

Glial Draper Rescues A β Toxicity in a *Drosophila* Model of Alzheimer's Disease

Arpita Ray, Sean D. Speese, and Mary A. Logan

Jungers Center for Neurosciences Research, Department of Neurology, Oregon Health and Science University (OHSU), Portland, Oregon 97239

Pathological hallmarks of Alzheimer's disease (AD) include amyloid- β (A β) plaques, neurofibrillary tangles, and reactive gliosis. Glial cells offer protection against AD by engulfing extracellular A β peptides, but the repertoire of molecules required for glial recognition and destruction of A β are still unclear. Here, we show that the highly conserved glial engulfment receptor Draper/MEGF10 provides neuroprotection in an AD model of *Drosophila* (both sexes). Neuronal expression of human A β 42^{arc} in adult flies results in robust A β accumulation, neurodegeneration, locomotor dysfunction, and reduced lifespan. Notably, all of these phenotypes are more severe in *draper* mutant animals, whereas enhanced expression of glial Draper reverses A β accumulation, as well as behavioral phenotypes. We also show that the signal transducer and activator of transcription (Stat92E), c-Jun N-terminal kinase (JNK)/AP-1 signaling, and expression of matrix metalloproteinase-1 (Mmp1) are activated downstream of Draper in glia in response to A β 42^{arc} exposure. Furthermore, A β 42-induced upregulation of the phagolysosomal markers Atg8 and p62 was notably reduced in *draper* mutant flies. Based on our findings, we propose that glia clear neurotoxic A β peptides in the AD model *Drosophila* brain through a Draper/STAT92E/JNK cascade that may be coupled to protein degradation pathways such as autophagy or more traditional phagolysosomal destruction methods.

Key words: amyloid; autophagy; Draper; *Drosophila*; glia

Significance Statement

Alzheimer's disease (AD) and similar dementias are common incurable neurodegenerative disorders in the aging population. As the primary immune responders in the brain, glial cells are implicated as key players in the onset and progression of AD and related disorders. Here we show that the glial engulfment receptor Draper is protective in a *Drosophila* model of AD, reducing levels of amyloid β (A β) peptides, reversing locomotor defects, and extending lifespan. We further show that protein degradation pathways are induced downstream of Draper in AD model flies, supporting a model in which glia engulf and destroy A β peptides to reduce amyloid-associated toxicity.

Introduction

One neuropathological feature of Alzheimer's disease (AD) is the formation of extracellular deposits of insoluble fibrillar amyloid- β

(A β) peptides (Holtzman et al., 2011; Nelson et al., 2012). These A β aggregates may adversely affect CNS function by sequestering protective molecules or by releasing small A β oligomers under certain physiological conditions (Rosenblum, 2014; Tipping et al., 2015; Jucker and Walker, 2015). Soluble A β oligomers can directly promote synaptic dysfunction (Selkoe, 2012; Rosenblum, 2014; Tipping et al., 2015) and may be an early causal factor in AD-related cognitive phenotypes. Although the precise mechanisms of A β -induced toxicity are enigmatic, there is compelling genetic and pharmacological evidence from model systems that reducing A β levels is largely protective (Lashuel et al., 2002; Wang et al., 2010; Miners et al., 2011; Baruch et al., 2016), emphasizing the need to understand how brain A β levels are normally kept in check.

Genome-wide association studies and genetic analyses of AD models support the notion that glial cells are coupled to AD

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Correspondence should be addressed to Dr. Mary Logan, Jungers Center for Neurosciences Research, Department of Neurology, Oregon Health and Science University, 3181 Southwest Sam Jackson Park Road, Portland, OR 97239. E-mail: loganm@ohsu.edu.

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pathogenesis. For example, mutations in the microglial receptor Trem2 (triggering receptor expressed on myeloid cells 2) are associated with increased AD risk (Guerreiro et al., 2013; Jonsson et al., 2013). The immunoreceptor CD33/Siglec-3 is another well described AD susceptibility locus. CD33 mutations are associated with reduced microglial internalization of A β and increased fibrillar amyloid accumulation *in vivo* (Bradshaw et al., 2013; Griuciu et al., 2013; Malik et al., 2013). Unsurprisingly, one prominent area of AD research has focused on glial phagocytic function; multiple glial cell types (e.g., microglia and astrocytes) have the capacity to reduce A β levels and influence AD progression (Wyss-Coray et al., 2003; Herber et al., 2007; Demattos et al., 2012; Hong et al., 2016; Pomilio et al., 2016; Wes et al., 2016). Understanding precisely how glia recognize, internalize, and degrade amyloid-like peptides will provide additional molecular and genetic targets to pursue for disease treatment.

Drosophila offers a powerful *in vivo* model to rapidly explore A β -induced toxicity. Transgenic expression of human A β _{1–42} fragment (A β 42) results in age-dependent presentation of multiple molecular and behavioral phenotypes, including A β accumulation, neuronal hyperexcitability, defective mitochondrial function, locomotor dysfunction, and reduced lifespan (Finelli et al., 2004; Crowther et al., 2005; Iijima et al., 2008; Wentzell and Kretzschmar, 2010; Ping et al., 2015), mirroring the cellular and behavioral decline observed in other organisms (Bayer and Wirths, 2008; Woodruff-Pak, 2008; Götz and Ittner et al., 2008; Rivest, 2009). Interestingly, electron microscopy reveals that when human A β 42 is expressed in *Drosophila* neurons, A β is detected in glia, suggesting that fly glia internalize secreted A β peptides *in vivo* (Iijima et al., 2008). The molecules involved in glial engulfment of human A β peptides in *Drosophila*, however, have never been explored.

The highly conserved engulfment receptor Draper is required for glial clearance of apoptotic cells and degenerating neuronal projections in flies during development and in the adult CNS (MacDonald et al., 2006; Tasdemir-Yilmaz and Freeman, 2014). Draper signals through a tyrosine kinase-signaling cascade to drive cytoskeletal remodeling, alter glial gene expression, and promote phagocytic activity (MacDonald et al., 2006, 2013; Ziegenfuss et al., 2008). The vertebrate orthologs of Draper (MEGF10 and Jedi) and downstream effectors (e.g., Fyn-related kinase, GULP, Rac1) are also implicated in glial immunity, including glial clearance of degenerating neurons (Osada et al., 2009; Wu et al., 2009; Linnartz et al., 2010; Chung et al., 2013; Iram et al., 2016), indicating that the core components of glial engulfment machinery are conserved across species. Interestingly, overexpression of MEGF10 in cultured HeLa cells enhances engulfment of bath-applied A β (Singh et al., 2010), but the role of Draper/MEGF10 in the context of AD has never been explored *in vivo*.

Here, we show that human A β 42^{arc} activates Draper-dependent signaling cascades in adult *Drosophila* glia, including signal transducer and activator of transcription (Stat92E) and c-Jun N-terminal kinase (JNK)/AP-1-mediated transcription, matrix metalloproteinase-1 (Mmp1) upregulation, and induction of protein degradation pathways. Glial inhibition of Draper exacerbates molecular and behavioral A β 42^{arc}-associated phenotypes, whereas overexpression of Draper/MEGF10 partially rescues these defects, providing the first *in vivo* evidence that Draper offers protection against A β 42-induced toxicity.

Materials and Methods

Fly strains. The following *Drosophila* strains were used: *repo-Gal4* (MacDonald et al., 2006), *elavc155-Gal4* (BL458), *elav-Gal4* (BL8765), *App1-Gal4* (obtained from Doris Kretzschmar, OHSU; RRID:BDSC_32040),

UAS-A β 42^{arc} (BL33773 and BL33774), *UAS-Draper-I* (Logan et al., 2012), *UAS-Draper^{RNAi}* (MacDonald et al., 2006), *drpr Δ 5rec9* (Neukomm et al., 2014), *UAS-Jra^{RNAi}* (BL31595, RRID:BDSC_3159), *UAS-kayak^{RNAi}* (BL31391, RRID:BDSC_31391), *UAS-stat92e^{RNAi}* (VDRC 43866), *TRE-GFP*, and *10xStat92E-dGFP* (Bach et al., 2007). *UAS-MEGF10* transgenic flies were generated by subcloning mouse MEGF10 (cDNA clone MGC:100091, IMAGE:30620548) from pEGFP-N3 (kind gift from B. Carter, Vanderbilt University, Nashville, TN) into the pUAST vector and transgenic flies were generated using standard methods by BestGene.

Brain dissection and immunostaining. Adult fly brains of either sex were dissected, fixed, and stained using previously described methods (Purice et al., 2016). Fly heads were fixed in 4% paraformaldehyde + 0.01% Triton X-100 for 16 min while rocking at room temperature, then washed with PBST-1 (PBS containing 0.01% Triton X-100) for 3 \times 2 min at room temperature. Brains were dissected in ice-cold PBST-1, transferred to microcentrifuge tubes containing 4% paraformaldehyde + 0.1% Triton X-100, fixed while rocking at room temperature for 20 min, and then washed with PBST-2 (PBS containing 0.1% Triton X-100) for 3 \times 2 min at room temperature. For immunostaining, brains were blocked in Sea Block blocking buffer (ThermoFisher Scientific) for 15 min at room temperature, followed by incubation in primary antibodies diluted in PBST-2 overnight at 4°C. Brains were then washed in PBST-2 for 4 \times 30 min at room temperature, incubated in secondary antibodies diluted in PBST-2 for 2 h at room temperature in the dark, and washed in PBST-2 for 4 \times 30 min in the dark. After the final wash, any remaining liquid was removed from the brains with a glass pipette and replaced with VECTASHIELD Mounting Media (Vector Laboratories; RRID:AB_2336789).

Confocal imaging. After sitting for 1 h overnight at 4°C in the dark, brains for each single experiment were mounted on microscope slides under a single no. 1.5 cover glass in VECTASHIELD before imaging on a Zeiss LSM 700 laser scanning microscope equipped with a Zeiss 40 \times 1.4 numerical aperture oil-immersion lens. On rare occasions, a brain was visibly damaged in the central region from the dissection or transfer process; these brains were excluded from analysis.

Antibodies. Primary antibodies were used at the following dilutions: chicken anti-GFP (1:1000; ThermoFisher Scientific, A10262; RRID: AB_2534023), mouse anti-A β 6E10 (1:500; BioLegend, 39320), rabbit anti-dAtg8 (Shelly et al., 2009; 1:1000; kind gift from Sara Cherry, University of Pennsylvania, Philadelphia, Pennsylvania), rabbit anti-Ref(2)P (Wyers et al., 1995; 1:1000; kind gift from Tor Erik Rusten, University of Oslo, Norway), guinea pig anti-Draper (Shklover et al., 2015; 1:1000; kind gift from Estee Kurant, Israel Institute of Technology), mouse anti-MMP1 (Developmental Studies Hybridoma Bank, 14A3D2; RRID: AB_579782, 3A6B4; RRID:AB_579780, 3B8D12; RRID:AB_579781, 5H7B11; RRID:AB_579779) at 1:50 used at 1:1:1:1 ratio. Secondary antibodies: AlexaFluor 488 anti-chicken or anti-mouse (1:400; Life Technologies, 703-545-155; RRID:AB_2340375), RhodoRed anti-mouse (1:400; Life Technologies, 715-295-150; RRID:AB_2340831), AlexaFluor 647 anti-guinea pig (1:400; Life Technologies, 706-605-148; RRID: AB_2340476). Amyloid fibrillary deposits were detected by Thioflavin T (ThT) staining using previously described methods (Marcora et al., 2014). Briefly, immunostained brains were incubated in 1:1 solution of water–ethanol containing 1% ThT (Sigma-Aldrich) for 20 min, washed in 1:1 solution of ethanol–1 \times PBS, and mounted for confocal imaging on a Zeiss LSM 700 microscope as described above.

Aggregate and fluorescence intensity quantification. To quantify A β aggregates, fluorescence intensity was measured in a region of interest in the cortex region adjacent to the antennal lobes on each side of the brain. Fluorescence of Atg8, p62 (Ref2), GFP (for TRE-GFP or 10XSTAT92E-dGFP reporters), or Mmp1 was quantified by measuring the fluorescence intensity of three different regions of interest at standardized positions in or around the antennal lobe. Specifically, twenty-four 1 μ m sections were included in each quantification analysis. All image analyses were performed using Volocity Analysis software (PerkinElmer; RRID:SCR_002668).

Lifespan and climbing assay. For lifespan analysis, flies were collected at a density of 20 flies per vial. At least three vials were used per treatment

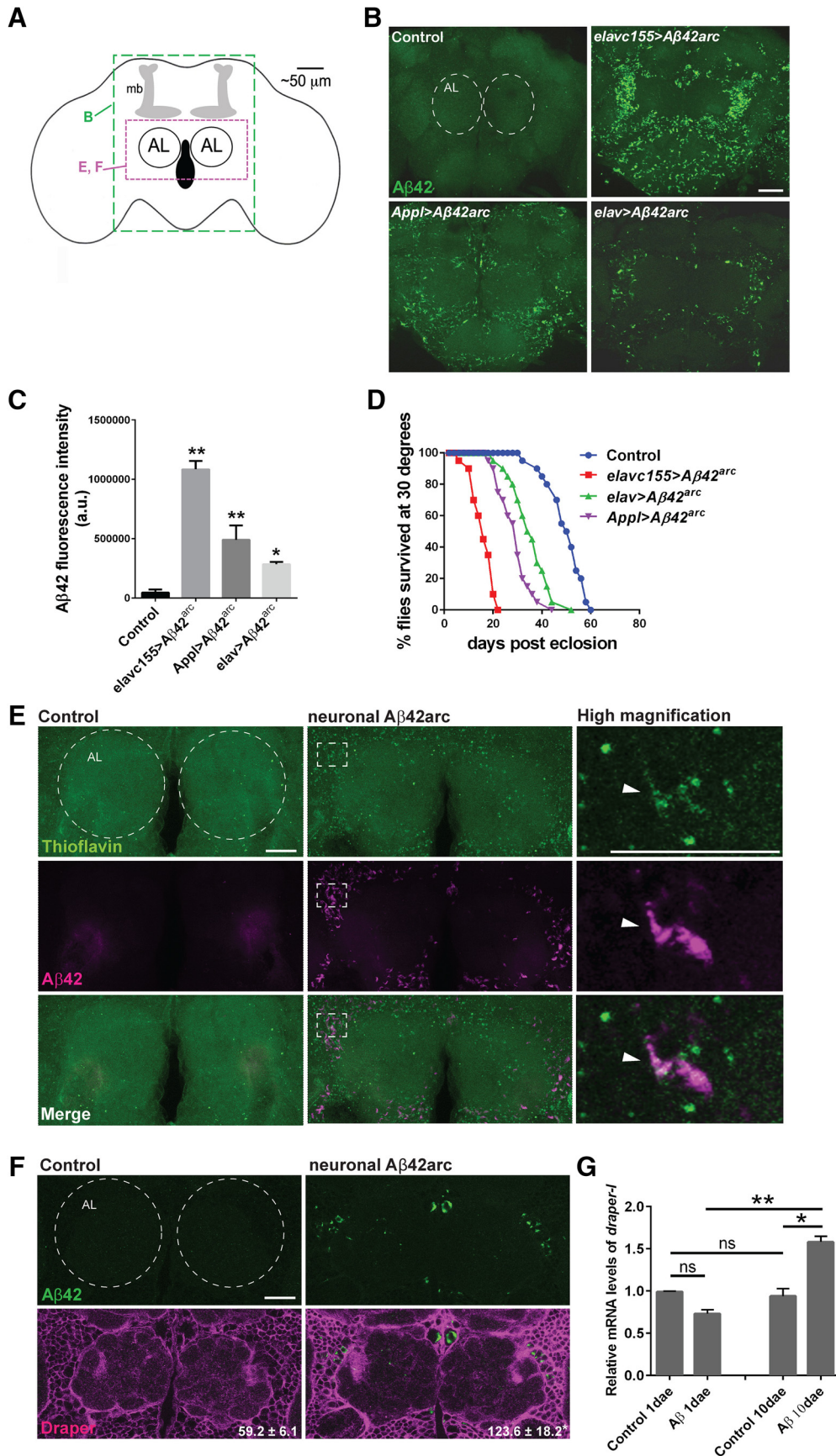


Figure 1. Glial Draper is upregulated in response to neuronal expression of human $A\beta_{42}^{arc}$. **A**, Schematic of the adult *Drosophila* brain showing relative location of the antennal lobes (AL) and mushroom bodies (mb). Green dotted box corresponds to brain region shown in **B**. Magenta dotted box shows brain region shown in **E** and **F**, and remaining confocal images throughout the paper. **B**, Representative confocal z-stack projections of adult brains expressing human $A\beta_{42}^{arc}$ under the control of various neuronal drivers. Genotypes: control (*Figure legend continues*.)

(total of 60 flies per genotype). Flies were passed to fresh vials every 3 d, and the number of dead flies was recorded. Locomotor function of flies was assessed using a negative geotaxis assay as reported by Bahadorani et al. (2008) with slight modifications. Briefly, 20 flies/trial were tapped to the bottom of an empty fly vial. After 7 s, the number of flies that climbed a minimum vertical distance of 8 cm was recorded. Each trial was repeated three times.

Quantitative RT-PCR. Total RNA was extracted from 15 to 20 fly heads using Trizol (Invitrogen) according to the manufacturer's instructions and quantified by Nanodrop Spectrophotometer. 100 ng of total RNA was then subjected to DNA digestion using DNase I (Ambion), immediately followed by reverse transcription using the Superscript II system (Invitrogen) with oligo(dT) primers. Quantitative PCR was performed on an ABI 7500 Fast Real-Time PCR machine using TaqMan master mix (Applied Biosystems) and the following TaqMan assays: Ribosomal Protein L32 (Applied Biosystems, standard Dm02151827_g1), Draper-I custom assay: F-primer, 50-TGTGATCATGGTTACGGAGGAC-30; R-primer, 50-CAGCCGGGTGGGCAA-30; probe, 50-CGCCTGCGATATAA-30.

Sectioning. Paraffin serial sections were prepared as described in Sunderhaus et al. (2016). Briefly, whole flies were fixed in Carnoy solution and washed in an ethanol series, followed by methylbenzoate. Sections were cut at 7 μ m thickness and imaged on a Zeiss LSM 700 laser scanning microscope. Neurodegenerative phenotypes were analyzed as described by Sunderhaus et al. (2016). The number of vacuoles in the central brain per section were quantified.

Experimental design and statistical analyses. Quantified data presented in all figures are shown as mean \pm SEM. Statistical details for each experiment are included in Figure legends, including number of flies used (*N*), statistical test (one-way ANOVA or unpaired, two-tailed Student's *t* test), and *post hoc* analysis (e.g., Tukey's test). For the lifespan assays, log rank (Mantel-Cox) test was used for analyses. *P* value for each test is indicated in the legends along with the value of the corresponding degrees of freedom (df), Student's *t* distribution, or ANOVA *F* distribution.

Data availability. Relevant transgenic strains and data relevant to this paper are available from the corresponding author.

Results

Neuronal expression of A β 42^{arc} triggers Draper upregulation in glia

To establish an *in vivo* model for exploring the role of Draper in A β -mediated pathogenesis, we first used three different pan-neuronal drivers (*elavc155-Gal4*, *elav-Gal4*, and *Appl-Gal4*) to express a highly pathogenic form of human A β 42 that carries the "Arctic" Swedish mutation Glu22Gly (A β 42^{arc}; Martin et al., 1995) fused to the N-terminal signal sequence of *Drosophila argos*

for secretion (Casas-Tinto et al., 2011). We compared A β peptide levels by immunostaining, as well as the lifespan of each genotype (Fig. 1*B–D*). Based on this analysis, we subsequently opted to use the *elav-Gal4* driver for the majority of our experiments as this driver induced moderate A β -related phenotypes that would allow us to discern enhancement and suppression following genetic manipulations. We also confirmed that a subset of *elav-Gal4*-driven A β 42^{arc} puncta colabeled with ThT, a marker of fibrillar amyloid plaques (Fig. 1*E*).

In adult flies, glia upregulate the engulfment receptor Draper at both the mRNA and protein level as they respond to degenerating axons following olfactory nerve axotomy (MacDonald et al., 2006; Doherty et al., 2009; Etchegaray et al., 2012; Logan et al., 2012). We wondered whether Draper might similarly be upregulated following exposure to human A β 42^{arc} peptides and performed Draper immunostaining on A β 42^{arc}-expressing flies (*elav-Gal4/+*; *UAS-A β 42^{arc}/+*) 10 d after eclosion (10 dae). We detected a significant increase in Draper in the central brain of 10-d-old adult A β 42^{arc} animals by immunostaining compared with age-matched controls (Fig. 1*F*), as well as increased *draper-I* transcript expression by quantitative PCR (Fig. 1*G*). Thus, within the first \sim 10 d of adulthood, neuronal expression of A β 42^{arc} in neurons triggers induction of Draper transcript and protein, suggesting that a Draper-dependent innate immune program is elicited in adult *Drosophila* glia in response to human A β 42^{arc}.

Loss of Draper enhances A β 42^{arc}-associated phenotypes

To determine whether Draper alters A β 42-related defects, we expressed A β 42^{arc} pan-neuronally in *draper-null* mutant flies and assessed several molecular and behavioral phenotypes. First, we detected a striking increase in A β 42 levels in the cortical region of the adult brain in *draper*-depleted flies (Fig. 2*A*). Notably, we detect more A β "puncta" in the antennal lobe neuropil in *draper* mutants compared with Draper-expressing flies (Fig. 2*A*, white arrowheads). Next, we assessed locomotor activity by performing negative geotaxis climbing assays. Although neuronal expression of A β 42^{arc} or loss of *draper* alone resulted in a partial climbing phenotype, this defect was notably exacerbated when A β 42^{arc} was expressed in *draper* mutant flies (Fig. 2*B*). Similarly, neuronal expression of A β 42^{arc} in a *draper* mutant background reduced adult lifespan, by \sim 50% compared with *draper* mutants or A β 42^{arc} expression alone (Fig. 2*C*).

Neuronal expression of A β 42 or A β 42^{arc} induces neurodegeneration in adult *Drosophila* (Iijima et al., 2004, 2008). Thus, we wondered if loss of Draper would exacerbate A β 42-related degeneration. Using vacuolar formation as a readout for neuronal integrity, we found that degeneration induced by neuronal expression of A β 42^{arc} was enhanced in *draper* mutant animals (Fig. 2*D,E*). Thus, these findings indicate that Draper reduces the overall A β 42^{arc} load in the adult brain and suggest that loss of Draper enhances A β 42-associated neurodegeneration, locomotor dysfunction, and shortened lifespan.

Glial expression of A β 42 phenocopies neuronal A β 42 expression in adult flies

APP is robustly expressed in neurons but also detected in mammalian oligodendrocytes, astrocytes, and microglia (Cahoy et al., 2008; Oberstein et al., 2015). Moreover, under certain conditions of CNS stress and injury, the mammalian *APP* gene is selectively targeted in glial cells through signaling of the cytokine transforming growth factor- β 1 and, subsequently, activation of the glial Smad transcription factors and the zinc finger nuclear factor CTCF (Amara et al., 1999; Burton et al., 2002; Lesné et al., 2003).

←

(Figure legend continued.) (*elav-Gal4/+*), *elavc155>A β 42arc* (*elavc155-Gal4/+*; *UAS-A β 42^{arc}/+*), *Appl>A β 42arc* (*Appl-Gal4/+*; *UAS-A β 42^{arc}/+*), *elav>A β 42arc* (*elav-Gal4/+*; *UAS-A β 42^{arc}/+*); 7-d-old flies immunostained with anti-A β . Scale bar, 20 μ m. Dotted circles outline the antennal lobes. **C**, Quantification of A β 42 fluorescence intensity in central brains of genotypes in **A**; mean \pm SEM. *N* \geq 19; $F_{(3,80)} = 40.99$; $*p < 0.05$ and $****p < 0.0001$; one-way ANOVA with Tukey's *post hoc* test. **D**, Lifespan analysis: *N* = 3 groups of 20 flies, *df* = 3, $p < 0.0001$ for each A β 42^{arc}-expressing strain compared with Control, log-rank (Mantel-Cox) test. **E**, Z-stack projections of the antennal lobe regions of control (*elav-Gal4/+*) or neuronal A β -expressing (*elav-Gal4/+*; *UAS-A β 42^{arc}/+*) flies immunostained for A β (magenta) and incubated with ThT (green). Dotted circles outline the antennal lobes. White dotted rectangle indicates region showing high-magnification images of a single confocal slice. Arrowhead points to representative example of A β and ThT puncta colocalization. **F**, Single confocal slice images of the antennal lobe regions of 10-d-old flies immunostained with anti-A β (green) and anti-Draper (magenta). Dotted circles outline the antennal lobes. Quantification of cortical Draper fluorescence intensity in control and A β -expressing brains written as mean \pm SEM, *N* \geq 16, $t = 2.809$, *df* = 38; $**p = 0.0078$; unpaired *t* test. **G**, Quantitative PCR analysis of *draper-I* transcript levels in control and neuronal A β -expressing flies 1 and 10 dae; mean \pm SEM plotted. *N* = 20; $**p < 0.01$, $***p < 0.001$, n.s., not significant; one-way ANOVA with Tukey's *post hoc* test. Scale bar, 20 μ m. Genotypes: (*elav-Gal4/+*) and (*elav-Gal4/+*; *UAS-A β 42^{arc}/+*).

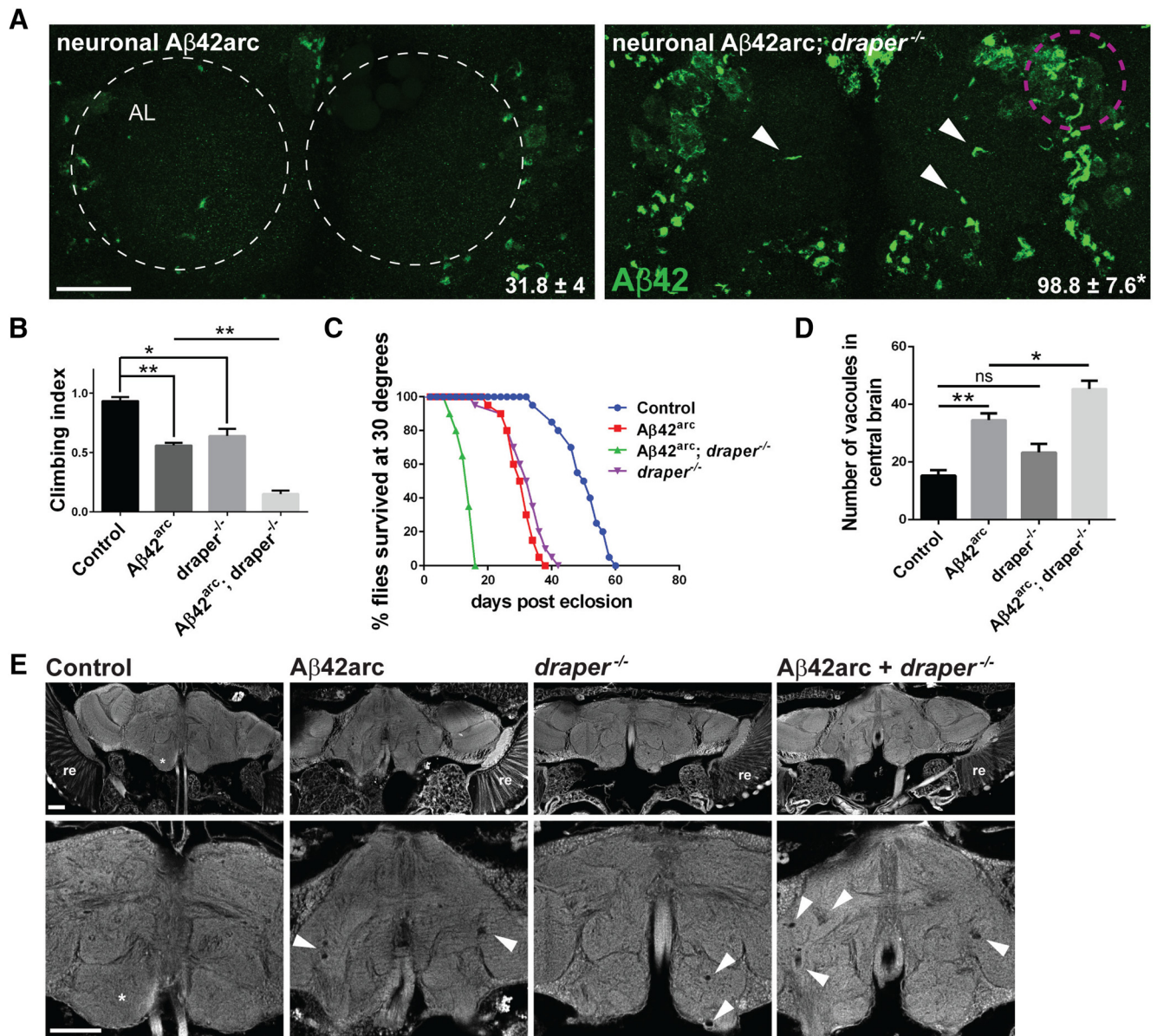


Figure 2. Loss of *draper* enhances Aβ42^{arc} levels, neurodegeneration, locomotor dysfunction, and reduced lifespan in human Aβ42^{arc}-expressing flies. **A**, Representative single confocal images of Aβ immunostaining (green) in the antennal lobe regions of the central brain (2 dae) following neuronal expression of Aβ42^{arc} in wild-type (*elav-Gal4/+; UAS-Aβ42^{arc}/+*) and *draper*-null (*elav-Gal4/+; UAS-Aβ42^{arc}, draper^{Δ5}/draper^{Δ5}*) background. White dotted circles outline the antennal lobes. Magenta circle shows representative region of interest used for quantifying Aβ levels. Arrowheads point to visible Aβ42 accumulation in the central region of the antennal neuropil of *draper* mutants. Single confocal slice located approximately mid-way through the anterior/posterior boundaries of the antennal lobes. Quantification of Aβ42 fluorescence intensity in the cortex region adjacent to neuropil regions written as mean ± SEM. *N* = 20, *t* = 7.823, *df* = 38; *****p* < 0.0001; unpaired *t* test. **B**, Quantification of locomotor climbing index of following genotypes: control (*elav-Gal4/+*), neuronal Aβ42^{arc} (*elav-Gal4/+; UAS-Aβ42^{arc}/+*), *draper*-null (*draper^{Δ5}/draper^{Δ5}*), and neuronal Aβ42^{arc}, *draper*-null flies (*elav-Gal4/+; UAS-Aβ42^{arc}, draper^{Δ5}/draper^{Δ5}*); mean ± SEM plotted. *N* = 3 groups of 20 7-d-old flies; *F*_(3,8) = 71.91; ***p* < 0.01, *****p* < 0.0001; one-way ANOVA with Tukey's *post hoc* test. **C**, Lifespan analysis of the genotypes shown in **B**. *N* = 3 groups of 20 flies, *df* = 3. Control versus neuronal Aβ42^{arc} flies: *p* < 0.0001. Control versus *draper*-null flies: *p* < 0.0001. Neuronal Aβ42^{arc} versus neuronal Aβ42^{arc}, *draper*-null flies: *p* < 0.0001; log rank (Mantel–Cox) test. **D**, Quantification of vacuoles in central brain region of 7-d-old flies. *N* ≤ 10 flies for each genotype; mean ± SEM plotted. *F*_(3,57) = 25.34; **p* < 0.05, *****p* < 0.0001; one-way ANOVA with Tukey's *post hoc* test. Genotypes same as in **B** and **C**. **E**, Representative images of 7 μm paraffin sections used for quantification in **D**. Arrowheads point to vacuoles indicating neurodegeneration. Asterisks indicate antennal lobe region. re, Retina. Scale bar, 20 μm.

It is unclear, however, how neuronal versus glial sources of Aβ peptides differentially contribute to AD pathology. Thus, we asked whether expression of Aβ42^{arc} in glia phenocopied the defects observed following neuronal expression of Aβ42^{arc}. Indeed, in flies expressing glial Aβ42^{arc}, we detected robust Aβ immunostaining (Fig. 3A–C), a subset of which colabeled with ThT (Fig. 3A). In addition, glial expression of Aβ42^{arc} inhibited locomotor activity, as assessed by a negative geotaxis climbing assay (Fig. 3D), and lifespan was reduced by ~50% compared

with control animals (Fig. 3E). Next, to knockdown glial Draper, we coexpressed *UAS-draper^{RNAi}* and *UAS-Aβ42^{arc}* with *repo-Gal4*. Notably, we detected a significant increase in Aβ42 throughout the central brain (Fig. 3B) and observed a modest further reduction in locomotor function (Fig. 3D) and lifespan (Fig. 3E). The fact that Aβ42 levels were increased when *UAS-draper^{RNAi}* was coexpressed with *UAS-Aβ42^{arc}* argues against Gal4 titration occurring due to the introduction of an additional UAS transgene; we also confirmed that Aβ42 levels were not significantly reduced

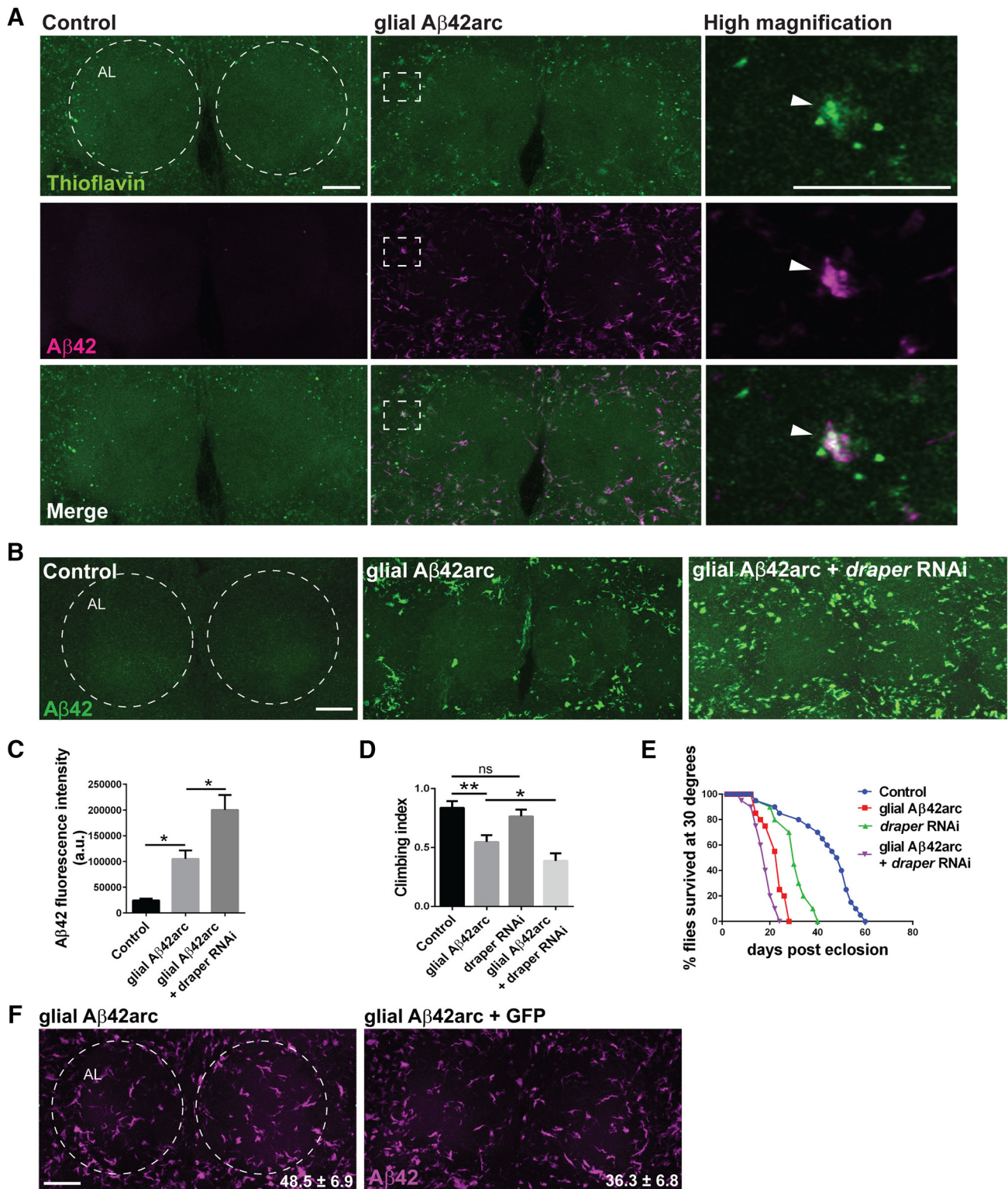


Figure 3. Glial expression of Aβ42^{arc} phenocopies neuronal Aβ42^{arc} expression. **A**, Z-stack projections of the antennal lobe regions of control (*repo-Gal4/+*) or glial Aβ-expressing (*UAS-Aβ42^{arc}/+; repo-Gal4/+*) flies immunostained for Aβ (magenta) and incubated with ThT (green). Dotted circles outline the antennal lobes (AL). White dotted rectangle indicates region shown in high-magnification images of single confocal slices. Arrowhead points to colocalization of glial Aβ and ThT. Scale bars, 20 μm. **B**, Images of anti-Aβ staining in driver Control (*repo-Gal4/+*), glial Aβ42^{arc} (*UAS-Aβ42^{arc}/+; repo-Gal4/+*), and glial Aβ42^{arc} + *draper* RNAi flies (*UAS-Aβ42^{arc}/draper^{RNAi}; repo-Gal4/+*); 7-d-old flies. Circles outline the AL. **C**, Quantification of Aβ42 fluorescence intensity in experiments depicted in **B**; mean ± SEM plotted. *N* ≥ 18; *F*_(2,57) = 21.92; ***p* < 0.01; one-way ANOVA with Tukey's *post hoc* test; a.u., arbitrary units. **D**, Locomotor assay, 15-d-old flies, mean ± SEM plotted. *N* = 3 groups of 20 flies, *F*_(3,8) = 37.14, **p* < 0.05, ***p* < 0.01, n.s., nonsignificant; one-way ANOVA with Tukey's *post hoc* test. **E**, Lifespan analysis: *N* = 3 groups of 20 flies; *df* = 3; Control versus glial Aβ flies: *p* < 0.0001; Control versus glial Aβ + *draper^{RNAi}* flies: *p* < 0.0001; Control versus *draper^{RNAi}* flies: *p* < 0.0001; glial Aβ versus glial Aβ + *draper^{RNAi}* flies: *p* < 0.0001; log rank (Mantel–Cox) test. Scale bar, 20 μm. Genotypes same as in **D**. **F**, Representative confocal z-stack projections of brains expressing glial Aβ42^{arc} alone (*UAS-Aβ42^{arc}/+; repo-Gal4*) or coexpressing glial Aβ42^{arc} and cytosolic GFP (*UAS-Aβ42^{arc}/+; repo-Gal4/UAS-GFP*); 8-d-old flies immunostained for Aβ42. Dotted circle outlines AL. Quantification of Aβ42 fluorescence intensity written as mean ± SEM. *N* ≥ 16, *t* = 1.258, *df* = 31; unpaired *t* test; *p* = 0.2177. Scale bar, 20 μm.

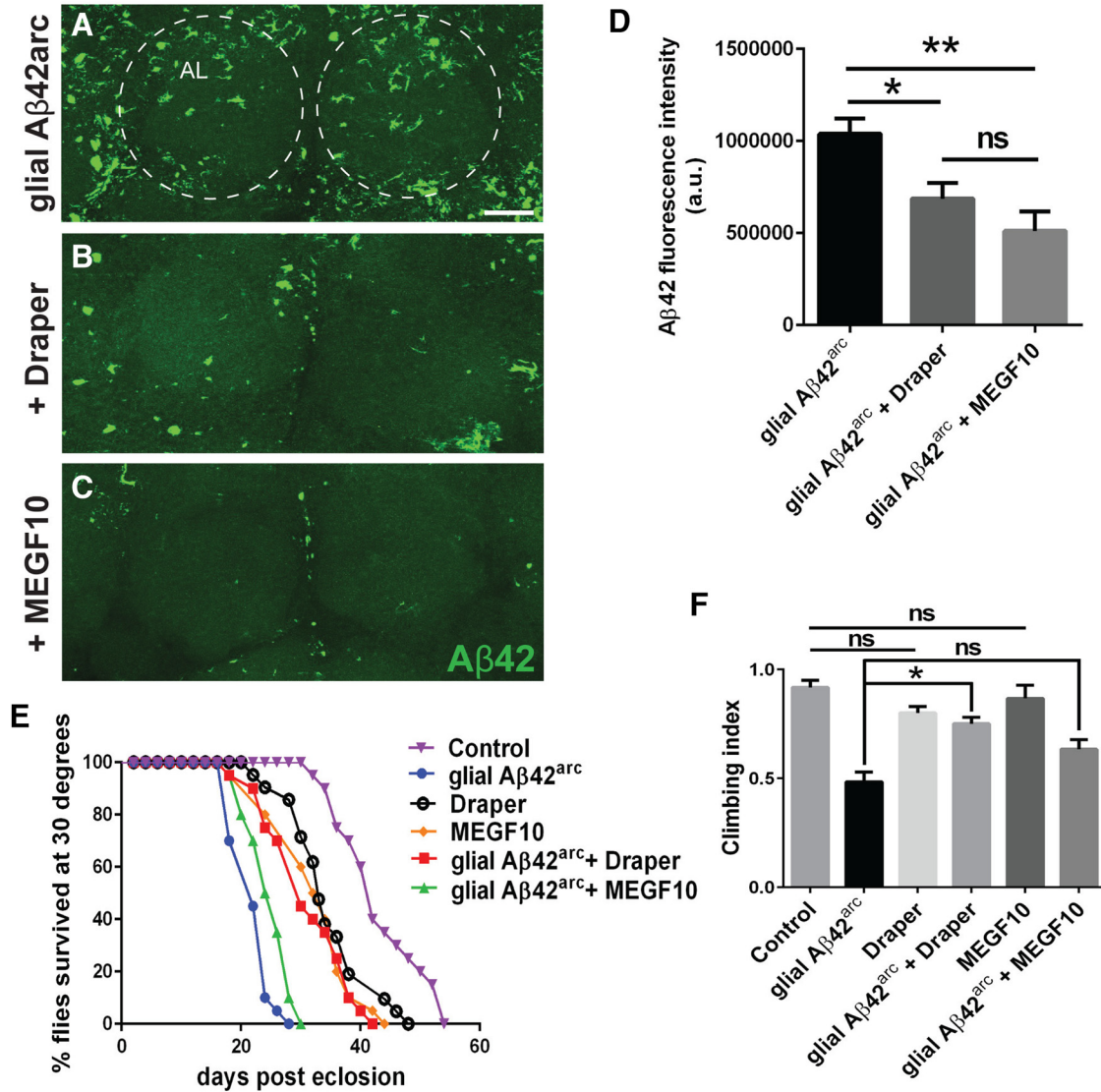


Figure 4. Overexpression of Draper/MEGF10 reverses Aβ accumulation, locomotor defects, and reduced lifespan in Aβ42^{arc}-expressing flies: *A–C*, Z-stack images of anti-Aβ stained brains expressing glial Aβ42^{arc} (*UAS-Aβ42^{arc}/+; repo-Gal4/+*), coexpressing glial Aβ42^{arc} and Draper (*UAS-Aβ42^{arc}/UAS-Draper-1; repo-Gal4/+*), or glial Aβ42^{arc} and mouse MEGF10 (*UAS-Aβ42^{arc}/+; repo-Gal4/UAS-MEGF10*); 7-d-old flies. Dotted circles outline antennal lobes. *D*, Quantification of Aβ42 fluorescence intensity for experiments shown in *A–C*; mean ± SEM plotted. *N* ≥ 16; *F*_(2,49) = 7.907; **p* < 0.05, ****p* < 0.001; one-way ANOVA with Tukey's *post hoc* test; n.s., not significant; a.u., arbitrary units. *E*, Lifespan analysis: *N* = 3 groups of 20 flies; *df* = 5; glial Aβ versus glial Aβ + Draper flies: *p* < 0.0001; glial Aβ versus glial Aβ + MEGF10 flies: *p* < 0.05; Control versus Draper: *p* < 0.001; Control versus MEGF10: *p* < 0.0001; log rank (Mantel–Cox) test. Genotypes: Control (*repo-Gal4/+*), glial Aβ42^{arc} (*UAS-Aβ42^{arc}/+; repo-Gal4/+*), Draper (*UAS-Draper-1/+*), MEGF10 (*UAS-MEGF10/+*), glial Aβ42^{arc} + Draper (*UAS-Aβ42^{arc}/UAS-Draper-1; repo-Gal4/+*), and glial Aβ42^{arc} + MEGF10 (*UAS-Aβ42^{arc}/+; repo-Gal4/UAS-MEGF10*). *F*, Negative geotaxis climbing assay results (20-d-old flies); mean ± SEM plotted. *N* = 3 groups of 20 flies; *F*_(5,12) = 14.97; ***p* < 0.01; n.s., not significant; one-way ANOVA with Tukey's *post hoc* test. Genotypes same as in *E*. Scale bar, 20 μm.

when cytosolic GFP (*UAS-GFP*) was coexpressed under the control of *repo-Gal4* (Fig. 3*F*). Together, these findings suggest that despite the cellular source of Aβ (neuronal versus glial), resultant molecular and behavioral defects are similar in adult flies, and also further bolster glial Draper as a protective molecule that minimizes Aβ42-related phenotypes.

Overexpression of glial Draper reverses Aβ-related phenotypes

Next, to determine whether boosting Draper levels could conversely rescue defects associated with human Aβ42 overexpression, we coexpressed *UAS-Draper-1* and *UAS-Aβ42^{arc}* with *repo-Gal4*. Overexpression of Draper resulted in a significant reduction of Aβ immunofluorescence throughout the central brain cortex (Fig. 4*A,B,D*), extended adult lifespan (Fig. 4*E*), and significantly en-

hanced the climbing of Aβ42^{arc}-expressing flies in negative geotaxis assays (Fig. 4*F*). Next, we asked whether glial expression of MEGF10, the mammalian homolog of Draper, could similarly reverse any defects in AD model flies. MEGF10 is required for glial engulfment of neuronal projections and apoptotic neurons in the developing mammalian nervous system (Wu et al., 2009; Chung et al., 2013; Iram et al., 2016). MEGF10 also shares basic structural features with Draper, including EGF-like motifs in the extracellular domain and intracellular immunoreceptor tyrosine-based activation motifs, which couple to conserved Syk tyrosine kinases that are required for phagocytic function (Logan et al., 2012; Scheib et al., 2012). Finally, in *ced-1* mutant worms, defective clearance of apoptotic cells is partially rescued by overexpression of human MEGF10 (Hamon et al., 2006), further highlighting the functional conservation of this family of recep-

tors across species. We used *repo-Gal4* to coexpress mouse MEGF10 and A β 42^{arc} and, as with Draper overexpression, we saw a significant reduction in A β immunostaining (Fig. 4A, C, D). Notably, we observed a very modest shift in the survival curve of MEGF10-expressing flies (Fig. 4E), and detected a trend in climbing index reversal, but this did not reach significance (Fig. 4F). It remains to be determined whether the weaker behavioral rescue observed with MEGF10 overexpression is due to differences in the extracellular region or an altered capacity for MEGF10 to couple to intracellular signaling pathways within *Drosophila* cells. Nonetheless, these results suggest that upregulating glial Draper/MEGF10 offers protection against A β -related molecular and behavioral phenotypes and also argues against the notion that enhancement of A β -related defects observed in *draper* mutants (Figs. 2, 3) are exclusively due to additive parallel effects.

JNK, Stat92e, and Mmp1 are activated upon A β 42 exposure and influence A β 42 levels in the brain

Following acute nerve injury in adult flies, two highly conserved transcription factors are activated downstream of Draper within responding glia: (1) Stat92E and (2) the heterodimer AP-1, which consists of Jra (homolog of c-Jun) and kayak (homolog of c-fos). These factors, in turn, target the *draper* locus to upregulate Draper levels as the glial cells become highly migratory and phagocytic to clear degenerating axons. Because we found that Draper was upregulated at the protein and transcript levels in A β 42^{arc}-expressing flies (Fig. 1F, G), we wondered whether these two transcriptional cascades are similarly activated in glia upon A β exposure. Both Stat92E and AP-1 activity can be readily monitored with well characterized *in vivo* reporter transgenes (MacDonald et al., 2013). First, we assessed activation of Stat92E by expressing human A β 42^{arc} with the neuronal *elav-Gal4* driver in flies that carried the *10XStat92E-GFP* reporter, which contains 10 Stat92E binding sites driving expression of destabilized GFP (dGFP). In A β -expressing flies, we observed a significant increase in dGFP levels (Fig. 5A, B) in a glial pattern in and around the antennal lobes (Doherty et al., 2009). We observed a similar significant increase in dGFP levels following glial-driven expression of A β (16.74 \pm 3.3 in control animals vs 29.8 \pm 5.1 following glial expression of A β 42^{arc}; $p < 0.05$). Next, we assessed activation of the *TRE-GFP* reporter, which contains multiple AP-1 binding sites controlling expression of GFP. In control flies, some basal *TRE-GFP* activation is apparent in the antennal lobes, but the GFP signal within and around the antennal lobes is significantly enhanced in A β -expressing flies (Fig. 5C, D). We also observed enhanced AP-1 activity following expression of human A β 42^{arc} in glia (41.1 \pm 6.7 in controls vs 77.6 \pm 14.3 following glial expression of A β 42^{arc}; $p < 0.05$). To determine whether Stat92E and AP-1, like Draper, influence A β levels in the *Drosophila* brain, we performed RNAi-mediated knockdown of *Stat92E*, *Jra*, and *Kayak* specifically in glia while coexpressing human A β 42^{arc}. Interestingly, glial depletion of *Stat92E*, *Jra*, or *Kayak* resulted in higher levels of A β in central brain (Fig. 5G, H). Finally, activation of the glial Draper receptor following acute axon injury also triggers transcriptional upregulation of the secreted matrix metalloproteinase Mmp1 (Purice et al., 2017). Notably, proper Mmp1 induction postinjury requires JNK/AP-1 and Stat92e signaling in responding glial cells (Purice et al., 2017). We discovered that neuronal expression of A β 42^{arc} also promotes a striking increase in Mmp1 levels by immunostaining in the central brain, and this upregulation is blocked in *draper* mutant flies (Fig. 5E, F). Collectively, these results suggest that glial Stat92E/AP-1 sig-

naling cascades are engaged when exposed to A β 42 peptides, perhaps in part driving the expression and release of Mmp1. Moreover, these transcriptional pathways influence A β levels in the CNS.

A β 42 induces Draper-dependent activation of Atg8 and p62

Increased activation of protein destruction pathways [ubiquitin-proteasome system (UPS), autophagy, etc.] has been reported in AD animal models and human AD postmortem tissue (Hong et al., 2014; Chen et al., 2015). Interestingly, autophagy signaling is upregulated in the developing *Drosophila* salivary gland in a Draper-dependent manner (McPhee and Baehrecke, 2010; Lin et al., 2017), although a connection between glial Draper/MEGF10 and autophagy has never been explored in the adult brain. We assessed expression of two markers that are associated with increased protein degradation (including autophagy), Atg8, and p62, in the central brain following neuronal expression of A β 42^{arc}. We observed little Atg8 or p62 staining in the central brain region of control animals, but detected a significant increase of both markers following neuronal expression of A β 42^{arc} (Fig. 6A–D). High-magnification images reveal that many Atg8/p62 puncta were either colocalized or juxtaposed to A β staining (Fig. 6A, C). Intriguingly, Atg8 and p62 upregulation was significantly reduced in *draper* mutants expressing neuronal A β 42^{arc} (Fig. 6A–D), suggesting that neuronal A β 42 alters the activity of protein degradation pathways in the adult brain, with a significant portion being Draper-dependent. Given our current analysis, it is not clear which puncta reside inside neurons versus glia. However, we favor the model that A β 42 peptides released from neurons are engulfed by glia in a Draper-dependent manner and shuttled through protein destruction pathways (UPS, autophagy, etc.) that include Atg8- and/or p62-positive compartments to promote destruction of these notoriously toxic protein fragments.

Discussion

Defective glial function is strongly implicated in the progression of AD (Akiyama et al., 2000), although the precise mechanisms that underlie glial contributions to disease pathogenesis are still unclear. Microglia and astrocytes can engulf amyloid peptides, likely through an array of cell surface receptors that act in concert to recognize and internalize A β in its various forms (Gold and El Khoury, 2015; Eugenin et al., 2016; Ries and Sastre, 2016), and, notably, many studies have identified AD susceptibility loci that encode factors required for proper glial phagocytic function (Hollingworth et al., 2011; Golde et al., 2013; Hickman and El Khoury, 2014). Here, we show that the conserved glial engulfment receptor Draper/MEGF10 provides protection in an *in vivo* *Drosophila* model of AD. Expression of pathogenic human A β 42^{arc} induces activation of a Draper/AP-1/STAT92E pathway in glia, which is known to trigger expression of the secreted metalloproteinase Mmp1 and promote glial phagocytic activity in response to acute neural injury (MacDonald et al., 2013; Doherty et al., 2014). We also show that loss of Draper exacerbates A β 42-induced phenotypes, including locomotor dysfunction and reduced longevity, while overexpression of glial Draper, or the homologous mammalian receptor MEGF10, partially rescues most of these phenotypes. Finally, our work also indicates that A β 42 expression triggers protein destruction pathways, largely in a Draper-dependent manner. Together, our findings suggest a mechanism whereby glia rely on the Draper receptor to activate a canonical Draper/JNK/STAT92E signaling cascade, internalize amyloid peptides, and perhaps shuttle them through Atg8/p62 protein degradation pathways, which attenuates A β 42-induced CNS dysfunction.

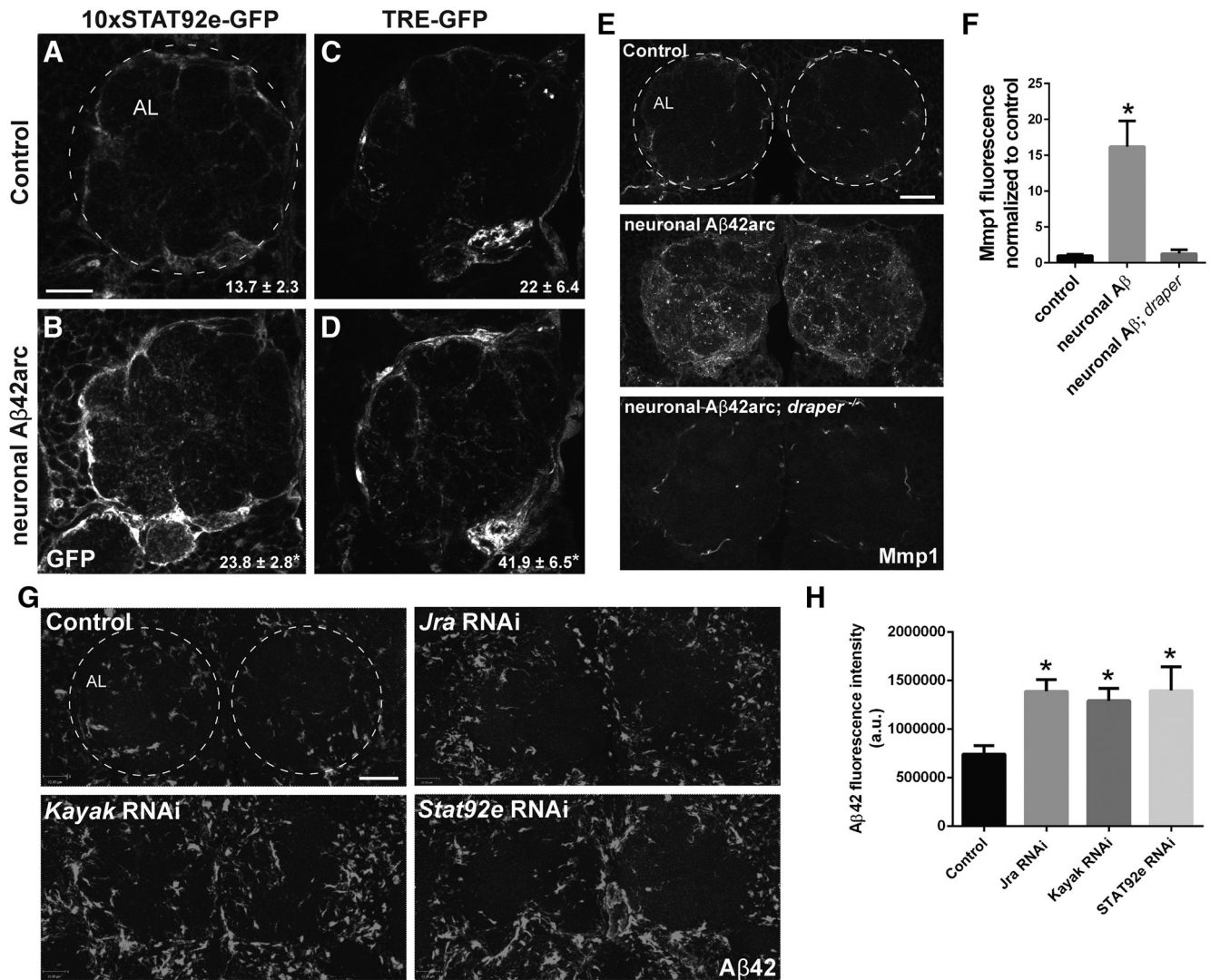


Figure 5. Expression of human Aβ42^{arc} promotes STAT92E and AP-1 signaling and upregulates Mmp1. **A–D**, Representative images (merged projection of 2 confocal sections) of single antennal lobes (7-d-old flies) showing GFP expressed in flies (expressing driver control or neuronal Aβ42^{arc}) that carry the STAT92E transcriptional reporter *10xSTAT92E-GFP* (**A**, **B**) or the JNK/AP-1 reporter *TRE-GFP* (**C**, **D**). Scale bar, 20 μm. Quantification of GFP written as mean ± SEM. Statistical data for **A** and **B**: $N \geq 16$; $t = 2.739$; $df = 40$; $*p < 0.05$; unpaired *t* test. Statistical data for **C** and **D**: $N \geq 16$; $t = 2.174$; $df = 30$; $*p < 0.05$; unpaired *t* test. Genotypes: **A** and **B**: Control (*elav-Gal4/+; 10xStat92E-dGFP/+*), neuronal Aβ42^{arc} (*elav-Gal4/+; UAS-Aβ42^{arc}/10xStat92E-dGFP*); **C**, **D**: Control (*elav-Gal4/+; TRE-GFP/+*), neuronal Aβ42^{arc} (*elav-Gal4/+; UAS-Aβ42^{arc}/TRE-GFP*). **E**, Representative single confocal images of Mmp1 immunostaining in the antennal lobe regions of 7-d-old control flies and flies expressing neuronal Aβ42^{arc} in wild-type or *draper-null* background. Genotypes: Control (*elav-Gal4/+*), neuronal Aβ42^{arc} (*elav-Gal4/+; UAS-Aβ42^{arc}/+*), neuronal Aβ42^{arc}, *draper-null* flies (*elav-Gal4/+; UAS-Aβ42^{arc}/draper^{Δ5}/draper^{Δ5}*). **F**, Quantification of Mmp1 fluorescence intensity in **E**; mean ± SEM, plotted. $N \geq 15$; $F_{(2,15)} = 13.27$; $**p < 0.01$; one-way ANOVA with Tukey's *post hoc* test. **G**, Representative confocal images of antennal lobe regions in brains immunostained for Aβ42. Flies (7-d-old) coexpressed Aβ42^{arc} and the noted RNAi constructs in glial cells. Control (*UAS-Aβ42^{arc}/+; repo-Gal4/+*), Jra RNAi (*UAS-Aβ42^{arc}/Jra^{RNAi}; repo-Gal4/+*), Kayak RNAi (*UAS-Aβ42^{arc}/Kayak^{RNAi}; repo-Gal4/+*), and Stat92E RNAi (*UAS-Aβ42^{arc}/Stat92E^{RNAi}; repo-Gal4/+*). **H**, Quantification of Aβ42 fluorescence intensity in experiment shown in **G**; mean ± SEM plotted. $N \geq 18$; $F_{(3,76)} = 4.097$; $*p < 0.05$; one-way ANOVA with Tukey's *post hoc* test; a.u., arbitrary units. Scale bar, 20 μm. Dotted circles in **A**, **E**, and **G** outline antennal lobes (AL).

Glia can detect fibrillar forms of Aβ through various cell-surface pattern recognition receptors, such as SCARA1 (scavenger receptor-A1), CD36, and Toll-like receptors (Malm et al., 2015). Soluble Aβ can also be internalized by microglia through fluid phase pinocytosis (Mandrekar et al., 2009; Li et al., 2013). In *Caenorhabditis elegans* the homolog of the Draper receptor, CED-1, recognizes necrotic cells by cell surface exposure of phosphatidylserine (Li and Zhou, 2016). Similarly, during *Drosophila* embryogenesis, two candidate ligands (Pretaporter and DmCaBP1) are presented by apoptotic cells and are likely bound by glial Draper to promote engulfment of dying neurons (Kuraishi et al., 2009; Okada et al., 2012). Thus, although Draper seems to be a requisite factor for glial recruitment to damaged neurons in the adult fly brain, it can serve as a true engulfment recognition receptor. Forced expres-

sion of the MEGF10 receptor in HeLa cells enhances phagocytosis of FITC-conjugated Aβ42 (Singh et al., 2010), raising the intriguing possibility that this family of receptors may contribute to recognition of extracellular Aβ. The extracellular domain (ECD) of Draper closely resembles the ECDs of the related mammalian receptors MEGF10, MEGF11, and Jedi; all contain multiple (>10) epidermal growth factor-like (EGF-like) domains (Wu et al., 2009). Notably, low density lipoprotein receptor-related receptor 1 (LRP1), a large endocytic receptor expressed by various cell types including glial cells, neurons, and vascular cells, binds directly to Aβ to promote uptake (Kanekiyo and Bu, 2014). Like Draper and its mammalian homologs, LRP1 possesses multiple EGF-like repeats in the ECD. It remains to be determined whether Draper and the related receptors can also directly bind Aβ, or cooperatively through coreceptors or

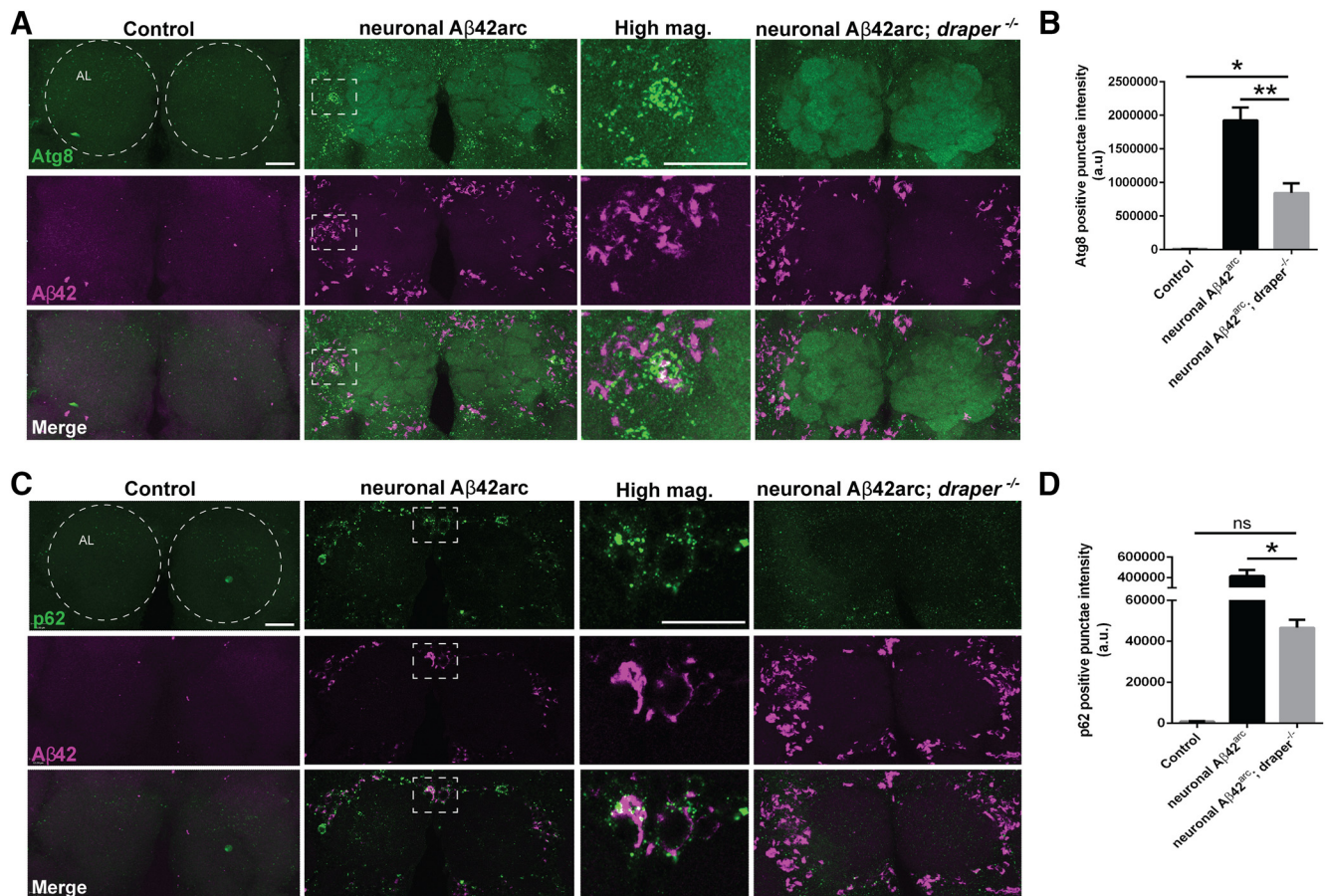


Figure 6. Human Aβ42 expression induces Draper-dependent activation of Atg8 and p62 in the adult fly brain. **A**, Representative confocal images of brains immunostained for Atg8 (green) and Aβ42 (magenta). Area of high-magnification image is indicated with dotted white box. Circles outline antennal lobes (AL). Control (*elav-Gal4/+*), neuronal Aβ42arc (*elav-Gal4/UAS-Aβ42^{arc}*), and neuronal Aβ42arc; draper (*elav-Gal4/+; UAS-Aβ42^{arc}; draper^{Δ5}/draper^{Δ5}*). **B**, Quantification of Atg8 fluorescence in **A**. Total Atg8 fluorescence intensity in the cortical regions adjacent to the antennal lobe neuropil was measured; mean ± SEM, plotted. $N \geq 15$; $F_{(2,45)} = 44.97$; $***p < 0.001$, $****p < 0.0001$; one-way ANOVA with Tukey's *post hoc* test; a.u., arbitrary units. **C**, Representative images of brains immunostained for p62 (green) and Aβ42 (magenta). Regions corresponding to high-magnification images are indicated with dotted white box. Control (*elav-Gal4/+*), neuronal Aβ42arc (*elav-Gal4/UAS-Aβ42^{arc}*), and neuronal Aβ42arc; draper (*elav-Gal4/+; UAS-Aβ42^{arc}; draper^{Δ5}/draper^{Δ5}*). **D**, Quantification of p62 fluorescence shown in **C**. Total p62 fluorescence was quantified from the cortical regions adjacent to the antennal lobes; mean ± SEM, plotted. $N \geq 13$; $F_{(2,39)} = 44.70$; $****p < 0.0001$; n.s., not significant; one-way ANOVA with Tukey's *post hoc* test; a.u., arbitrary units. Scale bars, 20 μm. Atg8- and p62-positive structures range from 0.1 to 1.5 μm. Average neuronal cell body size in the central brain is 3.1 ± 0.4 μm. All confocal images are 24 μm projections.

additional ligands, to facilitate glial engulfment of neurotoxic aggregates or soluble peptides.

A recent study revealed that in the developing mouse brain, the MEGF10 receptor recognizes apoptotic neurons that have become decorated with the secreted complement factor C1q, allowing astrocytes to phagocytically clear them from the CNS (Iram et al., 2016). Aβ can similarly be opsonized by secreted complement factors (Wyss-Coray and Rogers, 2012), and indeed the complement pathway is gaining recognition as a key player in AD pathogenesis (Wyss-Coray and Rogers, 2012; Hong et al., 2016). Together, these observations raise the intriguing possibility that complement may also direct glial recognition of amyloid via the MEGF10/Jedi family of engulfment receptors. Finally, Pearce et al. (2015) have recently shown that *Drosophila* glia internalize mutant human Huntingtin aggregates in a Draper-dependent manner in the adult brain, which implicates Draper as potential broad player in the transfer of the pathogenic protein aggregates in various neurodegenerative disorders.

In addition to their shared capacity to internalize amyloid peptides, mammalian microglia and astrocytes both release cytokines in response to Aβ, which is likely a robust trigger for microglial recruitment to Aβ deposit sites (Malm et al., 2015;

Guillot-Sestier and Town, 2013). In the adult *Drosophila* CNS, Draper, the downstream transcription factors AP-1 and STAT92E, and their transcriptional target *Mmp1* are all upregulated in response to acute nerve injury and are also all required for ensheathing glia to properly infiltrate neuropil regions and, subsequently, clear degenerating axonal debris (Logan et al., 2012; MacDonald et al., 2013; Doherty et al., 2014; Purice et al., 2017). Here, we show that Draper expression, AP-1/Stat92e activity, and *Mmp1* are also enhanced in Aβ42^{arc}-expressing flies. Mmps are indeed well known for accommodating cell migration in various cell types and contexts and, notably, have been coupled to AD symptomology in other models. Mmp expression is induced upon exposure to soluble and fibrillar Aβ in microglia and astrocytes (Deb et al., 2003; Yan et al., 2006; Ito et al., 2007), and Mmp overexpression in AD model mice attenuates Aβ oligomer formation and rescues cognitive defects (Fragkouli et al., 2014; Kaminari et al., 2017). It is still unclear to what extent migratory responses are elicited in *Drosophila* glia in response to Aβ and how *Mmp1* specifically contributes to Aβ processing and glial morphogenic responses in the adult fly brain. Future experiments that couple *in vivo* live imaging and single glial cell labeled clones will hopefully reveal how the Draper/*Mmp1* pathway governs glial recruitment

to sites of A β expression and glial recognition/internalization/degradation of A β peptides.

Enhanced autophagy is one viable mechanism by which both neurons and glia manage excessive amyloid peptides and other noxious proteins (Ling et al., 2009; Piras et al., 2016). Moreover, dysfunctional autophagy has indeed been implicated as a contributing factor to AD (Boland et al., 2008). Here, we show that human A β 42 peptides enhance expression of Atg8 and p62 in the adult *Drosophila* brain in a Draper-dependent manner, although the mechanistic significance of this finding is still unclear. Together, Atg8 and p62 promote ubiquitination of damaged cargo fated for destruction through autophagy (and other) cascades (Wurzer et al., 2015). Increased expression of Atg8 and p62 in AD model flies may indicate an accumulation of autophagosomes resulting from enhanced activation of glial autophagy. However, it is important to note that a build up of autophagosomes could instead reflect suppression of a downstream step in the pathway (e.g., phagosome maturation, lysosomal fusion or degradation; Mizushima et al., 2010). Finally, although Atg8 and p62 are often described as autophagy markers, these molecules can also be coupled to other degradation/destruction pathways (Galluzzi et al., 2017). More focused experiments, including genetic perturbation of autophagy regulators, will be essential to define precisely how autophagic flux and other protein degradation pathways are altered in glia in response to A β 42 overexpression and how Draper informs these events.

AD is marked by age-dependent progressive accumulation of extracellular aggregates in the brain and, notably, aged glia display reduced phagocytic function (Floden and Combs, 2011; Malm et al., 2015). Subtle deterioration of glial autophagy-lysosomal destruction pathways occurs normally with age and may enhance the aged brain's susceptibility to AD and related neurodegenerative disorders (Gorojod et al., 2015; Nikolettou et al., 2015). Our laboratory has recently shown that glial Draper levels decrease with age in adult *Drosophila* and that aged ensheathing glia are slow to phagocytically clear degenerating axons *in vivo* (Purice et al., 2016). Based on the high functional conservation between Draper and the MEGF10 family of receptors in glial engulfment responses (MacDonald et al., 2006; Wu et al., 2009; Chung et al., 2013) and their coupling to downstream signaling pathways (Osada et al., 2009; Wu et al., 2009; Linnartz et al., 2010), we anticipate that our work will provide new molecular insight into glial contributions to AD progression and potentially provide a new cohort of molecular targets for therapeutic intervention.

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