**Phf15**—a novel transcriptional repressor regulating inflammation in mouse microglia

Sandra E. Muroy¹, Greg A. Timblin¹, Marcela K. Preininger¹, Paulina Cedillo¹ and Kaoru Saijo¹,²

¹Department of Molecular and Cell Biology, University of California, Berkeley, Berkeley, CA 94720, USA
²Helen Wills Neuroscience Institute, University of California, Berkeley, Berkeley, CA 94720, USA

Correspondence to: Prof. Kaoru Saijo, Department of Molecular and Cell Biology, University of California, Berkeley, 439 Life Sciences Addition, Berkeley CA 94720, USA. E-mail: ksaijo@berkeley.edu; ORCID: 0000-0003-1656-1753

Received: date month year

Abstract

**Aim:** Excessive microglial inflammation has emerged as a key player in mediating the effects of aging and neurodegeneration on brain dysfunction. Thus, there is great interest in discovering transcriptional repressors that can control this process. We aimed to examine whether Phf15—one of the top differentially expressed genes in microglia during aging in humans—could regulate transcription of pro-inflammatory mediators in microglia.

**Methods:** RT-qPCR was used to assess Phf15 mRNA expression in mouse brain during aging. Loss-of-function (shRNA-mediated knockdown (KD)) and CRISPR/Cas9-mediated knockout (KO) of Phf15 and gain-of-function (retroviral overexpression (OE)) of murine Phf15 cDNA studies in a murine microglial cell line (SIM-A9) followed by immune activation with lipopolysaccharide (LPS) were used to determine the effect of Phf15 on pro-inflammatory factor (Tnfa, Il-1β, Nos2) mRNA expression. RNA-sequencing was used to determine global transcriptional changes after Phf15 knockout under basal conditions and after LPS stimulation.

**Results:** Phf15 expression increases in mouse brain during aging, similar to humans. KD, KO and OE studies determined that Phf15 represses mRNA expression levels of pro-inflammatory mediators such as Tnfa, Il-1β and Nos2. Global transcriptional changes after Phf15 KO showed that Phf15 specifically represses genes related to the antiviral (type I interferon) response and cytokine production in microglia.

**Conclusion:** We provide the first evidence that Phf15 is an important transcriptional repressor of microglial inflammation, regulating the antiviral response and pro-inflammatory cytokine production. Importantly, Phf15 regulates both basal and signal-dependent activation and controls the magnitude and duration of the microglial inflammatory response.

**Keywords:** Phf15, microglia, transcriptional repression, neuroinflammation

Introduction

Microglia are the resident myeloid-lineage cells of the brain. They actively provide homeostatic surveillance of the brain parenchyma playing critical roles during development, maintenance and repair throughout the life of an organism. As innate immune cells, however, microglia are also capable of mounting a full inflammatory response to environmental challenge in order to clear threats and restore homeostasis[14]. Microglia express pattern recognition receptors including Toll-like receptors (TLRs) to sense changes in their environment, such as infection by pathogens or endogenous danger signals. They can then respond by releasing pro-inflammatory mediators such as Tumor necrosis factor alpha (TNFα), Interleukin 1 beta (IL-1β), Interleukin 6 (IL-6), reactive oxygen species (ROS) and reactive nitrogen species (RNS) including nitric oxide (NO) to protect against threats[3,5,7].

Although beneficial when their production is tightly controlled, deregulated or sustained microglial production of inflammatory mediators can lead to collateral damage of surrounding neurons and other cells[5,7,9]. Thus, the transition to an activated state, as well as, timely resolution of the inflammatory
response, must be tightly regulated. Increasing evidence suggests that during aging, microglia lose
domestic function and acquire a pro-inflammatory phenotype that exacerbates aging-related brain
dysfunction[8]. Indeed, aberrant microglia activation has been found in many types of age-related
neurodegenerative conditions for example, Parkinson’s disease (PD) and Alzheimer’s disease (AD) which
are marked by inflammatory processes involving glia, and microglia in particular[9-11].

Since excessive production of pro-inflammatory mediators is neurotoxic[8,12-14], various molecular
mechanisms exist to regulate transcriptional repression of inflammatory gene expression. For example, 
basal state repression, that is, before the arrival of an activating signal, is generally carried out via
recruitment of co-repressor complexes that prevent initiation of inflammatory gene transcription. After
stimulation by an activating signal, additional mechanisms can maintain quiescence by restraining active
transcription. Finally, numerous mechanisms mediate the timely resolution of the inflammatory response at
the transcriptional level, including transrepression mechanisms that can remove transcription factors from
inflammatory gene promoters[8,15-18].

Studies have also highlighted an important role for chromatin modifications in the transcriptional
control of inflammatory gene expression[19,20]. A recent study by Soreq et al.[21], which compared
transcriptional profiles of different brain cell types and regions throughout healthy human aging found
microglial gene expression profiles as being one of the most predictive markers of biological age in the
brain[21]. The same study identified a relatively unknown gene, PHD finger protein 15 (PHF15) among the
top 25 differentially expressed genes in microglia during aging. Work in embryonic stem cells, and
sequence and structural similarity to other members of the PHF family, indicate that PHF15 is a putative
chromatin-mediated gene regulator[22,23].

Given that aging skews microglia towards a pro-inflammatory phenotype, and that PHF15 was
found to be highly upregulated during non-pathological aging, we sought to determine whether Phf15
might regulate microglial inflammatory function. We found that Phf15 strongly represses pro-inflammatory
gen expression, regulating both basal and signal-dependent activation and modulating the magnitude and
duration of the mouse microglial inflammatory response. Importantly, Phf15 seems to regulate pro-
inflammatory and Interferon type I (IFN-I)-dependent gene expression. Increased IFN-I tone and pro-
inflammatory cytokine expression are both hallmarks of the aging brain[24-28]. Our findings suggest that
Phf15 is an important novel repressor of microglial inflammatory function that might work to counteract
age-induced inflammation in the healthy, aging brain.

METHODS

Animals
Adult male C57Bl6/J mice were purchased from The Jackson Laboratory and maintained on a 12:12-h
light–dark cycle (lights on at 0700 hours) with ad libitum access to food and water and aged for ~2.5, ~14
or ~20 months. All animal care and procedures were approved by the University of California, Berkeley
Animal Care and Use Committee.

shRNA-mediated knockdown of Phf15 in murine microglial cells
pGIPZ Lentiviral mouse Jade2 shRNA constructs or a control scrambled shRNA were purchased from
Dharmacon (Lafayette, CO). Lentivirus was packaged via co-transfection of each pGIPZ-shRNA with
pCMV-VSV-G (Addgene plasmid #8454)[29] and pCMV-dR8.2 (Addgene plasmid #8455)[29] into HEK
293T cells using Lipofectamine 3000 reagent (Life Technologies, Carlsbad, CA) according to the
manufacturer’s instructions. Viral supernatant was harvested after 48 hours and incubated with SIM-A9
murine microglial cells in SIM-A9 complete medium (DMEM/F12, Life Technologies, Carlsbad, CA),
10% fetal bovine serum (FBS; GE Healthcare Life Sciences, Chicago, IL), 5% horse serum (HS; GE
Healthcare Life Sciences, Chicago, IL), 1% Pen-Strep (Life Technologies, Carlsbad, CA). After 48 hours,
GFp+ cells were sorted by FACS on an Aria Fusion (BD Biosciences, San Jose, CA; UC Berkeley Cancer
Research Laboratory), expanded and subcultured for immune stimulation experiments. Percent knockdown
was determined via RT-qPCR.

Overexpression of Phf15 in murine microglial cells
A Phf15 overexpression vector was constructed by cloning the full length Phf15 cDNA (Mus musculus) PHD finger protein 15, mRNA cDNA clone MGC:143877 IMAGE:40094330) obtained from Dharmacon (Lafayette, CO) into a pMYs-IREs-GFP retroviral vector (Cell Biolabs Inc, San Diego, CA). Virus expressing the full length Phf15 cDNA or empty vector control were co-transfected with pCL-10 A1 (Addgene plasmid #15805)[30] in HEK293T cells using Lipofectamine 3000 (Life Technologies, Carlsbad, CA) reagent according to the manufacturer’s instructions. SIM-A9 cells were incubated with virus for 24 hrs and then sorted via FACS on an Aria Fusion, expanded and subcultured for immune stimulation experiments. Fold overexpression was verified via RT-qPCR.

Generation of Phf15 knockout microglia

Phf15 knock out (KO) SIM-A9 cells were generated using the Alt-R CRISPR-Cas9–mediated gene editing system (guide RNA sequence ACTACATCCTGGCGGACCCGTGG) from IDT (Coralville, IA) using CRISPRMAX Lipofectamine reagent (IDT) as per the manufacturer’s instructions. ATTO 550+ cells were single-cell sorted on an Aria Fusion. Clones were screened for Phf15 deletion using PCR (primers Forward: agcacagttaacacctct and Reverse: gaccaagtctgatggctg) followed by restriction digest with BglI (New England Biolabs, Ipswich, MA). Percent decrease in Phf15 mRNA transcript expression was determined via RT-qPCR (primer sequences are listed in Supplementary Table 1).

Immune stimulation

For all immune stimulation time course experiments, cells (knockdown, knockout, overexpression and respective controls) were subcultured in 24-well plates at a density of 10^5 cells/well (in triplicate) and stimulated with LPS (final concentration of 100 ng/ml; Sigma Aldrich, St. Louis, MO), CpG ODN (final concentration of 2.5 uM; Invivogen, San Diego, CA) or Poly(I:C) (final concentration of 25 uM; Sigma Aldrich, St. Louis, MO) for 1, 6, 12 or 24 hrs. No stimulation controls received an equivalent volume of sterile 1xPBS (Invitrogen, Carlsbad, CA).

RNA extraction

Mice were sacrificed according to the approved protocol. Brains were isolated and frontal cortical areas were dissected, flash frozen and stored at −80 °C. RNA was extracted using a bead homogenizer (30 seconds, setting ‘5’; Bead Mill, VWR) in Trizol reagent (ThermoFisher, Waltham, MA). Total RNA was extracted using the Direct-zol RNA miniprep kit (Zymo Research, Irvine, CA) according to the manufacturer’s instructions. For cell lines, after immune stimulation, media was aspirated and wells were washed 2x with ice-cold 1xPBS (Invitrogen, Carlsbad, CA). RNA was extracted using the Direct-zol RNA miniprep kit (Zymo Research, Irvine, CA).

Real-Time Quantitative PCR (RT-qPCR)

cDNA was reversed transcribed from total RNA using the SuperScript™ III First-Strand Synthesis System kit (ThermoFisher, Waltham, MA) following the manufacturer’s instructions. RT-qPCR was run using SYBR green (Roche) on a QuantStudio 6 (ThermoFisher, Waltham, MA) real-time PCR machine. All RT-qPCR primers are specific to the desired template, span exon-exon junctions and capture all transcript variants for the specific gene under study. Ct values were normalized to the housekeeping gene Hprt.

Primer sequences used in this study are listed in Supplementary Table 1.

RNA-seq library preparation and analysis

RNA was extracted from a total of n= 3 replicates per condition (Phf15 KO or control) and was used to prepare libraries for RNA sequencing using the KAPA mRNA HyperPrep Kit according to the manufacturer’s instructions (KAPA Biosystems, Wilmington, MA). Libraries were quality control checked via Qubit (ThermoFisher, Waltham, MA) and via RT-qPCR with a next generation sequencing (NGS) library quantification kit (Zymo Research, Irvine, CA). RNA sequencing (1 lane) was performed on a HiSeq4000 sequencing system (Illumina Inc., San Diego, CA; UC Berkeley Genomics Sequencing Laboratory). Sequencing reads were aligned to the Mus musculus reference genome assembly GRCm38 (mm10) using Spliced Transcripts Alignment to a Reference (STAR) aligner[31]. Count data was analyzed with Hypergeometric Optimization of Motif EnRichment (HOMER) software for next-generation sequencing analysis (http://homer.ucsd.edu/homer/ngs/index.html) which uses the R/Bioconductor package.
DESeq\textsuperscript{2}\textsuperscript{[32]} to perform differential gene expression analysis. To adjust for multiple comparisons, DESeq\textsuperscript{2} uses the Benjamini-Hochberg procedure to control the false discovery rate (FDR) and returned FDR adjusted p values and log2fold expression changes between Phf15 KO and control conditions for each gene. Genes were filtered by adjusted p value (adjusted p < 0.01 for upregulated genes or 0.05 for downregulated genes) and log2 fold change in expression (greater than 1.5 log2fold change for upregulated genes and less than -1.5 for downregulated genes). Too few downregulated genes (< 200) passed the more stringent adjusted p < 0.01 cutoff for robust downstream biological function analysis, so the adjusted p value threshold was lowered to p < 0.05. Results were visualized using the R package EnhancedVolcano\textsuperscript{[33]}.

Lists of upregulated and downregulated genes were input into Metascape\textsuperscript{[34]}, a gene annotation and analysis tool, to determine enriched biological themes within the gene lists.

**Motif enrichment**

Transcription factor binding sites (‘motifs’) were analyzed using HOMER (http://homer.ucsd.edu/homer/ngs/index.html).

**Statistical Analysis**

Relative mRNA expression of Phf15 in mouse frontal cortical areas was analyzed using ordinary one-way ANOVA with post hoc Tukey’s multiple comparisons to compare expression levels across age. Percent knockdown and time course experiments measuring expression levels of inflammatory markers (Tnfa, Nos2, Il-1β) between control and Phf15 shRNAs shPhf15-1 and shPhf15-2 after immune stimulation (with LPS, CpG-ODN or Poly(I:C)) were analyzed via Unpaired t-tests between each shRNA versus control shRNA within timepoint. Fold overexpression or percent reduction and time course experiments for Phf15 overexpression and knockout cell lines were analyzed using Unpaired t-tests (overexpression or knockout vs. respective control) within each time point. P < 0.05 was considered significant in all experiments.

**RESULTS**

**Aging increases Phf15 expression in mouse brain.**

To investigate whether Phf15 increases in mouse brains similar to humans\textsuperscript{[21]}, we measured Phf15 mRNA expression in mouse frontal cortical brain areas across age. We were interested in frontal cortical regions because of their involvement in mediating various aspects of cognitive function and because they are selectively affected in several aging-related neurodegenerative conditions like PD, AD and frontotemporal dementia (FTD)\textsuperscript{[35,36]}.

We found that compared to young (~2.5-month-old) mice, old (~20-month-old) mice had significantly elevated Phf15 mRNA levels in frontal cortical areas (Figure 1). Middle-aged (~14-month-old) mice showed a trend towards increased Phf15 mRNA expression that did not reach statistical significance. Our data suggest that Phf15 expression increases in mouse frontal cortical regions upon normal aging, similar to what was previously reported in humans\textsuperscript{[21]}.

**Knockdown of Phf15 increases the magnitude of the microglial inflammatory response.**

To determine whether Phf15 regulates microglial inflammatory function, we performed loss-of-function studies via shRNA-mediated knockdown (KD) in a murine microglial cell line, SIM-A9, followed by immune activation with lipopolysaccharide (LPS), a component of gram-negative bacterial cell walls and Toll-like receptor 4 (TLR4) agonist. We chose LPS because 1) Intraperitoneal and/or intracranial administration of LPS in mice lead to increased microglial activation, neuroinflammation, neuronal loss including loss of dopaminergic neurons in the substantia nigra in a mouse model of PD\textsuperscript{[8]} as well as, cognitive and neurological deficits\textsuperscript{[37]}, 2) Aged individuals show increased systemic levels of LPS in the bloodstream\textsuperscript{[38]} which are associated with increased inflammation and microglial activation\textsuperscript{[39]} and 3) In humans, TLR4 activation is linked to age-related pathologies like PD and AD\textsuperscript{[40-42]}. Thus, LPS serves as a relevant aging-related physiological immune stimulant.

KD of Phf15 resulted in a significant reduction in Phf15 mRNA transcript levels of 52% or 60% for cell lines shPhf15-1 or shPhf15-2, respectively (Figure 2A), as well as, significantly increased mRNA expression of Tnfa, a pro-inflammatory cytokine, after KD with shPhf15-2 at 0, 1, 6 and 12 hours after LPS.
stimulation (Figure 2B). Similarly, mRNA levels of Nos2, the enzyme that catalyzes the production of NO, were significantly elevated at 1, 6 and 12 hours post stimulation for shPhf15-2 and 0, 6 and 12 hours for shPhf15-1 (Figure 2D). Overall, our experiments show that ~50-60% KD, the equivalent of a “heterozygous” condition, results in increased expression of pro-inflammatory mediators over a 12 hour time course that resolves and falls below control levels by 24 hours after immune stimulation. Importantly, microglial inflammatory function was elevated in the absence of immune stimulation (0 hour time point, Figures 2B, D and No stimulation condition, Figures 2C, E), suggesting a loss of repressive mechanisms that inhibit basal state inflammatory gene transcription.

We repeated the immune activation time course experiments in Phf15 KD cells using two separate immune stimulants specific to two distinct TLRs to test the pathway specificity of the inflammatory response. CpG Oligodeoxynucleotide (CpG ODN), a synthetic bacterial and viral DNA mimic targets TLR9 ligand and Polyinosinic:polycytidylic acid (Poly(I:C)), a synthetic viral dsRNA mimic targets TLR3. Although TLR4 uses both the Myeloid differentiation primary response 88 (MyD88) and TIR-domain-containing adapter-inducing interferon-β (TRIF) downstream adapters to transduce its inflammatory cascade, TLR9 and TLR3 utilize MyD88 or TRIF respectively (Supplementary Figure 1)[43,44].

Immune stimulation with CpG ODN and Poly(I:C) both yielded similar results to those obtained with LPS stimulation (Supplementary Figures 2 and 3, respectively) denoting no adapter selectivity and confirming that Phf15 antagonizes gene expression downstream of both the MyD88 and TRIF signaling pathways.

Genetic deletion of Phf15 increases the magnitude and prolongs the duration of the microglial inflammatory response.

Since our KD strategy resulted in ~50% reduction in Phf15 mRNA expression, we next performed CRISPR/Cas9-mediated genetic deletion of Phf15 in SIM-A9 microglial cells followed by immune activation with LPS. Knockout (KO) of Phf15 (Figure 3A) resulted in significantly increased LPS-induced expression of Tnfα (Figure 3B), Il-1β (Figure 3D) and Nos2, albeit to a lesser extent (Figure 3F) over a 24-hour time course. Importantly, mRNA levels of both Tnfα and Il-1β remained elevated at 24 hours compared to control cells, denoting a prolonged inflammatory response and failure to return to steady-state. mRNA expression of Nos2 showed a significant upregulation over 12 hours (0, 1 and 12 hour timepoints) but had returned to control levels by 24 hours (Figure 3F). Notably, basal expression of all 3 genes was significantly elevated, with a 4-fold increase in Tnfα, 14-fold increase in Il-1β and 32-fold increase in Nos2 when comparing KO versus control cells Figures 3C, E, G).

Time course experiments after stimulation of TLR9 with CpG-ODN (Supplementary Figure 4) and TLR3 with Poly(I:C) (Supplementary Figure 5) in Phf15 KO cells again yielded similar results to LPS stimulation in Phf15 KO microglial cells, denoting no difference in downstream adapter selectivity and confirming our prior KD results.

Overall, KO of Phf15 resulted in a more severe phenotype compared to our KD results, increasing the magnitude and prolonging the duration of the microglial inflammatory response. Taken together, our KD and KO results indicate that Phf15 functions to restrict microglial inflammatory output, regulating the magnitude and duration, as well as, basal inhibition of the inflammatory response.

Overexpression of Phf15 in microglia results in a dampened inflammatory response

To further test the role of Phf15 as a repressor of pro-inflammatory genes, we carried out gain-of-function studies of Phf15 in SIM-A9 cells. Overexpression (OE) via retroviral delivery of the full-length murine Phf15 cDNA (Figure 4A) resulted in significantly decreased expression of Tnfα at 6 hours (Figure 4B), Il-1β (0, 6, 12 hours; Figure 4D) and Nos2 (0, 6, 24 hours; Figure 4F). Notably, basal levels of both Il-1β and Nos2 were also significantly decreased (Figures 4E, G). Time course experiments following stimulation with CpG-ODN (Supplementary Figure 6) and Poly(I:C) (Supplementary Figure 7) likewise yielded similar results as LPS stimulation of Phf15 OE microglia, displaying no adapter selectivity.

Taken together, our OE results show a dampened microglial inflammatory response, revealing a reciprocal response phenotype compared to our KD and KO experiments. Collectively these results confirm that Phf15 functions to repress both basal and stimulus-dependent inflammatory gene expressions in microglia.
**Loss of Phf15 affects global expression of genes involved in antiviral responses and regulation of inflammatory processes**

To examine global transcriptional changes as a result of Phf15 deletion in microglia, we carried out RNA-sequencing (RNA-seq) on Phf15 KO SIM-A9 cells under no stimulation conditions and 6 hours post LPS stimulation. We chose to examine the no stimulation condition (0 hour time point) based on our KD and KO time course results which showed that baseline is one of the most consistently and strongly deregulated time points. Importantly, elevated or ‘leaky’ pro-inflammatory mediator expression at baseline might result in chronic inflammation leading to neurodegeneration. Similarly, 6 hours after LPS stimulation corresponded to the peak of the transcriptional inflammatory response, with large increases in magnitude for both IL-1β and Nos2. Differential gene expression analysis revealed that 466 genes with log2 fold change > 1.5 and p adj < 0.01 were up-regulated and 309 genes with log2 fold change < -1.5 and p adj < 0.05 were downregulated (Figure 5A). Biological theme enrichment analysis using Metascape[34] on the upregulated genes revealed that the most enriched biological process categories under basal conditions were “response to virus” and “cytokine production” (Figure 5B, C). Under the “response to virus” category, there was significant upregulation of various interferon-stimulated genes (ISGs), for example Ifit1, Ifit3, Irf7, Ifg15, Oas2 and Oasl2 (Figure 5C). The downregulated genes show more variability in the types of pathways affected, largely involving growth, differentiation and glial cell migration processes (Figure 5A and Supplementary Figure 8A).

Motif analysis for transcription factor (TF) binding sites enriched in the promoters of the upregulated genes at baseline revealed consensus motifs for Interferon (IFN) stimulated response element (ISRE, IRF binding motif), and motifs for IFN response factor 3 (IRF3) and IRF8 in the top 5 best matches. Also enriched were Activator protein 1 (AP-1) and nuclear factor kappa-light-chain-enhancer of activated B cells p65 subunit (NF-kB -p65) motifs. Both can regulate expression of canonical pro-inflammatory cytokines such as Tnfα and Il-1[45,46] (Figure 5D). Motif enrichment for the set of downregulated genes revealed motifs for Twist-related protein 2 (Twist2) and basic helix–loop–helix (bHLH) MIST1 (BHLHA15). Twist2 has been shown to mediate cytokine downregulation after chronic NOD2 (a bacterial peptidoglycan sensor) stimulation[47]. MIST1 has been shown to induce and maintain secretory architecture in cells specialized for secretion[48]( Supplementary Figure 8B).

Differential gene expression analysis after 6 hours of LPS stimulation in KO versus control cells revealed 576 up-regulated genes (log2 fold change > 1.5 and p adj < 0.01) and 322 down-regulated genes (log2 fold change < -1.5 and p adj < 0.05) (Figure 6A). Interestingly, by 6 hours after LPS administration, some of the most enriched biological process categories in KO cells were related to “cytokine secretion” and “immunoregulatory interaction” (Figure 6B and C), denoting a strong increase in magnitude of expression of genes involved in regulating the secretion of pro-inflammatory mediators. The downregulated genes at 6 hours after LPS stimulation in KO cells relative to control again displayed more variability, but did show decreases in biological process categories related to “regulation of defense response” and “cytokine production”, indicating negative regulation of these processes in Phf15 KO cells compared to control (Supplementary Figure 9A).

Motif enrichment analysis for TF binding sites enriched in the promoters of upregulated genes at the 6-hour time point revealed consensus sequences for AP-1, a key regulator of microglia reactivity in inflammation[49](Figure 6D). Motif enrichment for the set of downregulated genes revealed ISRE, such as IRF1 and IRF3 motifs (Supplementary Figure 9B), supporting the observation that there is a negative “regulation of defense response” by 6 hours post stimulation. It is interesting to note that a functional transition from cytokine production to cytokine secretion seems to occur in the 6 hour period after LPS activation.

Taken together, our RNA-seq results confirm that Phf15 is a repressor of microglial inflammatory gene expression, regulating the antiviral response - specifically, IFN-1-dependent responses - as well as processes related to pro-inflammatory cytokine production and release.

**DISCUSSION**

Our results show that Phf15 inhibits microglial expression of pro-inflammatory mediators under basal and signal-dependent activation, regulating both the magnitude and duration of the inflammatory response. Genetic deletion of Phf15 in a microglial cell line followed by stimulation with LPS lead to an exaggerated pro-inflammatory response with increased production of Tnfα, Il-1β and Nos2 over a time
course of 24 hours. Importantly, levels of pro-inflammatory factors remained elevated at 24 hours
demonstrating a sustained and prolonged response. Consistent with our LPS stimulation of TLR4 results,
similar results were obtained after TLR9 and TLR3 activation confirming that Phf15 is a general negative
regulator and controls both the MyD88 and TRIF downstream signal transduction pathways
(Supplementary Figure 1). Overexpression of Phf15 showed a dampened microglial inflammatory
response, highlighting a reciprocal response phenotype that further supports our loss-of-function results.

Prolonged inflammation can damage surrounding healthy tissue, eventually resulting in neuronal
degeneration and loss, and negatively affecting brain function. For example, levels of Tnfα are seen to
rapidly rise in experimental models of PD and are highly toxic to dopaminergic neurons[12,13,50]. Similarly,
high levels of TNFα are a hallmark of PD in humans[51-53]. Additionally, both TNFα and IL-1β are
involved in maintaining proper synaptic plasticity at physiological levels[54,55] and overproduction of these
cytokines can result in neuronal death via excitotoxicity and cognitive dysfunction[56,57].

Our studies further demonstrate that Phf15 can regulate both basal and signal-dependent
microglial inflammatory gene expression. KD and KO of Phf15 in microglial cell lines resulted in
significantly increased levels of pro-inflammatory cytokine gene expression 1) without stimulation and 2)
after immune activation, while OE had the reverse effect. The inflammatory response is a tightly controlled
process in immune cells in order to protect against unintended damage to healthy tissue. Even in aged
microglia, where production and secretion of pro-inflammatory mediators is generally increased, this
process is dependent upon treatment with immune stimulating[48,58,59]. Increased pro-inflammatory cytokine
gene expression without stimulation denotes constitutive or ‘leaky’ expression of inflammatory mediators,
simulating a state of low-grade but constant activation. Similarly, hyperresponsiveness to immune stimuli
combined with a lack of resolution of the inflammatory response can lead to a state of chronic
inflammation. All three can trigger pathological chronic inflammation in the brain which is detrimental to
brain function.

Importantly, distinct molecular mechanisms regulate transcriptional control of different phases
(modules) of the inflammatory response and it is noteworthy that Phf15 might be involved in regulating
several of these. Basal inflammatory function, for example, is generally regulated by co-repressors such as
nuclear receptor co-repressor (NCOR), silencing mediator of retinoid and thyroid receptors (SMRT) and
REST co-repressor 1, (RCOR1 or CoREST) that block poised promoters from active transcription,
preventing ‘leaky’ expression of primary response genes (e.g., TNFα, Type I IFNs, Il-1β, etc.)[19].
Significantly increased inflammatory gene transcription under baseline conditions, as observed in our
Phf15 KD and KO experiments, suggests a loss of this repressive mechanism.

After stimulation by an activating signal, additional mechanisms can maintain quiescence by
restraining active transcription. For example, nuclear receptors like peroxisome proliferator-activated
receptor-γ (PPARγ), glucocorticoid receptor (GR) and liver X receptors (LXRs) can inhibit the signal-
activated exchange of co-repressors for co-activators at poised promoters, inhibiting the initiation of
transcription[19,57]. Lastly, several mechanisms regulate resolution of inflammation at the transcriptional
level, including transrepression mechanisms that can remove transcription factors like NF-κB, from
inflammatory gene promoters, effectively blocking expression of secondary response genes, that is, genes
which require chromatin-modification as well as protein synthesis for their induction (for example Nos2
and ISGs)[9,13,58]. Timely resolution of an inflammatory response is crucial in order to limit cellular and
tissue damage caused by prolonged or chronic inflammation. Our results suggest that Phf15 may be
involved in regulating all three of the abovementioned mechanisms.

But how might Phf15 be involved in regulating transcriptional repression of the inflammatory
response? PHF15 was first described in embryonic stem cells as an E3 ligase that directly targets Lysine-
specific demethylase 1 (LSD1, Kdm1a) - a key demethylase of histone 3 lysine 4 - for degradation[22].
LSD1 has been identified as a member of the CoREST co-repressor complex[60,61] which is required for
transcriptional repression of inflammation in microgliia[9]. We therefore initially hypothesized that increased
levels of Phf15 upon aging might lead to decreased levels of LSD1 and increased microglial inflammatory
output. Our results, however, demonstrate that Phf15 itself inhibits microglial inflammatory function, thus,
its purported mechanism for inhibition is likely not via degradation of LSD1.

Interestingly, the global transcriptional changes caused by Phf15 deletion are highly similar to
age-associated transcriptional changes in microglia that have been previously reported[9,62,63]. In particular,
a study by Deczkowska et al.[64], found “immune system process” and specifically “response to virus”
among the most highly upregulated biological categories for differentially expressed genes in microglia of young (2-month old) versus aged (22-month old) mice, consistent with our results in Phf15 KO microglia. Notably, a study by Hammond et al.\textsuperscript{[63]}, which used single-cell RNAseq to look at microglia profiles throughout the mouse lifespan, found subpopulations in aged (P540) mouse brains which were largely 1) inflammatory, that is, they upregulated IL-1β, Tnfα and other cytokines or 2) IFN-I-responsive, upregulating ISGs, particularly Ifit3, Ifr7, Isg15, Oasl2, Ifitm3, and Rtp4, compared to younger adult (P100) brains. Similarly, a recent study from the Tabula Muris Consortium which produced a single-cell transcriptomic atlas of 23 tissues and organs across the Mus musculus life span, confirmed that microglia in the aged (P540 and P720) brain are enriched for IFN-I-responsive genes and upregulate a similar set of genes including Ifit3, Ifr7, Isg15, Oasl2, Ifitm3, and Rtp\textsuperscript{4}[65]. The genes upregulated by the interferon-responsive microglia clusters in both these studies are highly similar to those upregulated in our Phf15 KO cells under basal conditions (see Figure 5A and C). Because ISGs can modulate inflammation\textsuperscript{[64]}, it is possible that interferon-responsive microglia could play a role in contributing to the inflammatory signature found in the aged brain. Interestingly, among the set of downregulated genes in Phf15 KO cells at baseline and 6 hours after LPS stimulation, is Myocyte Enhancer Factor 2C (Mef2C). Mef2C is an important checkpoint inhibitor that restrains microglial activation in response to pro-inflammatory insults and is lost in brain aging via IFN-I mediated downregulation\textsuperscript{[64,66]}. Thus, an increase in Phf15 expression in microglia during healthy aging could putatively work to counteract not only microglial activation but increased IFN-I in the aged brain as well.

Notably, a recent study by Readhead et al.\textsuperscript{[67]} found that several virus species are commonly present in the aged human brain. Among them, human herpesvirus 6A and 7 (HHV-6A and HHV-7) were highly upregulated in the brain of AD patients and were found to modulate host genes associated with AD risk, for example, Amyloid precursor protein (APP) processing. APP is the precursor molecule whose proteolysis forms amyloid-β (Aβ) and formation of Aβ plaques has long been thought of as the driving force behind Alzheimer’s disease\textsuperscript{[62]}. Aβ has more recently been found to have antimicrobial properties, conferring increased resistance against infection from both bacteria and viruses\textsuperscript{[63]}. APP is among the significantly upregulated genes under basal conditions in our Phf15 KO cells (log2 fold change=t1.492 and p adj <0.0001; see Figure 5A). Upregulation of APP due to loss of Phf15 in mouse microglia is thus consistent with our data showing Phf15 regulation of the antiviral microglial response.

Altogether, our results show that Phf15 is a novel repressor of microglial inflammatory gene expression, regulating both the magnitude and time-to-resolution of the inflammatory response. Importantly, Phf15 also serves to repress baseline inflammatory output in the absence of immune activation. Putatively, increases in Phf15 during healthy aging could help counteract brain inflammation and protect brain health.

Future studies will determine the mechanism of action of Phf15. For example, the identity of its binding partner proteins, its genome-wide binding sites and associated histone marks to determine the specific gene regulatory regions it interacts with (e.g. active enhancers or promoters). Additionally, studies in Phf15 KO mice will elucidate whether loss of Phf15-mediated repression of pro-inflammatory factors is sufficient to induce cognitive decline or exacerbate LPS-induced neurotoxicity of dopaminergic neurons in the substantia nigra.

DECLARATIONS

Acknowledgements

We thank Prof. Ellen Robey for helpful comments on the manuscript and Wendy Yan for technical assistance.

Author’s contributions

Designed and performed experiments, analyzed data, and wrote the manuscript: Muroy, SE
Performed experiments and analyzed data: Timblin, GA, Preininger, MK
Performed experiments: Cedillo, P
Designed experiments and wrote the manuscript: Saijo, K.
Availability of data and materials
Sequencing data will be deposited in NCBI Gene Expression Omnibus (GEO).

Financial support and sponsorship
This work was supported by the Berkeley Fellowship to S.E.M., ADA Postdoctoral fellowship to G.A.T., NSF GRFP to M.K.P., and R01HD092093 and Pew Scholarship to K.S.

Conflicts of interest
All authors declared that there are no conflicts of interest.

Ethical approval and consent to participate
All procedures were approved by the Animal Care and Use Committee of the University of California, Berkeley (Animal Use Protocol AUP-2017-02-9539).

Consent for publication
Not applicable.

Copyright
The authors.

References


**Figure Legends**

**Figure 1. Phf15 expression increases in aged mouse frontal cortical areas.** Phf15 mRNA expression was significantly elevated in frontal cortical areas of old (~20-month-old; red bar) mice compared to young (~2.5 month old; black bar) mice. Data are mean ± SEM (n = 4 young, n = 5 middle aged, n = 12 old). One-way ANOVA with Tukey’s post hoc comparisons between age groups: **p<0.01
Figure 2. Knockdown of Phf15 increases the magnitude of the microglial inflammatory response. (A)
Knockdown efficiency for anti-Phf15 shRNAs shPhf15-1 (blue bar, 52% knockdown) and shPhf15-2 (red bar, 60% knockdown) Data are mean ± SEM (n = 3 per condition). Unpaired t-tests between shPhf15-1 or shPhf15-2 and shCtrl cells: asterisks indicate **p<0.01. 24-hour time course experiments showing relative mRNA expression levels of Tnfα (B) and Nos2 (D) after LPS stimulation of shRNAs shPhf15-1 and shPhf15-2 compared to shCtrl (control scrambled shRNA). “No stimulation” 0 hr time point is shown for Tnfα (C) and Nos2 (E). Data are mean ± SEM (n = 3 per condition). Unpaired t-tests for shPhf15-1 or shPhf15-2 and shCtrl cells for individual timepoints: asterisks indicate *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.
LPS, lipopolysaccharide; Tnfα, tumor necrosis factor alpha; Nos2, nitric oxide synthase, inducible.

Figure 3. Knockout of Phf15 increases the magnitude and duration of inflammatory gene expression. (A)
Percent reduction in Phf15 transcript expression in Phf15 knockout SIM-A9 microglia (Phf15 KO, red bar) compared to control (Ctrl, open bar). 24-hour time course experiments showing relative mRNA expression levels of Tnfα (B), Il-1β (D), and Nos2 (F) after LPS stimulation. Baseline (0 hr time point, No stimulation) expression of Tnfα (C), Il-1β (E), and Nos2 (G) are displayed separately from time course experiments. All data are mean ± SEM (n = 3 per condition). Unpaired t-tests between Phf15 KO and control cells for percent reduction and for individual timepoints: asterisks indicate *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.
LPS, lipopolysaccharide; Tnfα, tumor necrosis factor alpha; inducible; Il-1β, Interleukin 1 beta; Nos2, nitric oxide synthase.

Figure 4. Phf15 overexpression decreases the microglial inflammatory response. (A) Fold overexpression (OE) of Phf15 in SIM-A9 microglia (red bar) versus control cells (Ctrl, open bar). 24-hour time course experiments showing relative mRNA expression levels of Tnfα (B), Il-1β (D), and Nos2 (F) after LPS stimulation. Baseline (0 hour time point, No stimulation) expression of Tnfα (C), Il-1β (E), and Nos2 (G) are displayed separately from time course experiments. All data are mean ± SEM (n = 3 per condition). Unpaired t-tests between Phf15 OE and control cells for fold-overexpression and for individual time points: asterisks indicate *p<0.05, **p<0.01.
LPS, lipopolysaccharide; Tnfα, tumor necrosis factor alpha; inducible; Il-1β, Interleukin 1 beta; Nos2, nitric oxide synthase.

Figure 5. Loss of Phf15 affects the expression of genes involved in viral response and regulation of inflammatory processes in the absence of immune stimulation
(A) Volcano plot representing the RNA-seq results. Orange dots represent differentially expressed genes in Phf15 knockout microglia compared to control (upregulated genes at a cutoff of log2fold change > 1.5 and p adj < 0.01; downregulated genes at a cutoff of log2fold change < -1.5 and p adj < 0.05). (B) GO analysis for significantly upregulated genes showing biological process categories related to response to virus and inflammatory response. (C) Upregulated genes associated with response to virus and inflammatory response in the No stimulation (baseline) condition. Relative FPKM values were obtained by normalizing FPKM values of Phf15 knockout SIM-A9 microglia to control FPKM values for each gene (n = 3 per condition). Statistics are by DESeq2: asterisks indicate **p<0.01, #p<0.0001. (D) Top 5 enriched transcription factor binding motifs for the set of upregulated genes in the No stimulation (baseline) condition.

Figure 6. Knockout of Phf15 affects the expression of genes involved in inflammatory factor secretion and immunoregulatory processes after LPS stimulation
(A) Volcano plot representing the RNA-seq results. Orange dots represent differentially expressed genes in Phf15 knockout microglia 6 hours after LPS administration compared to control (upregulated genes at a cutoff of log2fold change > 1.5 and p adj < 0.01; downregulated genes at a cutoff of log2fold change < -1.5 and p adj < 0.05). (B) GO analysis for upregulated genes shows biological process categories associated with cytokine secretion and immunoregulatory interaction. (C) Upregulated genes associated with cytokine secretion and immunoregulatory interaction biological process categories 6 hours post LPS stimulation. Relative FPKM values were obtained by normalizing FPKM values of Phf15 knockout SIM-A9 microglia to control FPKM values for each gene (n = 3 wells per condition). Statistics are by DESeq2: asterisks indicate **p<0.01, $p<0.001, #p<0.0001. (D) Transcription factor binding motifs for the set of upregulated genes 6 hours after LPS stimulation are enriched for Activator protein 1 (AP-1).
Fig. 1.

**Phf15**

Relative mRNA expression

- young (~2.5 mos)
- middle aged (~14 mos)
- old (~20 mos)

**P<0.01**
**Fig. 2**

**Phf15**

**Time course**

**No stimulation**

**Tnfα**

**Nos2**
**Fig. 3**

A. Relative mRNA expression of Phf15 in Ctrl and Phf15 KO cells.

B. Time course of Tnfα expression following LPS stimulation.

C. No stimulation showing increased Tnfα expression in Phf15 KO cells.

D. Time course of IL-1β expression following LPS stimulation.

E. No stimulation showing increased IL-1β expression in Phf15 KO cells.

F. Time course of Nos2 expression following LPS stimulation.

G. No stimulation showing increased Nos2 expression in Phf15 KO cells.
**Fig. 4**

(A) Relative mRNA expression of *Phf15*.

(B) Time course of *Tnfα* expression.

(C) No stimulation of *Tnfα* expression.

(D) Time course of *Il-1β* expression.

(E) No stimulation of *Il-1β* expression.

(F) Time course of *Nos2* expression.

(G) No stimulation of *Nos2* expression.
**Fig. 5**

**A**

- **Log**₂ fold change vs. adjusted P values for 309 genes and 466 genes.
- Genes such as Ifit1, Ifit3, Isg15, Oas2, Oasl2, Rtp4, Tlr3, Irf7, C3, App, Mef2c, Pdcd1, Rgs2, Cxcl10, Tgfb2, Oas2, Ifit1, Rtp4, Tnf, C3 are highlighted.

**B**

- Upregulated genes with significant GO terms:
  - GO:0010876: lipid localization
  - GO:1901342: regulation of vasculature development
  - CORUM:146: Src-dynamin-synapsin complex
  - mmu04620: Toll-like receptor signaling pathway
  - GO:0045123: cellular extravasation
  - GO:0098609: cell-cell adhesion
  - GO:0043410: positive regulation of MAPK cascade
  - GO:0071346: cellular response to interferon-gamma
  - R-MMU-1280215: Cytokine Signaling in Immune system
  - GO:0032635: interleukin-6 production
  - mmu04610: Complement and coagulation cascades
  - GO:0006935: chemotaxis
  - GO:0050778: positive regulation of immune response
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - GO:0006935: chemotaxis
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis
  - mmu00600: complement and coagulation cascades
  - mmu00051: chemotaxis

**C**

- Relative FPKM for Response to virus and Inflammatory response.
- Key genes: Ifit1, Ifit3, Isg15, Nos2, Oas2, Oasl2, Rtp4, Tlr3, Irf7, C3, Tnf, Il1b, Nos2, Cxcl10.

**D**

- Motif Name | P-value
- IRF | 1e-6
- AP-1 | 1e-5
- IRF3 | 1e-5
- NFkB-p65 | 1e-5
- IRF8 | 1e-5
Figure 6

A.

A volcano plot showing the log2 fold change and adjusted P-value for 322 upregulated and 576 downregulated genes.

B.

A bar chart showing the upregulated genes with their associated biological processes.

C.

A bar chart comparing the relative FPKM of cytokine secretion and immunoregulatory interaction in Ctrl and Phf15 KO conditions.

D.

A table listing the motifs and their corresponding names and P-values.

### Table: Motif Name, P-value

<table>
<thead>
<tr>
<th>Name</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>AP-1</td>
<td>1e-5</td>
</tr>
<tr>
<td>AP-1</td>
<td>1e-5</td>
</tr>
</tbody>
</table>

Fig. 6