Non-visual light modulates behavioral memory and gene expression in *C. elegans*

Zhijian Ji[1, §], Bingying Wang[1, §], Rashmi Chandra[1, §], Junqiang Liu[1, §], Supeng Yang[1, 2],

Yong Long[3], Michael Egan[1, 2], Noelle L'Etoile[4], Dengke K. Ma[1, 5, 6, *]

[1]Cardiovascular Research Institute, University of California San Francisco, San

Francisco, CA 94158, USA.

[2]Department of Molecular Cell Biology, University of California, Berkeley, Berkeley, CA

94720, USA.

[3]Key Laboratory of Breeding Biotechnology and Sustainable Aquaculture, Institute of

Hydrobiology, Chinese Academy of Sciences, Wuhan 430072, China.

[4]Department of Cell and Tissue Biology, University of California San Francisco, San

Francisco, CA 94158, USA.

[5]Department of Physiology, University of California San Francisco, San Francisco, CA

94158, USA.

[6]Innovative Genomics Institute, University of California, Berkeley, Berkeley, CA 94720,

USA.

[§] Equal contribution

*Correspondence: Dengke.Ma@ucsf.edu

Abstract

Visible light influences a range of physiological processes, yet how animals respond to it independently of the visual system remains largely unknown. Here, we uncover a previously undescribed light-induced transcriptional pathway that modulates behavioral plasticity in *C. elegans*, a roundworm without eyes. We demonstrate that ambient visible light or controlled-intensity visible-spectrum LED activates an effector gene *cyp-14A5* in non-neuronal tissues through the bZIP transcription factors ZIP-2 and CEBP-2. Light induction of *cyp-14A5* is more prominent at shorter wavelengths but is independent of the known blue light receptors LITE-1 and GUR-3 in *C. elegans*. This bZIP-dependent genetic pathway in non-neuronal tissues enhances behavioral adaptability and olfactory memory, suggesting a body-brain communication axis. Furthermore, we use the light-responsive *cyp-14A5* promoter to drive ectopic gene expression, causing synthetic light-induced sleep and rapid aging phenotypes in *C. elegans*. These findings advance our understanding of light-responsive mechanisms outside the visual system and offer a new genetic tool for visible light-inducible gene expression in non-neuronal tissues.

Introduction

Visible light is crucial for image formation and regulating various physiological processes through the visual system, yet how animals respond to ambient light independently of sight remains poorly understood. Recent studies have uncovered diverse non-visual photoreception mechanisms that modulate a range of biological processes, from circadian rhythms to stress responses and metabolic homeostasis(Andrabi et al., 2023; Cronin and Johnsen, 2016; Do and Yau, 2010; Van Gelder, 2008). These mechanisms often involve specialized light-sensitive proteins, such as opsins and cryptochromes, widely expressed in body locations, including the skin, brain, and peripheral organs. For example, mammalian melanopsin-expressing retinal ganglion cells play critical roles in systemic light responses largely independent of image formation(Berson et al., 2002; Hattar et al., 2003; Lucas et al., 2003; Shi et al., 2024). In the nematode roundworm *C. elegans*, blue light photoreception requires the light-activated ion channels LITE-1 and GUR-3 in specific neurons, influencing aversive behaviors and cellular physiology(Bhatla and Horvitz, 2015a, 2015b; Edwards et al., 2008; Gong et al., 2016; Hanson et al., 2023). Visible light irradiation can also generate photo-oxidative reactive oxygen species in animals(De Magalhaes Filho et al., 2018; Liebel et al., 2012; Mahmoud et al., 2010). Despite these advances, the molecular pathways and physiological outcomes of non-visual light sensing and responses remain understudied, raising intriguing questions about the mechanistic basis and functional implications of light as an environmental cue beyond vision.

We previously studied how genes encoding cytochrome P450 (CYP) proteins respond to and mediate effects of exposure to environmental stresses in *C. elegans*(Keller et al.,

2014; Ma et al., 2013). Among various transcriptional reporters we generated for CYP-

encoding genes to monitor environmental regulation, we serendipitously discovered that

the *cyp-14A5* promoter-driven GFP expression is particularly sensitive to ambient visible

light exposure. Building upon this initial finding, we conduct transcriptome profiling to

identify light-inducible genes in addition to *cyp-14A5*, determine key transcriptional

regulators of *cyp-14A5*, and show that the light-inducible CYP-14A5 promotes

behavioral plasticity and olfactory memory in *C. elegans*. The findings also provide a

genetic tool to use light-inducible *cyp-14A5* promoter to flexibly and ectopically drive

gene expression.

Results

Light activates expression of *cyp-14A5* and other genes in *C. elegans*

Cytochrome P450 proteins comprise a highly conserved superfamily of heme-containing

monooxygenases critical for metabolizing endogenous and xenobiotic

compounds(Denisov et al., 2005). We constructed transcriptional reporters for genes

encoding CYPs in *C. elegans* and found that *cyp-14A5p::GFP* was drastically up-

regulated by bright-field transmission light from a microscope inadvertently left on

overnight. Using controlled light versus dark conditions, we confirmed the finding from

an integrated *cyp-14A5p::GFP* reporter and observed its robust widespread GFP

expression in many tissues induced by moderate-intensity (500-3000 Lux, 16-48 hr

duration) LED light exposure (**Fig. 1A**). The level of GFP expression increased

proportionally with both light intensity and duration (**Fig. 1B**), the condition of which

does not impact ambient temperature (**Fig. S1A-S1D**). Other common stresses,

including transient 32 °C heat shock, constant 24-hr hypoxia or starvation did not

apparently induce *cyp-14A5p::GFP* (**Fig. S1E-S1H**). Together, these data suggest that

cyp-14A5p::GFP induction is finely tuned to ambient light conditions.

To determine CYP-14A5 protein expression pattern, we constructed a translational GFP

reporter (*cyp-14A5p::cyp-14A5::GFP*) and observed robust light-induced expression of

CYP-14A5::GFP in many of the non-neuronal tissues, including the pharynx, hypoderm

and intestine (**Fig. 1C**). The transcriptional reporter exhibited similar patterns of non-

neuronal GFP induction by light (**Fig. 1A**). The translational reporter reveals the CYP-

14A5::GFP pattern indicative of the endoplasmic reticulum structure (**Fig. 1C**),

consistent with the known subcellular localization of most CYPs to ER

membranes(Neve and Ingelman-Sundberg, 2010).

To explore how eyeless *C. elegans* responds to ambient visible light independently of a

visual system, we conducted transcriptomic profiling by RNA-seq in *C. elegans* exposed

to controlled light or dark conditions. We found that defined visible light exposure (1500

Lux, 24 hr duration) to a synchronized population of young adults (24 hrs post L4)

triggered a robust genome-wide transcriptional response, including 7902 genes

differentially regulated (adjusted *P* value < 0.05, **Fig. 1D** and **Table S1**). Among these,

cyp-14A5 was one of the most strongly upregulated genes (**Fig. 1E**). Gene ontology

(GO) analysis of the light-induced transcriptome reveals their significant enrichment in

several pathways, including transmembrane signaling, pathogen and stress responses,

protein phosphorylation, cellular homeostasis and metabolisms (**Fig. S2**).

ZIP-2 and CEBP-2 are essential for light-induced transcriptional responses

We next investigated the molecular regulators driving *cyp-14A5* activation in response

to light. To test if it requires previously identified blue-light receptors LITE-1 or GUR-3,

we crossed the *cyp-14A5p::GFP* reporter with *lite-1* and *gur-3* double loss-of-function

mutants. Surprisingly, light-induced GFP expression was preserved in *lite-1gur-3* double

mutants, indicating that *cyp-14A5* activation operates through an alternative, non-visual

light-sensing mechanism (**Fig. 2A**). Prolonged photonic light exposure may also cause

photo-oxidation of DNA and genotoxicity, leading to DNA damage and ATM protein-

dependent check points and transcriptional responses(Ciccia and Elledge, 2010; De

Magalhaes Filho et al., 2018; Schuch et al., 2017). However, loss of the DNA damage

sensor ATM-1 did not apparently affect light-induced *cyp-14A5p::GFP* (**Fig. 2A**). These

findings underscore the existence of a novel light-responsive pathway in *C. elegans*,

distinct from previously characterized photoreceptive systems.

To identify transcriptional regulators driving *cyp-14A5* activation in response to light, we

adopted an RNAi-based screening strategy, focusing initially on approximately 400

genes encoding transcription factors, including those responding to various types of

stresses. Knockdown of the expression of genes encoding TF from a previously

assembled RNAi library or selected for mediating various common stress responses

(hypoxia, oxidative stress, heat shock etc.) did not appear to affect *cyp-14A5* activation

in response to light (**Fig. 2B**). Interestingly, we identified from such screen two bZIP-

type transcription factors, ZIP-2 and CEBP-2, as critical mediators of light-induced *cyp-*

14A5 transcription (**Fig. 2B**). Knockdown or genetic ablation of either *zip-2* or *cebp-2*

abolished light-induced *cyp-14A5p::GFP* expression (**Fig. 2B, 2C**). ZIP-2 and CEBP-2

have been previously identified(Dunbar et al., 2012; Estes et al., 2010; Kniazeva and

Ruvkun, 2025; Reddy et al., 2016) to cooperate in a regulatory complex and mediate

transcriptional responses to translational inhibition caused by the bacterial pathogen

Pseudomonas aeruginosa PA14. In these studies, the *irg-1*p::GFP transcriptional

reporter was robustly activated by PA14 as a well-established target for ZIP-2 and

CEBP-2. Interestingly, we found *irg-1*p::GFP was not activated by the same light

condition (1500 Lux, 24 hrs) that reliably induced *cyp-14A5*p::GFP (**Fig. 2D**). Although

ZIP-2 can be activated by pathogen stresses through ribosomal inhibition and

subsequent selective ZIP-2 translation(Dunbar et al., 2012; Estes et al., 2010; Kniazeva

and Ruvkun, 2025; Reddy et al., 2016), our results suggest the specific roles of ZIP-2 in

mediating light-induced *cyp-14A5* but not *irg-1* reporter expression, suggesting the

involvement of additional stress context-specific factors in these processes.

We further explored conditions and mechanisms leading to light-induced *cyp-*

14A5p::GFP. To test potential effects of ultraviolet (UV) irradiation from our visible light

LED, we used a UV-masking shield to block UV irradiation. However, this did not affect

visible LED light-induced *cyp-14A5p::GFP* expression (**Fig. 2E**). In addition, we found

that the LED light exposure of equal intensities (1500 Lux, 24 hrs) but at different

wavelengths (red, green, blue) led to differential *cyp-14A5p::GFP* expression (**Fig. 2F,**

2G), showing stronger effects of shorter wavelengths in the visible-light spectrum. A

pseudo-open reading frame (uORF) in the 5' untranslated region (UTR) of *zip-2* mRNA

inhibits the ribosomal translation of the ZIP-2 main open reading frame (mORF) in the

context of PA14 pathogen exposure(Dunbar et al., 2012). However, constitutive

expression of *zip-2* uORF by the *rpl-28* promoter did not affect light-induced *cyp-*

14A5p::GFP (**Fig. 2H**). Furthermore, a CRISPR phospho-site knock-in mutation of *eif-*

2alpha(S49A) did not affect global translation(Ma et al., 2023), yet abolished light-

induced *cyp-14A5p::GFP* (**Fig. 2I**). As the eukaryotic eIF2alpha complex facilitates

translational switch from uORF to mORF upon stress-induced ribosomal stall at

uORF(Brito Querido et al., 2024; Costa-Mattioli and Walter, 2020; Mir et al., 2024),

these results suggest that it is the *zip-2* uORF translational inhibition, not the uORF

protein product function, that mediates visible light-increased ZIP-2 translation and *cyp-*

14A5p::GFP expression (**Fig. 2J**).

Light-induced CYP-14A5 enhances behavioral memory

Although EIF-2alpha and ZIP-2/CEBP-2 functions appear essential for light-induced up-

regulation of *cyp-14A5*, the *zip-2* or *cyp-14A5* loss-of-function null mutants show no

apparent body-size, morphological, feeding, defecation or developmental defects under

dark or LED light treatment (1500 Lux for 16 or 24 hrs) conditions (**Fig. S3**). These data

suggest that transient visible light exposure or light-induced *cyp-14A5* activation by ZIP-

2 does not broadly impact development, aging or physiology, unlike long-term visible

light exposure, which has been shown to robustly shorten lifespans in *C. elegans*(De

Magalhaes Filho et al., 2018).

The lack of obvious morphological and basal behavioral defects led us to explore

whether light exposure influences other aspects of *C. elegans* biology, particularly

behavioral plasticity and associative memory formation that might require integration of

body physiology. Specifically, we chose a learning paradigm in which animals learn to

avoid an innately attractive odor butanone after it is paired with aversive

stimuli(Chandra et al., 2023; Kauffman et al., 2010). *C. elegans* can consolidate this

learning into a long-lasting memory for up to 16 hours once the repetitive training is

followed by sleep and recovery post learning(Chandra et al., 2023). Using this

conditioning protocol (**Fig. 3A**), we observed that animals exposed to ambient light

(approximately 500–1000 Lux) during olfactory associative learning and recovery

exhibited significantly enhanced memory retention compared to those maintained in

darkness (**Fig. 3B**). To pinpoint the critical period for light exposure, we deprived

animals of light in two-hour intervals immediately post learning. Interestingly, light

deprivation during the first 2–4 hours post learning resulted in markedly impaired

memory retention (**Fig. 3C**). These results suggest that environmental light exposure

enhances aversive cue association post learning and is not required for learning itself

but is required post learning concurrent with sleep for consolidation of memory(Chandra

et al., 2023).

Does the light-modulated behavioral memory consolidation require light activation of the

ZIP-2 pathway? To address this question, we examined the behavioral memory of two

independent *zip-2* deletion mutants as compared to wild type (*cebp-2* mutants are

pleiotropically sick and thus not included). We found that both the *ok3730* and *tm4246*

deletion mutations of *zip-2* caused significantly impaired memory consolidation but not

learning (**Fig. 3D**). Strikingly, the loss-of-function mutation of *cyp-14A5*, but not *F43C1.7*

(another ZIP-2 target gene induced by visible light), also impaired memory retention as

zip-2 (**Fig. 3E**), indicating a crucial role of the ZIP-2/CYP-14A5 regulatory axis in

mediating light-modulated memory consolidation. To further delineate the role of CYP-

14A5, we performed tissue-specific rescue experiments in the behavioral memory

assay. We found that hypoderm-specific expression of *cyp-14A5* restored the

behavioral memory in the *cyp-14A5* mutant (**Fig. 3F**). We observed similar degrees of

rescue by two independently derived lines expressing hypoderm-specific *dpy-7p::cyp-*

14A5 transgenes. These findings strongly suggest that hypodermal induction of CYP-

14A5 by ZIP-2 plays a central role in mediating light-modulated behavioral memory.

The *cyp-14A5* promoter as a versatile tool for light-inducible gene expression

The light-responsive nature of the *cyp-14A5* promoter prompted us to explore its

potential as a tool for controlling gene expression. We generated synthetic constructs

driving the expression of diverse effectors under the *cyp-14A5* promoter to confer

striking organismal phenotypes. We previously found that *zip-10* expression promotes

organismal phenoptosis(Pandey and Ma, 2022; Wang et al., 2023). Driven by the *cyp-*

14A5 promoter, light-induced *zip-10* expression indeed caused a robust light-dependent

rapid aging or phenoptosis-like phenotype with markedly shortened median and

maximal lifespans (**Fig. 4A-4D**). We confirmed that LED light exposure markedly

induced *zip-10* expression, as evidenced by robust ZIP-10-tagging mCherry

fluorescence in major non-neuronal tissues of transgenic animals, only after light (1500

Lux, 24 or 48 hrs) exposure (**Fig. 4C**).

To test organismal behavioral outcomes, we expressed *nlp-22* under the *cyp-14A5*

promoter. *nlp-22* was previously identified as a sleep-promoting

neuropeptide(Bringmann, 2018; Nelson et al., 2013; Van der Auwera et al., 2020),

overexpression of which can cause drastic reduction of pumping and locomotion speed,

characteristic of sleep behaviors in *C. elegans*. We found that *cyp-14A5p::nlp-22* can

indeed trigger striking behavioral quiescence upon light exposure (1500 Lux, 24 or 48

hrs), as quantified by pumping rates, bending frequencies and locomotion speed (**Fig.**

4E-4G). Quantitative analysis by WormLab reveals that the behavioral quiescence

induced by *nlp-22* corresponded to characteristic bouts of sleep **(Fig. S4**). These proof-

of-concept studies demonstrate that the *cyp-14A5* promoter enables light-dependent

ectopic induction of gene expression, offering a flexible tool for probing gene function,

studies of organismal biology, behaviors and synthetic physiology applications.

226 Discussion

Our findings uncover a previously unknown light-induced transcriptional pathway in *C.*

elegans that operates independently of known visual light receptors. Our study also

establishes a functional link between ambient light and behavioral plasticity through a

ZIP-2/CYP regulatory axis. The discovery of this pathway and its organismal functions

opens exciting avenues for understanding body-brain communication and how

environmental cues such as light can shape physiological and behavioral processes.

The specificity of this pathway is particularly intriguing, as *cyp-14A5* is robustly induced

by light at wavelength and intensity that do not apparently alter ambient temperature

(**Fig. S1**). Previous studies identified *cyp-14A5* as one of many genes moderately

regulated by bacterial pathogens(Sinha et al., 2012; Troemel et al., 2006; Wong et al.,

2007), yet the classic pathogen-inducible gene reporter *irg-1p::GFP* was not apparently

activated by light conditions that induced *cyp-14A5*p::GFP. This specificity raises

important questions about how ZIP-2 and *cyp-14A5* are selectively activated by light, or

to different degrees. Given the crucial roles of ZIP-2 and eIF2alpha we discovered for

light-induced expression of *cyp-14A5* and the established role of the uORF at the 5'

untranslated region of *zip-2* RNA in ZIP-2 regulation(Dunbar et al., 2012), it is plausible

that light may regulate ZIP-2 translation by *zip-2* RNA photo-oxidation at specific sites,

eIF2alpha phosphorylation and specialized ribosomal signaling(D'Orazio and Green,

2021; Genuth and Barna, 2018; Sinha et al., 2024). Further investigation into the

upstream signaling events and the molecular sensors linking light exposure to ZIP-

2/CEBP-2 activation is warranted.

Our behavioral assays demonstrate that light exposure enhances olfactory associative

memory, providing direct evidence for the functional relevance of light-induced *cyp-

14A5* expression. Interestingly, light exposure appears to exert its effects during a

specific temporal window hours following learning, suggesting that light-induced

transcriptional changes post learning play a key role in memory consolidation. The

discovery of *cyp-14A5* as a key effector in this pathway also provides new insights into

how non-neuronal tissues contribute to behavioral plasticity. Our findings suggest that

light-induced CYP-14A5 and CYP-dependent metabolic or signaling changes in the

hypoderm may communicate with the nervous system to influence behavioral memory.

This body-brain communication axis highlights the importance of systemic integration in

mediating complex physiological and behavioral responses to environmental

cues(Aghayeva et al., 2021; Fukuda et al., 2025; Liu et al., 2022; Zhang et al., 2018).

Beyond its biological significance, the light-inducible *cyp-14A5* promoter offers a useful

new tool for gene expression studies in *C. elegans*. The ability to drive ectopic gene

expression in response to light provides a versatile system for temporally controlled genetic manipulations. Our demonstration of light-induced sleep and mortality phenotypes through ectopic gene expression illustrates the potential applications of this tool in studying diverse biological processes in synthetic biology and physiology. Previous studies have used heat shock or drug-inducible promoters for temporally controlled gene expression in *C. elegans*(Monsalve et al., 2019; Stringham et al., 1992; Wei et al., 2012). The light-inducible *cyp-14A5* promoter provides an alternative, simple-to-implement approach and might be particularly useful when the drug-inducible system is cumbersome, or heat shock effects are undesirable.

While our study uncovers a novel light-responding mechanism with functional consequences in *C. elegans*, several limitations exist. First, the precise molecular mechanism by which visible light activates ZIP-2 and/or CEBP-2 remains unclear, as does the upstream signaling cascade linking light exposure to transcriptional activation. Second, although we demonstrate a functional connection between light-induced *cyp-14A5* expression and behavioral outcomes, the exact molecular interplay between peripheral transcriptional changes and neural plasticity requires further exploration. Finally, while the *cyp-14A5* promoter serves as a useful genetic tool, it does not confer tissue specificity, and its ectopic effector expression requires control for light effects. These limitations provide fertile ground for future research to build upon our findings.

Materials & Methods

***C. elegans* strains**

C. elegans strains were grown on nematode growth media (NGM) plates seeded with

Escherichia coli OP50 at 20 °C with laboratory standard procedures unless otherwise

specified. The N2 Bristol strain was used as the reference wild type(Brenner, 1974).

Mutants and integrated transgenes were back-crossed at least five times. Genotypes of

strains used are as follows: *dmaIs156 IV [cyp-14A5p:: cyp-14A5::GFP; unc-*

54p::mCherry], agIs17 IV [irg-1p::gfp], dmaEx [dpy-7p::cyp-14A5; myo-2p::mCherry],

dmaEx [cyp-14A5p::zip-10::mCherry; myo-2p::mCherry], dmaEx [cyp-14A5p::nlp-22;

myo-2p::mCherry], cebp-2 (tm5421) I, eif-2alpha(rog3) I, zip-2(tm4248) III, zip-2(ok3730)

III, cyp-14A5(gk152) V.

PCR fusion constructs were used to generate transgenes(Hobert, 2002), using primer

sequences:

DM1310_*cyp-14A5*Pro c5p TCAACCACATCTTCCGATCA;

DM1311_*cyp-14A5*Pro to GFP c3p

CGACCTGCAGGCATGCAAGCTgatctttgttggacagaatagtttt;

DM2857_*dpy-7*p to *cyp-14A5* codutr Forward TGTCTCTGACGCCTGTGAGT;

DM2858_*dpy-7*p to *cyp-14A5* codutr Reverse

GATAAAGCAACGATGAAAACGCTCATTTTGTTTTCACAGAGCGGTAGA;

DM2944_*zip-2*uORF to *rpl-28*p-GOI-mCherry-5utr fusion F

CATCATAAAATAATTTATTTCCAGGTAAAATGTATCACGCAAAGACAACCACCG;

DM2945_*zip-2*uORF to *rpl-28*p-GOI-mCherry-5utr fusion

catgttatcttcttcacccttt gaggagccAAGCTCCCGTGGGAAGCTTGTG;

DM2948_*zip-10* to *cyp-14A5*p-GOI-mCherry-5utr fusion F

aaaactattctgtccaacaaagatcaaaATGACAACAATGACTAATTCTCTTATTTC;

DM2949_*zip-10* to *cyp-14A5*p-GOI-mCherry-5utr fusion R

catgttatcttcttcaccctttgaggagccGGAATGGTTGATTTGATTATTGAGTTG

DM2952_*nlp-22*cod::3utr to *cyp-14A5*p-GOI fusion

aaaactattctgtccaacaaagatcaaaATGCGTTCCATAATCGTCTTCATCG;

DM2953_*nlp-22*cod::3utr to *cyp-14A5*p-GOI fusion R   cggttccactttctcatgagt

Fluorescence microscopy and imaging

SPE confocal (Leica) and epifluorescence microscopes were used to capture fluorescence images. Animals were randomly picked at the same stage and treated with 1 mM levamisole in M9 solution (31742-250MG, Sigma-Aldrich), aligned on a 2% agar pad on a slide for imaging. Identical setting and conditions were used to compare experimental groups with control. For quantification of GFP fluorescence, animals were outlined and quantified by measuring gray values using the ImageJ software. The data were plotted and analyzed by using GraphPad Prism10.

For light-induced reporter imaging, reporter animals (synchronized young adults, 24 hrs post L4) were exposed to white light (1500 Lux for 16 or 24 hrs, by Viribright 12-Watt, 800 Lumen, LED Desk Lamp Dimmable Office Lamp). For blue, green (SPE confocal, Leica), and red light (HQRP 660 nm 14w LED pure red) conditions, animals of the same stage were exposed to the same intensities (1500 Lux, 16 or 24 hours). Control groups from the same batch of animals were maintained in darkness by opaque shields. Light intensities and temperature were quantitatively measured by digital light meters and thermometers.

RNA sequencing

A synchronized population of wild-type young adult (24 hrs post L4) animals were exposed to LED light (1500 lux, 24 hr duration, Viribright 12-Watt, 800 Lumen, LED Desk Lamp Dimmable Office Lamp). Control groups from the same batch of animals were maintained in darkness by opaque light shields. Four independent biological replicates were used for both light-treated and control groups. For sample collection, the animals were washed down from NGM plates using M9 solution and bacteria-cleaned with M9 washing in centrifuge tubes, homogenized by tissue disruptors and subjected to RNA extraction using the RNeasy Mini Kit from Qiagen. 1 mg total RNA from each sample was used for sequencing library construction. The libraries were constructed and sequenced for paired end 150 bp by DNBseq (Innomics). The cleaned RNAseq reads were mapped to the genome sequence of *C. elegans* using hisat2 and the mapped reads were assigned to the genes using featureCounts(Kim et al., 2015; Liao et al., 2014). The abundance of genes was expressed as RPKM (Reads per kilobase per million mapped reads) and identification of differentially expressed genes (Table S1) was performed using the DESeq2 package(Love et al., 2014).

C. elegans **behavioral assays**

The olfactory behavioral memory assay was as described previously with modification(Chandra et al., 2023; Kauffman et al., 2010). Briefly, one day old adult worms (24 hrs post L4) were washed with S basal buffer (0.1 M NaCl, 0.05 M K_3PO_4, pH 6.0) off

10 cm NGM plates and into microfuge tubes, where they were washed three times with

S basal buffer. The animals were split in two groups; one group was added to a microfuge

tube of S basal media and the other group was added to a microfuge tube of 1:10,000

dilution of butanone in S basal. The microfuge tubes were then rotated for 80 minutes.

The odor training includes three 80-minute cycles of training with odor, or a control buffer

interspersed with two 30-minute periods of feeding with OP50 *E. coli* bacteria. For

chemotaxis assay, 1 µL of (1 M) NaN_3 was pipetted onto the odor and diluent spots in 10

cm plastic petri dishes. 1 µL of 200 proof ethanol was added to the diluent spot and 1 µL

of 1:1000 butanone was added to the odor spot, while S basal or butanone-trained worms

were dropped onto the middle of 10 cm plastic petri dishes. The recovery period was

either under darkness or ambient light (approximately 600 Lux) for 16 hrs or were kept

under darkness for 2 or 4 hr periods followed by light exposure and chemotaxis to assay

behavioral memory.

For sleep analysis induced by *cyp-14A5p::nlp-22*, the bending angles, moving average

speed, and track length of *C. elegans* after 48 hours of exposure to either light or dark

conditions were analyzed using WormLab. In such experiment, a synchronized population

of young adult (24 hrs post L4) animals of indicated genotype or transgene expression

were used. After light exposure or control dark treatment, they were transferred to a fresh

NGM plate seeded with a small OP50 bacterial lawn and allowed to settle for at least ten

minutes to recover at room temperature. After the recovery period, a one-hour recording

session was conducted using WormLab. Bending angles were calculated as described in

the referenced method as a metric for sleep behaviors(Chandra et al., 2023). Moving

average speed was determined by tracking the displacement of the worms over time.

Statistics

Numerical data were analyzed using GraphPad Prism 10 Software (Graphpad, San

Diego, CA) and presented as means ± S.D. unless otherwise specified, with P values

calculated by unpaired two-tailed t-tests (comparisons between two groups), one-way

ANOVA (comparisons across more than two groups) and two-way ANOVA (interaction

between genotype and treatment), with post-hoc Tukey and Bonferroni's corrections.

The lifespan assay was plotted and quantified using Kaplan–Meier lifespan analysis,

and P values were calculated using the log-rank test.

Acknowledgment

Some strains were provided by the *Caenorhabditis* Genetics Center (CGC), which is

funded by the NIH Office of Research Infrastructure Programs (P40 OD010440), and by

Dr. E. Troemel. We also thank the *C. elegans* Reverse Genetics Core Facility

(University of British Columbia), National Bioresource Project (S. Mitani, Tokyo

Women's Medical University, Tokyo, Japan), Wormbase.org (NIH grant #U24

HG002223 to P. Sternberg), Wormatlas.org (NIH grant #OD010943 to D.H. Hall.), Aging

Atlas (Dr. M. Wang) and CenGen (cengen.org) for their immensely helpful resources.

The work was supported by NIH grants (R35GM139618 to D.K.M.), BARI Investigator

Award (D.K.M.), and UCSF PBBR New Frontier Research Award (D.K.M.)

Author Contributions

D.K.M. designed and analyzed the *C. elegans* experiments, contributed to project conceptualization and wrote the manuscript. B.W. made the initial observation on *cyp-14A5* induction by light and performed RNAi screens and reporter imaging. Z.J. prepared RNA-seq samples and characterized light effects on the *cyp-14A5* reporter, cellular, behavioral and physiological phenotypes of various mutants with assistance from W.Y. and M.E. Y.L. analyzed the RNA-seq data. R.C. designed, performed and analyzed the behavioral memory assays. J.L. designed, performed and analyzed the light-induced sleep and phenoptotic aging assays. N.L., Y.L., B.W., Z.J., R.C., J.L. contributed to research materials, project conceptualization and editing manuscript.

Competing Interest Statement: The authors declare no competing interests.

Figures and figure legends

Figure 1 Visible light exposure activates the CYP-encoding gene *cyp-14A5* in a genetic program in *C. elegans*. A, Representative epifluorescence and brightfield

images showing *cyp-14A5*p::GFP induction by visible light exposure (1500 Lux, 24 hrs),

in synchronized young adults (24 hrs post L4). Scale bar: 50 µm. B, Bubble plot

showing fold induction of *cyp-14A5p::GFP* as a function of light intensity (Lux) and

duration (hours of light_dark indicated in Y axis). C, Schematic of *cyp-14A5*

transcriptional and translational GFP reporters. The translational reporter shows non-

neuronal (indicated by arrows) induction of CYP-14A5::GFP by light (1500 Lux, 24 hrs).

Scale bar: 50 µm. D, Volcano plot showing genes differentially regulated by light (1500

Lux, 24 hrs), with *cyp-14A5* highlighted, in synchronized young adults (24 hrs post L4).

E, Heat map of top-ranking visible light-regulated genes (top 30 including *cyp-14A5*).

B

RNAi	cyp-14A5p::GFP induction by light (1500 Lux)
Control	+++++
skn-1	+++++
hsf-1	+++++
hif-1	+++++
hlh-30	+++++
daf-16	+++++
pqm-1	+++++
xbp-1	+++++
atfs-1	+++++
sta-2	+++++
zip-2	-
cebp-2	-
TF lib (387 clones)	+++++

Figure 2 Light induction of *cyp-14A5*p::GFP requires the transcription factors ZIP-2 and CEBP-2. A, Representative epifluorescence images showing light-induced *cyp-14A5*p::GFP expression in *lite-1 gur-3* double and *atm-1* single loss-of-function mutants. Scale bar: 50 μm. B, Summary of RNAi screens identifying ZIP-2 and CEBP-2 as

essential transcriptional regulators of light-induced *cyp-14A5p::GFP* expression. C,

Representative epifluorescence images showing light-induced *cyp-14A5p::GFP*

expression in wild type, *zip-2* and *cebp-2* loss-of-function mutants. Scale bar: 50 µm. D,

Representative epifluorescence images showing light-induced *cyp-14A5p::GFP*

expression and no light-induced *irg-1p::GFP* expression in wild type animals. Scale bar:

50 µm. E, Representative epifluorescence images showing light-induced *cyp-*

14A5p::GFP expression unaffected by a UV shield. Scale bar: 50 µm. F, Representative

epifluorescence images showing light-induced *cyp-14A5p::GFP* expression by red,

green, blue LED light sources of equal intensities. Scale bar: 50 µm. G, Quantification of

E and F. *** indicates *P* < 0.001, n.s., non-significant. H, Representative

epifluorescence images showing light-induced *cyp-14A5p::GFP* expression unaffected

in *rpl-28p::zip-2uORF* transgenic animals. Scale bar: 50 µm. I, Representative

epifluorescence images showing light-induced *cyp-14A5p::GFP* expression abolished in

eif-2alpha mutants. Scale bar: 50 µm. J, Schematic model for light-induced transition of

zip-2 mRNA from translating uORF to mORF, leading to increased ZIP-2 and

subsequent increased transcriptional *cyp-14A5* expression in cooperation with CEBP-2.

Other molecular players are omitted and uORF and mORF are separated for clarity.

Figure 3 Light promotes behavioral plasticity and memory consolidation via a ZIP-2/CYP axis in hypodermis. A, Schematic of behavioral setup to test effects of dark/light on olfactory memory. B, Wild-type learning and memory after 16 hours of dark exposure. 7 trials, 50-200 animals per trial/condition. Two-way ANOVA shows significant differences in chemotaxis (CI) under ambient light conditions (approximately 600 Lux) but not when the assay plates were placed in the dark. Learning (LI) indices reflect the differences between buffer- and butanone-treated animals, attenuated under dark (one-way ANOVA). Pairwise t-tests of the amount of memory retention under light and dark recovery reveal the degree of memory loss under dark. C, Dark exposure timeline shows that exposing animals to dark immediately after training (0-2 hr, Dark) hampered memory retention, whereas dark conditions for the 2–4-hour period is less sufficient to induce memory loss (two-way ANOVA). The lack of differences between buffer and butanone-trained animals is reflected in the respective LIs (one-way ANOVA). D, Two different loss-of-function alleles of *zip-2(tm4246)* or *zip-2(ok3730)* both showed impaired memory, but learning remained intact (two-way ANOVA). 5-10 trials, 50-200 animals per trial/condition. E, Memory impairment of *cyp-14A5(gk152)* but not *F43C1.7* null mutant animals (two-way ANOVA for CIs and One-way ANOVA for LIs. 7-14 trials, 50-200 animals per trial/condition. F, Memory defects of *cyp-14A5(gk152)* mutants are rescued by hypodermal expression of wild-type *cyp-14A5*. Two independent transgenic lines show similar results with comparison of pairwise differences in LIs and the amount of memory rescued by hypodermal *cyp-14A5* (Cis: Two-way ANOVA; Lis: One-way ANOVA). * indicates $P < 0.05$, ** indicates $P < 0.01$, *** indicates $P < 0.001$, **** indicates $P < 0.0001$, n.s., non-significant.

Figure 4 Light-induced gene expression drives organismal phenotypes, including sleep and shortened lifespans. A, Schematic of synthetic constructs for light-inducible *nlp-22* and *zip-10::mCherry* using the *cyp-14A5* promoter. B, Representative compound epifluorescence images showing light-induced *cyp-14A5p::zip-10::mCherry* activation. Scale bar: 50 µm. Pharyngeal muscle-specific *myo-2p::mCherry* was used as a co-

injection marker. C, Representative confocal fluorescence images showing light-induced

cyp-14A5p::zip-10::mCherry activation (1500 Lux, 24 hrs starting at 24 hrs post L4) in

major non-neuronal tissues (hypoderm, intestinal cells indicated by arrows). Scale bar:

50 μm. D, Representative lifespan curves showing that light-induced *zip-10* can

markedly shorten lifespan through transient light exposure (1500 Lux, 24 hrs starting at

24 hrs post L4). **** indicates $P < 0.0001$. E, Representative bright field images showing

quiescent sleep behaviors by light-induced *cyp-14A5p::nlp-22* expression through

transient light exposure (1500 Lux, 24 hrs starting at 24 hrs post L4). F, Quantification of

population bending frequencies for transient light-treated (1500 Lux, 24 hrs starting at

24 hrs post L4) control wild type and *cyp-14A5p::nlp-22* animals. G, Quantification of

population track lengths for control wild type and *cyp-14A5p::nlp-22* animals with

transient light (1500 Lux, 24 hrs starting at 24 hrs post L4) or darkness treatments. ***

indicates $P < 0.001$, **** indicates $P < 0.0001$, n.s., non-significant.

Figure S1 *cyp-14A5p::GFP* induction responds primarily to visible light exposure rather than changes in ambient oxygen, nutrient or temperature. A, Schematic of the setup for measurements of light intensity and temperature at a plane (in parallel to LED visible light sources) where animals are exposed to LED light in NGM plates. B, Measurements of temperature at the 600 Lux light intensity showing no change of temperature over 24 hrs. C, Measurements of temperature at the 1500 Lux light intensity showing no change of temperature over 24 hrs. D, Measurements of temperature at the 3000 Lux light intensity showing no change of temperature over 24 hrs. E-H, Representative bright-field and epifluorescence images showing no apparent

505   *cyp-14A5p::GFP* induction by transient exposure to heat shock (F), constant exposure

506   to 24 hrs of hypoxia (G) or starvation (H). Scale bar: 50 μm.

A

Gene ontology analysis
by WormCat:

B   Gene ontology analysis
by WormEnrichr:

Figure S2 Gene ontology analysis of light-induced transcriptomic changes. A,

Starburst plot of gene ontology analysis of light-induced genes using WormCat

(http://www.wormcat.com/). B, Table summary of gene ontology analysis of light-

induced genes using WormEnrichr (https://maayanlab.cloud/WormEnrichr/).

Figure S3 No apparent effects of short-term transient visible LED light exposure

on development, morphology, simple behaviors and lifespans. A, Representative

bright-field images showing no apparent effects of visible light exposure (1500 Lux, 24

hrs) on the body lengths and gross morphology of wild type, *cebp-2*, and *zip-2* loss-of-

function mutants. Scale bar: 50 μm. B. Representative images showing the movement

tracks of wild type, *cyp-14A5*, and *zip-2* loss-of-function mutants under dark and light

(1500 Lux, 24 hrs) conditions. C, Quantification of track lengths of wild type, *cyp-14A5*,

and *zip-2* loss-of-function mutants under dark and light (1500 Lux, 24 hrs) conditions. D,

Quantification of pumping rates of wild type, *cyp-14A5*, and *zip-2* loss-of-function

mutants under dark and light (1500 Lux, 24 hrs) conditions. E, Quantification of

defecation behaviors of wild type, *cyp-14A5*, and *zip-2* loss-of-function mutants under

dark and light (1500 Lux, 24 hrs) conditions. F, Lifespan curves of wild-type animals

under conditions of dark or transient LED light exposure for various indicated durations.

Figure S4 WormLab analysis reveals sleep bouts caused by light-induced *cyp-14A5p::nlp-22* expression. (A) Representative tracking of moving angles for body posture and average speed for control animals under dark conditions (N=15). (B) Representative tracking of moving angles for body posture and average speed for control animals after light exposure conditions (1500 Lux, 24 hrs, N=13). (C) Representative tracking of moving angles for body posture and average speed for *cyp-14A5p::nlp-22* transgenic animals under dark conditions (N=12). (B) Representative tracking of moving angles for body posture and average speed for *cyp-14A5p::nlp-22* transgenic animals after light exposure conditions (1500 Lux, 24 hrs, N=13).

References

Aghayeva U, Bhattacharya A, Sural S, Jaeger E, Churgin M, Fang-Yen C, Hobert O. 2021. DAF-16/FoxO and DAF-12/VDR control cellular plasticity both cell-autonomously and via interorgan signaling. *PLoS Biol* **19**:e3001204. doi:10.1371/journal.pbio.3001204

Andrabi M, Upton BA, Lang RA, Vemaraju S. 2023. An Expanding Role for Nonvisual Opsins in Extraocular Light Sensing Physiology. *Annu Rev Vis Sci* **9**:245–267. doi:10.1146/annurev-vision-100820-094018

Berson DM, Dunn FA, Takao M. 2002. Phototransduction by retinal ganglion cells that set the circadian clock. *Science* **295**:1070–1073. doi:10.1126/science.1067262

Bhatla N, Horvitz HR. 2015a. Light and hydrogen peroxide inhibit C. elegans Feeding through gustatory receptor orthologs and pharyngeal neurons. *Neuron* **85**:804–818. doi:10.1016/j.neuron.2014.12.061

Bhatla N, Horvitz HR. 2015b. Light and hydrogen peroxide inhibit C. elegans Feeding through gustatory receptor orthologs and pharyngeal neurons. *Neuron* **85**:804–818. doi:10.1016/j.neuron.2014.12.061

Brenner S. 1974. The genetics of Caenorhabditis elegans. *Genetics* **77**:71–94.

Bringmann H. 2018. Sleep-Active Neurons: Conserved Motors of Sleep. *Genetics* **208**:1279–1289. doi:10.1534/genetics.117.300521

Brito Querido J, Díaz-López I, Ramakrishnan V. 2024. The molecular basis of translation initiation and its regulation in eukaryotes. *Nat Rev Mol Cell Biol* **25**:168–186. doi:10.1038/s41580-023-00624-9

Chandra R, Farah F, Muñoz-Lobato F, Bokka A, Benedetti KL, Brueggemann C, Saifuddin MFA, Miller JM, Li J, Chang E, Varshney A, Jimenez V, Baradwaj A, Nassif C, Alladin S, Andersen K, Garcia AJ, Bi V, Nordquist SK, Dunn RL, Garcia V, Tokalenko K, Soohoo E, Briseno F, Kaur S, Harris M, Guillen H, Byrd D, Fung B, Bykov AE, Odisho E, Tsujimoto B, Tran A, Duong A, Daigle KC, Paisner R, Zuazo CE, Lin C, Asundi A, Churgin MA, Fang-Yen C, Bremer M, Kato S, VanHoven MK, L'Étoile ND. 2023. Sleep is required to consolidate odor memory and remodel olfactory synapses. *Cell* **186**:2911-2928.e20. doi:10.1016/j.cell.2023.05.006

Ciccia A, Elledge SJ. 2010. The DNA damage response: making it safe to play with knives. *Mol Cell* **40**:179–204. doi:10.1016/j.molcel.2010.09.019

Costa-Mattioli M, Walter P. 2020. The integrated stress response: From mechanism to disease. *Science* **368**:eaat5314. doi:10.1126/science.aat5314

Cronin TW, Johnsen S. 2016. Extraocular, Non-Visual, and Simple Photoreceptors: An Introduction to the Symposium. *Integr Comp Biol* **56**:758–763. doi:10.1093/icb/icw106

De Magalhaes Filho CD, Henriquez B, Seah NE, Evans RM, Lapierre LR, Dillin A. 2018. Visible light reduces C. elegans longevity. *Nat Commun* **9**:927. doi:10.1038/s41467-018-02934-5

Denisov IG, Makris TM, Sligar SG, Schlichting I. 2005. Structure and chemistry of cytochrome P450. *Chem Rev* **105**:2253–2277. doi:10.1021/cr0307143

Do MTH, Yau K-W. 2010. Intrinsically photosensitive retinal ganglion cells. *Physiol Rev* **90**:1547–1581. doi:10.1152/physrev.00013.2010

D'Orazio KN, Green R. 2021. Ribosome states signal RNA quality control. *Mol Cell* **81**:1372–1383. doi:10.1016/j.molcel.2021.02.022

Dunbar TL, Yan Z, Balla KM, Smelkinson MG, Troemel ER. 2012. C. elegans detects pathogen-induced translational inhibition to activate immune signaling. *Cell Host Microbe* **11**:375–386. doi:10.1016/j.chom.2012.02.008

Edwards SL, Charlie NK, Milfort MC, Brown BS, Gravlin CN, Knecht JE, Miller KG. 2008. A novel molecular
solution for ultraviolet light detection in Caenorhabditis elegans. *PLoS Biol* **6**:e198.
doi:10.1371/journal.pbio.0060198
Estes KA, Dunbar TL, Powell JR, Ausubel FM, Troemel ER. 2010. bZIP transcription factor zip-2 mediates
an early response to Pseudomonas aeruginosa infection in Caenorhabditis elegans. *Proc Natl
Acad Sci U S A* **107**:2153–2158. doi:10.1073/pnas.0914643107
Fukuda A, Sato K, Fujimori C, Yamashita T, Takeuchi A, Ohuchi H, Umatani C, Kanda S. 2025. Direct
photoreception by pituitary endocrine cells regulates hormone release and pigmentation.
Science **387**:43–48. doi:10.1126/science.adj9687
Genuth NR, Barna M. 2018. Heterogeneity and specialized functions of translation machinery: from
genes to organisms. *Nat Rev Genet* **19**:431–452. doi:10.1038/s41576-018-0008-z
Gong J, Yuan Y, Ward A, Kang L, Zhang B, Wu Z, Peng J, Feng Z, Liu J, Xu XZS. 2016. The C. elegans Taste
Receptor Homolog LITE-1 Is a Photoreceptor. *Cell* **167**:1252-1263.e10.
doi:10.1016/j.cell.2016.10.053
Hanson SM, Scholüke J, Liewald J, Sharma R, Ruse C, Engel M, Schüler C, Klaus A, Arghittu S, Baumbach
F, Seidenthal M, Dill H, Hummer G, Gottschalk A. 2023. Structure-function analysis suggests that
the photoreceptor LITE-1 is a light-activated ion channel. *Curr Biol* **33**:3423-3435.e5.
doi:10.1016/j.cub.2023.07.008
Hattar S, Lucas RJ, Mrosovsky N, Thompson S, Douglas RH, Hankins MW, Lem J, Biel M, Hofmann F,
Foster RG, Yau K-W. 2003. Melanopsin and rod-cone photoreceptive systems account for all
major accessory visual functions in mice. *Nature* **424**:76–81. doi:10.1038/nature01761
Hobert O. 2002. PCR fusion-based approach to create reporter gene constructs for expression analysis in
transgenic C. elegans. *Biotechniques* **32**:728–730. doi:10.2144/02324bm01
Kauffman AL, Ashraf JM, Corces-Zimmerman MR, Landis JN, Murphy CT. 2010. Insulin signaling and
dietary restriction differentially influence the decline of learning and memory with age. *PLoS Biol
***8**:e1000372. doi:10.1371/journal.pbio.1000372
Keller J, Ellieva A, Ma DK, Ju J, Nehk E, Konkel A, Falck JR, Schunck W-H, Menzel R. 2014. CYP-13A12 of
the nematode Caenorhabditis elegans is a PUFA-epoxygenase involved in behavioural response
to reoxygenation. *Biochem J* **464**:61–71. doi:10.1042/BJ20140848
Kim D, Langmead B, Salzberg SL. 2015. HISAT: a fast spliced aligner with low memory requirements. *Nat
Methods* **12**:357–360. doi:10.1038/nmeth.3317
Kniazeva M, Ruvkun G. 2025. Translation elongation defects activate the Caenorhabditis elegans ZIP-2
bZIP transcription factor-mediated toxin defense. *Proc Natl Acad Sci U S A* **122**:e2423578122.
doi:10.1073/pnas.2423578122
Liao Y, Smyth GK, Shi W. 2014. featureCounts: an efficient general purpose program for assigning
sequence reads to genomic features. *Bioinformatics* **30**:923–930.
doi:10.1093/bioinformatics/btt656
Liebel F, Kaur S, Ruvolo E, Kollias N, Southall MD. 2012. Irradiation of skin with visible light induces
reactive oxygen species and matrix-degrading enzymes. *J Invest Dermatol* **132**:1901–1907.
doi:10.1038/jid.2011.476
Liu Y, Zhou J, Zhang N, Wu X, Zhang Q, Zhang W, Li X, Tian Y. 2022. Two sensory neurons coordinate the
systemic mitochondrial stress response via GPCR signaling in C. elegans. *Dev Cell* **57**:2469-
2482.e5. doi:10.1016/j.devcel.2022.10.001
Love MI, Huber W, Anders S. 2014. Moderated estimation of fold change and dispersion for RNA-seq
data with DESeq2. *Genome Biol* **15**:550. doi:10.1186/s13059-014-0550-8
Lucas RJ, Hattar S, Takao M, Berson DM, Foster RG, Yau K-W. 2003. Diminished pupillary light reflex at
high irradiances in melanopsin-knockout mice. *Science* **299**:245–247.
doi:10.1126/science.1077293

Ma DK, Rothe M, Zheng S, Bhatla N, Pender CL, Menzel R, Horvitz HR. 2013. Cytochrome P450 drives a
HIF-regulated behavioral response to reoxygenation by C. elegans. *Science* **341**:554–558.
doi:10.1126/science.1235753
Ma Z, Horrocks J, Mir DA, Cox M, Ruzga M, Rollins J, Rogers AN. 2023. The integrated stress response
protects against ER stress but is not required for altered translation and lifespan from dietary
restriction in Caenorhabditis elegans. *Front Cell Dev Biol* **11**:1263344.
doi:10.3389/fcell.2023.1263344
Mahmoud BH, Ruvolo E, Hexsel CL, Liu Y, Owen MR, Kollias N, Lim HW, Hamzavi IH. 2010. Impact of
long-wavelength UVA and visible light on melanocompetent skin. *J Invest Dermatol* **130**:2092–
2097. doi:10.1038/jid.2010.95
Mir DA, Ma Z, Horrocks J, Rogers A. 2024. Stress-Induced Eukaryotic Translational Regulatory
Mechanisms. *J Clin Med Sci* **8**:1000277.
Monsalve GC, Yamamoto KR, Ward JD. 2019. A New Tool for Inducible Gene Expression in
Caenorhabditis elegans. *Genetics* **211**:419–430. doi:10.1534/genetics.118.301705
Nelson MD, Trojanowski NF, George-Raizen JB, Smith CJ, Yu C-C, Fang-Yen C, Raizen DM. 2013. The
neuropeptide NLP-22 regulates a sleep-like state in Caenorhabditis elegans. *Nat Commun*
4:2846. doi:10.1038/ncomms3846
Neve EPA, Ingelman-Sundberg M. 2010. Cytochrome P450 proteins: retention and distribution from the
endoplasmic reticulum. *Curr Opin Drug Discov Devel* **13**:78–85.
Pandey T, Ma DK. 2022. Stress-Induced Phenoptosis: Mechanistic Insights and Evolutionary Implications.
Biochemistry (Mosc) **87**:1504–1511. doi:10.1134/S0006297922120082
Reddy KC, Dunbar TL, Nargund AM, Haynes CM, Troemel ER. 2016. The C. elegans CCAAT-Enhancer-
Binding Protein Gamma Is Required for Surveillance Immunity. *Cell Rep* **14**:1581–1589.
doi:10.1016/j.celrep.2016.01.055
Schuch AP, Moreno NC, Schuch NJ, Menck CFM, Garcia CCM. 2017. Sunlight damage to cellular DNA:
Focus on oxidatively generated lesions. *Free Radic Biol Med* **107**:110–124.
doi:10.1016/j.freeradbiomed.2017.01.029
Shi Y, Zhang J, Li X, Han Y, Guan J, Li Yilin, Shen J, Tzvetanov T, Yang D, Luo X, Yao Y, Chu Z, Wu T, Chen Z,
Miao Y, Li Yufei, Wang Q, Hu J, Meng J, Liao X, Zhou Y, Tao L, Ma Y, Chen J, Zhang M, Liu R, Mi Y,
Bao J, Li Z, Chen X, Xue T. 2024. Non-image-forming photoreceptors improve visual orientation
selectivity and image perception. *Neuron* S0896-6273(24)00840–7.
doi:10.1016/j.neuron.2024.11.015
Sinha A, Rae R, Iatsenko I, Sommer RJ. 2012. System wide analysis of the evolution of innate immunity in
the nematode model species Caenorhabditis elegans and Pristionchus pacificus. *PLoS One*
7:e44255. doi:10.1371/journal.pone.0044255
Sinha NK, McKenney C, Yeow ZY, Li JJ, Nam KH, Yaron-Barir TM, Johnson JL, Huntsman EM, Cantley LC,
Ordureau A, Regot S, Green R. 2024. The ribotoxic stress response drives UV-mediated cell
death. *Cell* **187**:3652-3670.e40. doi:10.1016/j.cell.2024.05.018
Stringham EG, Dixon DK, Jones D, Candido EP. 1992. Temporal and spatial expression patterns of the
small heat shock (hsp16) genes in transgenic Caenorhabditis elegans. *Mol Biol Cell* **3**:221–233.
doi:10.1091/mbc.3.2.221
Troemel ER, Chu SW, Reinke V, Lee SS, Ausubel FM, Kim DH. 2006. p38 MAPK regulates expression of
immune response genes and contributes to longevity in C. elegans. *PLoS Genet* **2**:e183.
doi:10.1371/journal.pgen.0020183
Van der Auwera P, Frooninckx L, Buscemi K, Vance RT, Watteyne J, Mirabeau O, Temmerman L, De Haes
W, Fancsalszky L, Gottschalk A, Raizen DM, Nelson MD, Schoofs L, Beets I. 2020. RPamide
neuropeptides NLP-22 and NLP-2 act through GnRH-like receptors to promote sleep and
wakefulness in C. elegans. *Sci Rep* **10**:9929. doi:10.1038/s41598-020-66536-2

Van Gelder RN. 2008. Non-visual photoreception: sensing light without sight. *Curr Biol* **18**:R38-39.
doi:10.1016/j.cub.2007.11.027
Wang C, Long Y, Wang B, Zhang C, Ma DK. 2023. GPCR signaling regulates severe stress-induced
organismic death in Caenorhabditis elegans. *Aging Cell* **22**:e13735. doi:10.1111/acel.13735
Wei X, Potter CJ, Luo L, Shen K. 2012. Controlling gene expression with the Q repressible binary
expression system in Caenorhabditis elegans. *Nat Methods* **9**:391–395. doi:10.1038/nmeth.1929
Wong D, Bazopoulou D, Pujol N, Tavernarakis N, Ewbank JJ. 2007. Genome-wide investigation reveals
pathogen-specific and shared signatures in the response of Caenorhabditis elegans to infection.
Genome Biol **8**:R194. doi:10.1186/gb-2007-8-9-r194
Zhang B, Gong J, Zhang W, Xiao R, Liu J, Xu XZS. 2018. Brain-gut communications via distinct
neuroendocrine signals bidirectionally regulate longevity in C. elegans. *Genes Dev* **32**:258–270.
doi:10.1101/gad.309625.117
691