes in

transcription overall. Nevertheless, if tau pathology is inhibiting LSD1 function, we would

expect that the genome-wide expression changes induced by tau might be exacerbated by a

reduction in LSD1. The RNA-seq analysis detected 54 significant gene expression changes in

PS19 Tau mice compared to $Lsd1^{+/+}$ (Fig S8 A,B), and 271 significant gene expression changes

in PS19;$Lsd1^{\Delta/+}$ mice compared to $Lsd1^{+/+}$ (Fig S8 C,D). Importantly, $Lsd1^{\Delta/+}$ mice had only 4

gene expression changes observed genome-wide (Fig. S8 E,F), indicating that the partially

reduced level of LSD1 expression had very little effect on transcription on its own. This is

consistent with the lack of phenotype in these animals.

We first examined the relationship between tau-induced expression changes and the

effects of *Lsd1* heterozygosity by comparing the transcriptional changes observed in PS19 Tau

mice with PS19;$Lsd1^{\Delta/+}$ mice. In PS19 Tau mice that do not yet have significant

neurodegeneration, we identified 54 genes (36 up and 18 down) that were differentially

expressed. Of these 54 genes, 50 were changed in the same direction in PS19;$Lsd1^{\Delta/+}$ mice

(93%). In addition, amongst the 50 genes changed in the same direction, 36 (72%) had

exacerbated expression in PS19;$Lsd1^{\Delta/+}$ mice compared to PS19 Tau mice (Fig. 4A). Based on

this overlap, we further compared the expression changes between PS19 Tau mice and

PS19;$Lsd1^{\Delta/+}$ mice genome-wide. Amongst the transcripts that were changed in both PS19 Tau

mice and PS19;$Lsd1^{\Delta/+}$ mice compared to $Lsd1^{+/+}$ mice, 71% changed in the same direction

(either up or down). Consistent with this overlap in gene expression, Gene Set Enrichment

Analysis demonstrated that the pathways that are affected in both PS19 Tau mice and

PS19;*Lsd1*$^{\Delta/+}$ mice are very similar (Fig. S8 G-J). However, the genes affected in both sets of

mice tended to be further exacerbated in PS19;*Lsd1*$^{\Delta/+}$ mice compared to PS19 Tau mice.

Amongst the 71% of genes that changed in the same direction in both PS19 Tau mice and

PS19;*Lsd1*$^{\Delta/+}$ mice, 76% of these transcripts had a higher fold-change in PS19;*Lsd1*$^{\Delta/+}$ mice

compared to PS19 Tau mice (Fig. 4B).

Overexpression of LSD1 rescues neurodegeneration in the hippocampus of PS19 Tau mice

Our data demonstrate that reduction of LSD1 protein exacerbates the tauopathy phenotype in

PS19 Tau mice. Based on this, we considered the possibility that overexpression of LSD1 might

counter the loss of LSD1 from the nucleus and protect against neurodegeneration in PS19 Tau

mice. To address this possibility, we injected PS19 Tau mice with a neuronal specific virus

(AAV-DJ driven by the synapsin promoter) expressing either the full length LSD1 protein with

an N-terminal HA tag (hereafter referred to as PS19- LSD1 inj) or a control virus expressing

only the HA tag (hereafter referred to as PS19- HA inj). Additionally, to control for the effects of

viral injection, we injected Wild Type littermates with the HA only expressing virus (hereafter

referred to as WT- HA inj). All injections were performed directly into the hippocampus at 8-8.5

months, when tau pathology is already present throughout the nervous system. Immunolabeling

for the HA tag demonstrated that the virus is specific to NeuN+ neurons (Fig. S9 A-D), with no

HA expression observed in IBA+ microglia (Fig. S9 E-H), or GFAP+ astrocytes (Fig. S9 I-L). It

also confirmed that virally expressed LSD1 is nuclear (Fig. S9 M) and confined to the

hippocampus (Fig. S9 N). After 3 months of overexpression, 11-11.5 month old mice were

euthanized, and the brains were analyzed. Injections resulted in a ~6-fold increase in expression

of LSD1 in the hippocampus compared to endogenous LSD1 in the PS19- HA inj mice, but no

increase in the cerebellum (Fig. S9 O,P). As expected, because the viral injections were restricted

to the hippocampus, the mice injected with LSD1 still developed paralysis (Movie S3). This

confirms that the tau transgene is expressed and functioning. Additionally, we did not observe a

difference in total levels of AT8 positive tau immunoreactivity (Fig. S9 Q-T). Therefore, any

modulation to the phenotype was not due to changes in tau pathology.

Injected mice were evaluated for cell death by neuronal cell counts in the hippocampus.

Injection of LSD1 virus into the hippocampus of PS19 Tau mice rescued the neurodegeneration

phenotype. At 11 months, compared to WT-HA inj control mice, 70% of the PS19-HA inj mice

had hippocampal cell counts that were below the lowest WT-HA inj control, while none of the

Tau mice injected with the LSD1 virus were below this level. Overall, we observed significantly

more neurons (P-value <0.05) spanning the pyramidal cell layer (84% of WT- HA inj CA1

counts) compared to their PS19- HA inj littermates (59% of WT- HA inj CA1 counts), such that

overall the neuronal cell count in PS19- LSD1 inj mice was not statistically different from the

WT- HA inj (Fig. 5A-D). Additionally, in the histological analysis we observed a large number

of cells infiltrating the hippocampus in PS19- HA inj mice compared to WT- HA inj littermates

(Fig. 5B vs. 5C). Marker analysis demonstrated that this was due to a strong inflammatory

response, with a large increase in the number of GFAP+ astrocytes (Fig. S10 A-C vs. D-F) and

TRL2+ activated microglia (Fig. S10 J-L vs. M-O, S-V vs. W,Z, EE). Injection of PS19 Tau

mice with LSD1 virus rescued this inflammatory response. For example, all but one (9 out of 10

analyzed) of the PS19- LSD1 inj mice had a reduction in the number of GFAP+ astrocytes (Fig.

S10 G-I vs. D-F) and TRL2+ activated microglia (Fig. S10 P-R vs. M-O, AA-DD vs. W-Z, EE).

Of note, the one PS19- LSD1 inj mouse where we did observe increased glial cells, similar to

PS19- HA inj mice, had the lowest neuronal cell count (74% of WT- HA inj CA1 neurons). It is

possible that this mouse was already undergoing neurodegeneration prior to the injection of the

LSD1 overexpression virus.

Although the number of hippocampal neurons in PS19- LSD1 inj mice did not differ

from WT- HA inj controls, in 6 of the 10 PS19- LSD1 inj mice we observed cells with abnormal

blebbed nuclei at varying numbers throughout the hippocampus (Fig. 5E). These abnormal cells

are rare in PS19- HA inj mice, which have a reduced overall number of cells in the pyramidal

cell layer compared to WT- HA inj control mice. One possibility is that these abnormal cells

with blebbing nuclei represent an intermediate state between a healthy neuron and a dying

neuron that is prolonged by rescue via LSD1 overexpression. Interestingly, these abnormal cells

also differed in the localization of HA-tagged LSD1. The four mice with normal nuclei had HA-

tagged LSD1 protein localized uniformly throughout the nucleus (Fig. 5F). In contrast, the six

mice with abnormal nuclear blebbing had some HA-tagged LSD1 that was mislocalized to the

cytoplasm (Fig. 5G). This includes the one PS19- LSD1 inj mouse that had an elevated number

of astrocytes and TRL2 positive microglia. Thus, the blebbing state correlates with when the

viral produced LSD1 begins to be sequestered in the cytoplasm, similar to the endogenously

produced LSD1.

DISCUSSION

In this study we investigate a potential downstream mediator of tau pathology in

neurodegenerative disease. We find that modulation of the chromatin modifying enzyme LSD1

can alter neurodegeneration in a tauopathy mouse model. Previously, we showed that LSD1

colocalizes with tau pathology in the cell body of neurons in AD cases (*28*). This suggested that

LSD1 might be disrupted in tauopathies such as AD, by being excluded from the nucleus. To

address this directly, we utilize the PS19 tauopathy mouse model. In these mice, we find that

LSD1 is sequestered in the cytoplasm, in some cases being completely depleted from the

nucleus. This provides the first cytological evidence that pathological tau can prevent LSD1 from

properly localizing to the nucleus in hippocampal and cortical neurons, where we have

previously shown it is continuously required.

Based on the ability of pathological tau to sequester LSD1, we hypothesized that

neuronal cell death may be due, at least partly, to LSD1 being sequestered in the cytoplasm and

depleted from the nucleus. In this case, reducing LSD1 levels should make it easier for tau to

deplete LSD1 from the nucleus, resulting in a faster progression of neurodegeneration and/or a

more severe neurodegenerative phenotype. Importantly, LSD1 heterozygosity alone induces only

4 significant gene expression changes and does not lead to any neurodegeneration. This suggests

that any effects observed in PS19;$Lsd1^{\Delta/+}$ mice are not simply due to LSD1 haploinsufficiency.

Normally, PS19 Tau mice develop paralysis and neurodegeneration, along with reduced survival.

In contrast, when we reduce LSD1 in the PS19 Tau mice, PS19;$Lsd1^{\Delta/+}$ mice die significantly

earlier, most likely due to the increased rate of paralysis. Additionally, PS19;$Lsd1^{\Delta/+}$ mice have

increased neuronal cell death and clearance in the hippocampus. This suggests that pathological

tau functions through LSD1 to cause neurodegeneration *in vivo* in mice.

PS19;$Lsd1^{\Delta/+}$ mice have a 31% reduction in LSD1 protein levels compared to PS19 Tau

mice from birth. This reduction should theoretically make mice sensitive to LSD1 depletion at

any time. However, tau pathology starts at 6-8 months in PS19 Tau mice. As a result, if *Lsd1*

heterozygosity is functioning by making it easier for pathological tau to deplete LSD1 from the

nucleus, we would not expect to see any exacerbation until after pathological tau is present. The

exacerbation of the PS19 Tau mouse neurodegenerative phenotype does not occur until after

pathological human tau was present. This suggests that the effect of *Lsd1* heterozygosity requires

the presence of pathological tau, placing LSD1 downstream of tau. Consistent with LSD1 being

downstream of pathological tau, we found no evidence that *Lsd1* heterozygosity affects the

expression of the tau transgene, or the buildup of pathological tau in PS19 Tau mice.

To test whether the functional interaction between pathological tau and reduced LSD1 is

specific, we used RNA-seq to determine whether the downstream molecular pathways altered in

PS19 Tau mice are exacerbated in PS19;*Lsd1$^{Δ/+}$* mice. This analysis was performed at the time of

earliest signs of neuronal distress, allowing us to assess molecular changes prior to cell death and

clearance. LSD1 heterozygosity induces only 4 significant expression changes. In addition, the

pathways are affected in both PS19 Tau mice and PS19;*Lsd1$^{Δ/+}$* mice are very similar. This

suggests that reducing LSD1 did not induce any additional neurodegeneration pathways. In

contrast, when LSD1 is reduced in PS19 Tau mice, the genome-wide expression changes

induced by pathological tau are specifically exacerbated. This suggest that the functional

interaction that we observe between pathological tau and reduced LSD1 is occurring through the

tau pathway.

Our previous data implicated LSD1 in the tau-mediated neurodegeneration pathway.

Utilizing the PS19 Tau mouse model, we now show a functional interaction between

pathological tau and LSD1. Importantly, because PS19 Tau mice do not have Aβ plaque

accumulation, this functional interaction is specific to tau. Based on these data we propose the

following model (Movie S4): in healthy hippocampal and cortical neurons, LSD1 is translated in

the cytoplasm and transported into the nucleus where it is continuously required to repress

inappropriate transcription. In tauopathy, pathological tau accumulates in the cytoplasm blocking

LSD1 from nuclear import. This interferes with the continuous requirement for LSD1, resulting

in neuronal cell death. Recently, it has been observed that the nuclear pore breaks down in AD

(*42-44*). It should be noted that this mechanism would potentially exacerbate the model that we

propose.

This model makes a direct prediction: if tau is predominantly functioning through LSD1,

then increasing the levels of LSD1 should rescue the tau-induced neurodegenerative phenotype.

To address this, we overexpressed LSD1 in the hippocampal neurons of PS19 Tau mice.

Overexpression of LSD1 specifically in hippocampal neurons rescues the neuronal cell death and

limits the inflammatory response. This rescue is neuronal specific, suggesting that the functional

interaction between LSD1 and tau is occurring in neurons. In addition, this rescue occurs despite

there being no effect on tau aggregation. This negates the possibility that the tau transgene is

simply not functioning when LSD1 is overexpressed. The ability of LSD1 overexpression to

overcome tau-mediated neurodegeneration in the presence of pathological tau aggregates,

provides further evidence that pathological tau is functioning through the inhibition of LSD1.

Importantly, overexpressing LSD1 should not prevent it from being sequestered. Rather

overexpressing LSD1 should make it more difficult for pathological tau to sequester all of the

LSD1 protein, allowing some LSD1 to be transported to the nucleus. Thus, overexpressing LSD1

would be expected to temporarily rescue the ability of pathological tau to kill neurons.

Consistent with this, LSD1 overexpression delays the effect of pathological tau rather than

permanently rescuing. In 60% of the mice, the surviving neurons have abnormal morphology,

and the overexpressed version of LSD1 is also sequestered. observation that neurons fail to

maintain their morphology when the overexpressed LSD1 begins to be sequestered in the

cytoplasm provides further support for the model that tau mediates neurodegeneration through

the sequestration of LSD1. Nevertheless, our data suggest that overexpression of LSD1 cannot

permanently overcome pathological tau. To permanently overcome pathological tau, it would

likely be necessary to permanently disrupt the interaction between pathological tau and LSD1.

This work is currently ongoing in the lab. Overall, our data establish LSD1 as a major

downstream effector of tau-mediated neurodegeneration. Based on these data, we propose that

the LSD1 pathway is a potential late stage target for intervention in tauopathies, such as AD.

MATERIALS AND METHODS

All mouse work, including surgical procedures, were approved by and conducted in accordance

with the Emory University Institutional Animal Care and Use Committee.

<u>Mouse tissue fixation</u>

Mice were given a lethal dose of isoflurane via inhalation, then transcardially perfused with ice

cold 4.0% paraformaldehyde in 0.1M phosphate buffer. Brain and spinal cord were dissected and

post fixed in cold paraformaldehyde solution for 2 hours. Brain weights and sizes were taken

from mice that were euthanized by cervical dislocation. Brain was dissected, immediately

weighed, imaged, and fixed in cold 4.0% paraformaldehyde in 0.1M phosphate buffer overnight.

In all cases, tissues were transferred to cold PBS, then serially dehydrated and embedded in

paraffin and serially sectioned into 8µm coronal sections.

<u>Histology and histological studies</u>

Hematoxylin and eosin staining was performed according to standard procedures. Briefly,

sections were dewaxed with xylenes and serial ethanol dilutions then stained with Eosin using

the Richard-Allan Scientific Signature Series Eosin-Y package (ThermoScientific). To derive

unbiased estimates of neuronal loss in the hippocampus, the number of primordial neurons in

CA1 and CA3 (corresponding approximately to bregma coordinates -2.0 mm and -3.0 mm) were

counted from 2 randomly selected regions in the field of a Zeiss Axiophot ocular graticule grid

and measured manually using digital micrographs of H&E-stained preparations. Investigators

were blinded to the genotype or treatment.

Immunohistochemistry and immunofluorescence

Sections were dewaxed with xylenes and serial ethanol dilutions, then treated with 3% hydrogen

peroxide at 40°C for 5 minutes to quench endogenous peroxidase activity, blocked in 2% serum

at 40°C for 15 minutes, and incubated with primary Ab (Table S1) overnight at 4°C. Slides were

washed, then incubated with biotinylated secondary Ab (Biotinylated Goat α Rabbit, 1:200,

Vector Labs BA-1000 or Biotinylated Goat α Mouse, 1:200, Vector Labs BA-9200) at 37°C for

30 minutes. Signal amplification was then carried out by incubating at 37°C for 1 hour with

Vector Labs Elite ABC reagent (PK-6200). Slides were developed with DAB for 1-5 minutes,

counterstained with hematoxylin for 1 minutes, and coverslipped. For immunofluorescence,

dewaxed sections were first rinsed with TBS. Antigen retrieval was performed by microwaving

at 10% power 2X for 5 minutes in 0.01M sodium citrate. Slides were then cooled, washed with

TBS, permeabilized in 0.5% Triton X-100 for 20 minutes, followed by blocking in 10% goat

serum 20 minutes. Primary Abs (Table S1) were incubated overnight at 4°C. Slides were then

washed and incubated in secondary Abs (Invitrogen A1 1001 and Invitrogen A11012) for 1 hour

at room temperature, followed by TBS washes, counterstained with DAPI, and then

coverslipped. For the assessment of tau accumulation, six random sections (sampling from CA1,

CA3, and cerebral cortex) per sample were manually counted using digital micrographs of AT8

stained preparations in the field of a Zeiss Axiophot ocular graticule grid. Investigators were

blinded to the genotype or treatment. Imagining for immunofluorescence of LSD1 staining was

performed on a spinning-disk confocal Nikon-Tie controlled with the software NIS Elements

(Nikon). Imaging for all other immunofluorescence staining was performed on an Eclipse Ti2

inverted microscope (Nikon, Toyko, Japan) controlled with the software NIS Elements (Nikon).

Image J software ((NIH, http://imagej.nih.gov/ij/) was used for viewing all images.

Protein Quantification

Protein levels were determined by homogenizing brains in 1 ml/g of tissue in ice-cold lysis

buffer (150mM NaCl, 1% Triton X-100, 0.5% Na-deoxycholate, 1% SDS, 50mM Tris, pH8.0) in

a dounce homogenizer, followed by end-over-end spin at 4°C for 2 hours, and centrifugation at

20,000 x g for 20 minutes at 4°C. Protein concentrations were determined following standard

BCA protocol (Pierce BCA Protein Assay Kit). Equal amounts of protein for each sample were

loaded and run on a 12% SDS-PAGE gel, transferred (Semi-dry transfer using BIO RAD Trans-

Blot Turbo Transfer System), blocked in 5% BSA, and probed with primary Ab (Table S1) over

night at 4°C. Blots were rinsed and stained with HRP-conjugated secondary Ab, and detected by

chemiluminescence using ChemiDoc MP Imaging System (BIO RAD). Protein levels were

normalized using total protein calculated using BIO RAD ImageLab software.

Quantitative analysis of paralysis

We performed experiments on PS19 Tau, $Lsd1^{\Delta/+}$, PS19;$Lsd1^{\Delta/+}$ mice at 6, 8, and 10 months.

For the rotarod experiments, mice were given two practice trials and then placed on the rotating

cylinder at 4rpm. Rotational speed then gradually increased over a 5-minute test session up to a

maximum rotational speed of 40rpm. Latency to fall off of the accelerating rotarod was used as

the dependent variable. We calculated the latency to fall, maximum speed in rotations per

minute, and distance traveled. For grid performance, mice were placed on a horizontal grid that

was then inverted so mice are hanging upside down by their paws. Mice were videotaped for 10

seconds, and then scored for forepaw and back paw distance traveled. Mice that could not hold

onto grid for 10 seconds were censored. Investigators were blinded to the genotypes for both

experiments.

MRI of brain atrophy

MRI studies were conducted on PS19 Tau, $Lsd1^{\Delta/+}$, PS19;$Lsd1^{\Delta/+}$ mice at 6 months and 10

months (*n*=3/genotype). Mice were anesthetized with isoflurane, and monitored for heart rate and

temperature changes while anesthetized. MRI measurements were performed using a 9.4 T/20

cm horizontal bore Bruker magnet, interfaced to an AVANCE console (Bruker, Billerica, MA,

USA). A two-coil actively decoupled imaging set-up was used (a 2 cm diameter surface coil for

reception and a 7.2 cm diameter volume coil for transmission). Axial T2-weighted images were

acquired with a RARE (Rapid Acquisition with Refocused Echos) sequence. Its imaging

parameters were as follows: TR = 3000 ms, Eff.TE = 64 ms, RARE factor = 4, field of view

(FOV) = 23.04 × 23.04 mm2, matrix = 192 × 192, Avg = 4, slice thickness (thk) = 0.6 mm,

number of slice(NSL)=20. Specific emphasis was placed on the neocortex and hippocampus in

the coronal images (1.0 – 4.0 mm posterior to the bregma).

RNA sequencing

9 month old $Lsd1^{+/+}$, $Lsd1^{\Delta/+}$, PS19 Tau, and PS19;$Lsd1^{\Delta/+}$ littermates (n=2 mice/genotype)

were euthanized by cervical dislocation, hippocampi were dissected and snap frozen with liquid

nitrogen in 1mL Trizol, and stored at -80°C. For RNA isolation, samples were thawed at 37°C

then kept on ice prior to homogenization with Polytron homogenizer with a 5 second pulse. After

a 5 minute incubation at room temperature, one tenth the sample volume of 1-bromo-

3chloropropane was added, mixed by inversion and incubated for 3 minutes at room temperature.

Samples were then centrifuged at 13,000 X g for 15 minutes at 4°C to separate the aqueous and

organic layers. As much of the aqueous layer was recovered as possible, then RNA was

precipitated with isoproponal. Pellets were then washed with 75% ethanol and resuspended in

50μL of dionized water. RNA library preparation and sequencing were performed by

HudsonAlpha Genomic Services Lab. RNA was Poly(A) selected and 300bp size selected.

Libraries were sequenced for 25 million 50bp paired end reads.

<u>RNA sequencing analysis</u>

The sequencing data were uploaded to the Galaxy web platform, and *we used the public server*

at <u>usegalaxy.org</u> *to analyze the data ((45, 46)).* FASTQ files were quality assessed using

FASTQC (v.0.11.7), trimmed using Trimmomatic (v.0.36.5) and minimum QC score of 20 and

minimum read length of 36bp. Paired-end reads were subsequently mapped to the GRCm38

genome using HISAT2 (v.2.1.0). Unmapped, unpaired and multiply mapped reads were removed

using Filter SAM or BAM (v.1.1.2). Assignment of transcripts to GRCm38 genomic features

was performed using Featurecounts (v.1.6.0.6) and the Ensembl GRCm38.93 gtf file.

Differentially expressed transcripts were determined using DESEQ2 (v.2.11.40.2) *((46))*. For all

datasets, a cutoff of adjusted p-value < 0.3 and abs ($\log_2$ fold change) > 0.58 was applied. TPM

values were calculated from raw data obtained from Featurecounts output. Subsequent

downstream analysis was performed using R and normalized counts and adjusted P-values from

DESEQ2 (v.2.11.40.2). Heatmaps were produced and hierarchical clustering was done using the

gplots package (v. 3.0.1) and normalized counts *((47))*. Volcano plots were produced using the

enhanced volcano package (v.0.99.16) and adjusted p-values *((48))*. Additionally, Gene Set

Enrichment Analysis (Pre-ranked list) was performed using the online platform WebGestalt *((49-*

52)). Custom R-scripts available upon request.

<u>Stereotaxic surgery and viral infusion</u>

All surgical procedures were approved by and conducted in accordance with the Emory

University Institutional Animal Care and Use Committee. Mice were anesthetized with

isoflurane (3% induction, 1-2% maintenance) and administered the analgesic meloxicam (5

mg/kg). Using a Stoeling Quintessential Stereotaxic Injector pump and Hamilton syringe, mice

were injected with either the AAV-DJ-LSD1- HA virus or the control AAV-DJ- HA virus into

both hippocampi. Each virus was injected into the rostral (AP: -2.5, ML:± 2.2, DV: -1.6, relative

to bregma) and caudal (AP: -3.1, ML:± 3.0, DV: -3.5) hippocampus of both hemispheres (four

injection sites total). Infusion volumes were 0.5 µL per injection site, administered at a rate of

0.15 µL/min. Following surgery, mice were monitored daily for the duration of the experiment.

Brains were extracted 3 months post-surgery which allows sufficient time for viral expression.

Injection accuracy was confirmed by HA positive staining, and those mice where staining was

outside the hippocampus or that did not fully reach hippocampus were censored.

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Contributions: A.K.E and D.J.K. conceived and designed the study and wrote the manuscript.

A.K.E. performed experiments with the help of A.C.W, S.M.K, and R.A.M under the direction

of D.J.K. D.A.M performed bioinformatics analysis on the RNA sequencing data. A.K.E,

A.C.W, S.M.K, and R.A.M analyzed all other data and interpreted results. All authors discussed

the results and commented on the manuscript. **Competing Interests:** The authors declare that

they have no competing interests. **Data and materials availability:** FastQ files for the RNA

sequencing experiments are bring deposited in the GEO and will be available upon publication.

Results from DESEQ2 are available in Data S1. Correspondence and requests for materials

should be addressed to D.J.K. (djkatz@emory.edu).

Fig. 1: LSD1 sequestration and tau accumulation in PS19 Tau mice. A-C, Representative immunofluorescence of 12 month old control Wild Type mice showing DAPI (**A**), LSD1 (**B**), and merged (**C**) in the cerebral cortex where LSD1 is localized specifically to DAPI positive nuclei. **D-F**, Representative image of the cerebral cortex in 12 month old PS19 Tau mice. Staining for DAPI (**D**), LSD1 (**E**), and merged (**F**) shows that LSD1 is localized outside the nucleus, and depleted from the DAPI positive nucleus. Arrows denote cells where LSD1 is localized outside of the nucleus, and asterisks denote LSD1 localized specifically to the nucleus. **G-I,** Representative immunofluorescence of 12 month old PS19 Tau mouse with staining for DAPI (**G**), AT8 positive hyper-phosphorylated tau (**H**) and merge (**I**) where hyper-phosphorylated tau accumulates in the cytoplasm of the cell body. Arrowheads denote hyper-phosphorylated tau. Scale bars=25µm.

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Fig. 2: Reduction of *Lsd1* exacerbates the PS19 Tau mouse paralysis phenotype. A, Lifespan curve showing that
no *Lsd1$^{\Delta/+}$* mice died before 18 months (orange, *n*=20). PS19;*Lsd1$^{\Delta/+}$* mice (purple, *n*=44) have a significant
reduction in survival compared to PS19 Tau mice with wild-type levels of *Lsd1* (green, *n*=37)(Log-rank Mantle-Cox
test ***P<0.005). **B-D**, Rotarod testing of latency to fall (in seconds) (**B**), rotations per minute (when the mouse fell)
(**C**), and distance traveled (in centimeters) (**D**) for mice at age 6, 8 and 10 months. *Lsd1$^{\Delta/+}$* (orange, *n*=10,11,14),
PS19 Tau (green, *n*=11,22,9), and PS19;*Lsd1$^{\Delta/+}$* (purple, *n*=8,17,11). Values are mean ± SEM (two-way analysis of
variance (ANOVA) with Tukey's post hoc test *P<0.05 **P<0.01, ns=not significant).

Fig. 3: Reduction of *Lsd1* exacerbates neurodegeneration in PS19 Tau mice. A,B, Average nuclei per area in the CA1 (**A**) and CA3 (**B**) regions of the hippocampus in 12 month old *Lsd1*$^{+/+}$, *Lsd1*$^{\Delta/+}$, PS19 Tau, and PS19;*Lsd1*$^{\Delta/+}$ mice. Quantification from histology represented in **Fig. S5 A-H**. Values are mean ± SD (**A**, *n*=13 & **B**, *n*=9). **C,** Representative image of the brains of 12 month old *Lsd1*$^{\Delta/+}$, PS19 Tau, and PS19;*Lsd1*$^{\Delta/+}$ littermates. **D,** Total brain weight of 12 month old littermates represented in **Fig. 3C.** Values are mean ± SD (*n*=5). For all graphs: one-way analysis of variance (ANOVA) with Tukey's post hoc test (two-sided) *P<0.05,****P<0.001. **E-J,** Representative image of T2- weighted RARE coronal MRI taken from 6 months (**E-G**) and 10 months (**H-jJ**) of age in *Lsd1*$^{\Delta/+}$ (**E,H**), PS19 (**F,J**), and PS19;*Lsd1*$^{\Delta/+}$ (**G,J**) mice (*n*=3). Arrow denotes region of hippocampal atrophy.

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Fig. 4: Molecular overlap between loss of LSD1 function and tauopathy. A, Histogram ($\log_2$ fold change) of the
54 genes that have significant changes in expression in the PS19 Tau mouse (green) and their corresponding
expression changes in the PS19;$Lsd1^{\Delta/+}$ mouse (purple). **B,** Scatter plot showing the correlation between the
genome-wide $\log_2$ fold change in gene expression between PS19 Tau and PS19;$Lsd1^{\Delta/+}$. The most significantly
changed genes in PS19;$Lsd1^{\Delta/+}$ mouse are shown in red (upregulated) and green (downregulated). All other genes
are shown in grey. Dotted line represents 1:1 relationship between gene expression changes in PS19 Tau vs.
PS19;$Lsd1^{\Delta/+}$. Exacerbated genes fall to the right of the dotted line in the positively correlated quadrant and to the
left of the dotted line in the negatively correlated quadrant. Genes with correlated expression changes are found in
the top right and bottom left quadrants, while genes that do not correlate are found in the opposite quadrants.

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Fig. 5: LSD1 overexpression rescues the neurodegenerative phenotype in the hippocampus of 11 month old
PS19 Tau mice. A-C, Representative image of H&E stained CA1 region of the hippocampus of 11 month old Wild
Type mice injected with HA control virus (WT- HA inj) (**A**), PS19 Tau mice injected with HA control virus (PS19-
HA inj) (**B**), and PS19 Tau mice injected with *Lsd1* overexpressing virus (PS19- LSD1 inj) (**C**). Square brackets
denote thickness of pyramidal layer of the CA1 of the hippocampus and curvy brackets denote hippocampal region
with or without infiltrating cells. **D,** Quantification of the average number of nuclei in the pyramidal layer of the
hippocampus per area per mouse from histology represented in **Fig. 5A-C**. Values are mean ± SD (*n*=10, one-way
analysis of variance (ANOVA) with Tukey's post hoc test, **p<0.01, ns=not significant). **E,** Representative H&E of
PS19- LSD1 inj mouse with abnormal nuclei blebbing in the CA1 region of the hippocampus. **E'-E''',** High
magnified image of cells denoted by arrows in **Fig. 5E** of individual nuclei that are either abnormally blebbed (**E',**
E") or normal (**E'''**). **F,G,** Immunohistochemistry staining of HA(LSD1) in 11 month PS19- LSD1 inj mice. HA is
either localized specifically to the nucleus in all nuclei (**F**) or in only a few nuclei while it is partially sequestered in
the cytoplasm in others (**G**). **F'-F''',** High magnified image of cells denoted by arrows in **Fig. 5F** of nuclear HA
localization in individual nuclei. **G'-G''',** High magnified image of cells denoted by arrows in **Fig. 5G** of individual
nuclei with HA(LSD1) either sequestered to the cytoplasm (**G', G"**) or confined to the nucleus (**G'''**). Scale
bars=50μm.