Neuronal Detection Triggers Systemic Digestive Shutdown in Response to Adverse Food Sources

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Summary

The ability to sense and adapt to adverse food conditions is essential for survival across species, but the detailed mechanisms of neuron-digestive crosstalk in food sensing and adaptation remain poorly understood. This study identifies a novel mechanism by which animals detect unfavorable food sources through olfactory neurons and initiate a systemic response to shut down digestion, thus safeguarding against potential harm. Specifically, we demonstrate that NSY-1, expressed in AWC olfactory neurons, detects *Staphylococcus saprophyticus* (SS) as an unfavorable food source, prompting the animal to avoid and halt digestion of SS. Upon detection, the animals activate the AWC^{OFF} neural circuit, leading to a systemic digestive shutdown, which is mediated by NSY-1-dependent STR-130. Additionally, NSY-1 mutation triggers the production of insulin peptides, including INS-23, which interact with the DAF-2 receptor to modulate SS digestion and affects the expression of intestinal BCF-1. These findings uncover a crucial survival strategy through neuron-digestive crosstalk, where the NSY-1 pathway in AWC neurons orchestrates food evaluation and initiates digestive shutdown to adapt effectively to harmful food sources.

Introduction

Food is a source of essential nutrients and also poses a risk of lethal toxins and pathogens. Animals, including humans, must respond to various food sources to ensure survival. The ability to detect and adapt to adverse food conditions is crucial for the survival of many species. Various sensory mechanisms have evolved to monitor food quality by detecting beneficial and harmful substances, include olfactory (Fiala, 2007; McLachlan et al., 2022; Sengupta et al., 1996), gustatory (Avery et al., 2021; Hukema et al., 2006; Scott, 2018), and gut chemosensory systems (Bargmann, 2006). Food allergies serve as a biological food quality control system, offering protection and benefits by promoting food avoidance behavior (Florsheim et al., 2021). Research by Plum et al. (Plum et al., 2023) and Florsheim et al. (Florsheim et al., 2023) provides evidence that the immune system's allergic response communicates with the brain in mice, leading to food avoidance. This avoidance behavior acts as a defense strategy, reducing the risk of exposure to harmful substances, including allergens.

The digestive system functions by transporting food through the gastrointestinal (GI) tract, where it is broken down into molecules that can be absorbed and utilized by the body's cells. Thus, shutdown of digestion may serve as a mechanism for eliminating indigestible or harmful substances, acting as a protective system in animals to avoid adverse food. Despite this, the interaction between neuronal food detection and intestinal digestion, particularly in assessing and adapting to harmful food, remains inadequately understood.

The free-living nematode *Caenorhabditis elegans* thrives in organic-rich environments where it encounters a variety of microorganisms as food (Felix and Braendle, 2010; Samuel et al., 2016; Schulenburg and Felix, 2017). *C. elegans* has evolved mechanisms to sense bacterial presence and food quality, which influence its feeding behaviors and digestive processes to adapt to its environment. Previous research has identified heat-killed *E. coli* as low-quality food, which the nematode avoids using its food-quality evaluation systems, such as the FAD-ATP-TORC1-ELT-2 pathway (Qi et al., 2017) and the UPR^{ER}–immunity pathway (Liu et al., 2024). Additionally, we have found that certain bacteria, like

Staphylococcus saprophyticus (SS), are classified as inedible, leading to shutting down digestion and stunted growth in the nematodes (Geng et al., 2022). However, we still need to determine whether SS represents harmful food for *C. elegans* and how the nematode senses SS and shuts down digestion to reject it. It is hypothesized that *C. elegans* may detect or assess inedible food, such as SS, and subsequently halt digestion as a survival strategy. This suggests that the cooperation between food sensing and digestive systems could form a systemic food quality control mechanism in animals, aimed at minimizing the adverse effects of harmful food.

In this study, we developed a model in *C. elegans* to investigate responses to harmful food and explored how the nematodes sense and avoid ingesting such food by shutting down their digestive systems. We identified a food quality control mechanism involving communication between neurons and the digestive system. This mechanism functions as a defense strategy to minimize the adverse effects of harmful food environments on the animals.

Results

Shutting Down Digestion as a Protective Mechanism for Survival in Larval *C. elegans*

Previous studies have shown that *Caenorhabditis elegans* cannot digest *Staphylococcus saprophyticus* (SS), which prevents their development (Figure 1A). In natural environments, *C. elegans* rely on various bacteria for nutrition and growth. However, SS is not a viable food source for *C. elegans*. Larval arrest, such as the dauer stage, serves as an adaptive mechanism for survival under unfavorable conditions, including limited food availability or extreme temperatures. We hypothesize that *C. elegans* can sense or evaluate inedible food, such as SS, and subsequently shut down their digestion to arrest development as a protective survival strategy (Figure 1B).

Our previous research demonstrated that *C. elegans* can assess and avoid low-quality food, like heat-killed *E. coli*, to adapt to nutrient-deficient conditions (Liu et al., 2024; Qi et al., 2017). To determine if *C. elegans* also detect SS as an unfavorable food source, we conducted two behavioral assays: food dwelling/avoidance and food

choice (Qi et al., 2017). In the food dwelling/avoidance assay, larval-stage animals

exhibited strong discrimination against SS compared to the standard food, OP50

(Figure 1C). In the food choice assay, the animals preferred OP50 over low-quality

food such as heat-killed *E. coli* (Figure S1A) or SS (Figure 1D). However, they could

not distinguish between heat-killed *E. coli* and SS (Figure S1B). These results suggest

that SS acts as an unfavorable food that *C. elegans* can detect and avoid.

In response to starvation, L1 larvae can enter a state of developmental arrest, pausing

their growth to survive (Baugh and Sternberg, 2006). To test whether *C. elegans* shut

down digestion of SS as a protective strategy upon sensing unfavorable food, we

performed a survival assay on L1 larvae fed with SS. We found that larvae unable to

digest SS still survived under SS feeding conditions (Figure S1C), similar to larvae

under L1 starvation. This suggests that shutting down digestion may be a protective

mechanism in larvae under SS feeding conditions.

Previously, we observed that activating larval digestion with heat-killed *E. coli* or *E.*

coli cell wall peptidoglycan (PGN) enabled the digestion of SS as food (Hao et al.,

2024). Additionally, when animals reached the L2 stage on a normal OP50 diet, they

could utilize SS as a food source to support growth (Figure S1D). These findings

suggest that once the digestive system is activated, *C. elegans* no longer detect SS as

unfavorable, leading to digestion. If SS is indeed an unfavorable or toxic food for *C.*

elegans, digesting it could result in physiological defects. We measured the lifespan

of L4 stage animals fed with SS or OP50. We found that SS consumption shortened

their lifespan (Figure 1E-F), indicating a cost associated with digesting unfavorable or

toxic food.

In conclusion, our data suggest that larval-stage *C. elegans* can sense and evaluate SS

as an unfavorable food source, leading to the shutdown of digestion to avoid

consumption, thereby protecting them and allowing adaptation to an unfavorable food

environment.

C. elegans Sense SS and Shut Down Digestion through NSY-1

We speculated that key factors in *C. elegans* are involved in sensing *Staphylococcus*

saprophyticus (SS) and shutting down its digestion. If these factors are mutated, the

animals would fail to detect SS as an unfavorable food source and would utilize it

(Figure S2A). To identify these factors, we conducted an unbiased forward genetic

screen to find mutant animals that cannot sense SS, thereby allowing its digestion and

supporting growth. One of the mutant alleles identified, *ylf6*, could digest SS and

exhibited a growth phenotype under SS feeding conditions (Figure S2B).

Whole-genome deep sequencing revealed that *ylf6* carries two mutations in the *nsy-1*

gene (H929Y, Q1191*) (Figure S2C).

To confirm that *nsy-1* is essential for shutting down SS digestion, we used an

independent *nsy-1* mutant allele, *ag3*, and found that *nsy-1(ag3)* mutants also digested

SS (Figure 2A). To determine whether *nsy-1* is crucial for sensing SS, we performed

two behavioral assays: food dwelling/avoidance and food choice. In the food

dwelling/avoidance assay, larval stage *nsy-1* mutant animals showed reduced

discrimination against SS compared to wild-type N2 animals (Figure 2B). In contrast

to wild-type N2 animals, *nsy-1* mutants preferred SS when given a choice between

two poor-quality foods, heat-killed *E. coli* and SS (Figure 2C, Figure S1B). These

results suggest that *nsy-1* is essential for *C. elegans* to sense and avoid SS.

Next, we examined whether larvae that cannot sense SS and do not shut down

digestion can adapt to SS environments. We measured the survival rate of *nsy-1*

mutants under SS feeding conditions and found that these mutants had a higher

mortality rate (Figure 2D).

Overall, these results indicate that *C. elegans* sense and detect unfavorable food, such

as SS, through *nsy-1*, and subsequently shut down digestion to protect themselves and

enhance survival.

NSY-1 Functions in AWC Neurons to Shut Down SS Digestion

The *nsy-1* gene in *C. elegans* encodes a MAP kinase kinase kinase (MAPKKK) that

operates in the AWC neurons (Kim et al., 2002; Sagasti et al., 2001), which are

essential for chemotaxis and odor sensation. The primary role of *nsy-1* in AWC

neurons is to regulate the asymmetric expression of odorant receptors, contributing to

neuronal asymmetry and diversity (Chuang et al., 2007; Sagasti et al., 2001). We

hypothesized that the shutdown of SS digestion in *C. elegans* is mediated by *nsy-1*

function in AWC neurons.

Firstly, we constructed a P*nsy-1*::GFP reporter strain and confirmed that *nsy-1* is expressed in the AWC neurons (Figure 3A). Secondly, we expressed *nsy-1* in the AWC neurons of *nsy-1* mutant animals and observed that the transgenic animals rescued the indigestion phenotype (Figure 3B). This indicates that *nsy-1* functions in AWC neurons to shut down SS digestion. Thirdly, we used CRISPR to construct a mutant strain that knocks out *nsy-1* specifically in AWC neurons (Figure S3). We found that *nsy-1* knockout in AWC neurons also resulted in the shutdown of SS digestion (Figure 3C).

These results collectively suggest that NSY-1 is functional in AWC neurons and is crucial for shutting down SS digestion in *C. elegans*.

AWC Neurons Exhibit OFF State in Sensing SS Food

In *C. elegans*, the expression of the *str-2* gene in AWC neurons indicates the ON state (AWC^{ON}) (Sagasti et al., 2001), which is associated with high cGMP levels and lower calcium activity, enabling the neuron to respond to specific odors. Conversely, the absence of *str-2* expression marks the OFF state (AWC^{OFF}), characterized by different odor responses, low cGMP levels, and higher calcium activity (Troemel et al., 1999). We aimed to investigate (1) whether AWC neurons exhibit different states under normal food (*E. coli* OP50) versus unfavorable food (SS) conditions and (2) whether the state of AWC neurons affects the ability of *C. elegans* to digest SS.

Using *str-2*::GFP as a marker for AWC neuron states (Troemel et al., 1999), we found that wild-type animals feeding on normal OP50 food typically exhibit one AWC^{OFF} and one AWC^{ON} neuron. However, when feeding on SS, the proportion of animals with the AWC^{OFF} state increased, with approximately 50% of animals exhibiting two AWC^{OFF} neurons (Figure 3D, E, F).

In *nsy-1* mutant animals feeding on OP50, *str-2*::GFP is expressed in both AWC neurons ($2AWC^{ON}$), consistent with previous studies (Chuang and Bargmann, 2005; Chuang et al., 2007; Sagasti et al., 2001; Troemel et al., 1999) (Figure 3D, E). Notably, both AWC neurons remained in the AWC^{ON} state in *nsy-1* mutants feeding on SS (Figure 3D, E). These results suggest that SS feeding induces an AWC^{OFF} state in wild-type animals, while the *nsy-1* mutation promotes an AWC^{ON} state even under

SS feeding conditions. This implies that the AWC^{OFF} state may inhibit SS digestion,

whereas the AWC^{ON} state promotes it.

The TIR-1-NSY-1-SEK-1-MAPK pathway plays a crucial role in regulating the

asymmetric AWC cell fate decision. Previous studies have shown that *str-2*::GFP

expression in both AWC cells (2AWC^{ON} phenotype) occurs in *tir-1*, *nsy-1*, and *sek-1*

mutant animals (Chuang and Bargmann, 2005; Sagasti et al., 2001; Troemel et al.,

1999). We found that *tir-1* mutant can grow under SS feeding conditions (Figure 3G),

indicating that *tir-1* mutant can digest SS similarly to *nsy-1* mutants. This

demonstrates that the AWC^{ON} state promotes SS digestion.

Overall, our data suggest that the state of AWC neurons is critical for sensing food in

C. elegans. When sensing SS food, animals exhibit an AWC^{OFF} state, which shuts

down digestion. Conversely, the AWC^{ON} state promotes the digestion of SS.

NSY-1 Shuts Down SS Digestion through Induction of STR-130

We have demonstrated that NSY-1 in AWC neurons detects unfavorable food and

shuts down digestion (Figure 3). To investigate the genes regulated by NSY-1 in

response to SS and their impact on SS digestion, we conducted a transcriptomic

analysis on L1 larval animals fed with normal food (OP50) or unfavorable food (SS)

for a short duration (4 hours). We speculated that some genes induced by SS food are

dependent on NSY-1 (Figure 4A), and their induction aids in shutting down SS

digestion.

RNA-seq data analysis revealed 304 NSY-1-dependent candidate genes responding to

SS (Figure 4B, Table S1). Enrichment analysis (Figure S4A, Table S2) of these

candidate genes showed mainly associations with biotic stimulus, defense responses,

xenobiotic stimulus, suggesting that NSY-1 positively regulates stress response

pathways to protect animals under harmful food, SS, feeding conditions. Moreover,

we found that sensory perception related genes (*sra-32, str-87, str-112, str-130,*

str-160, str-230) (Figure S4A, Table S2) were also enriched, with many genes being

G protein-coupled receptors (GPCRs), which mediate odor sensing (Buck and Axel,

1991). Our study indicated that wild-type *C. elegans* respond to SS by regulating

olfactory AWC neurons (Figure 3D, E), potentially influenced by GPCRs. We further

analyzed the dependence of these enriched GPCRs on NSY-1 under SS feeding

conditions (Figure S4B) and found that *str-130* is significantly upregulated in
response to SS, with its function strong being NSY-1 dependent (Figure 4C).

It has been shown that *str-130* is expressed in AWC^{OFF} neurons, based on transgenic
GFP reporter strains, *str-130p*::GFP (Vidal et al., 2018). Our data also show that
str-130 expression is induced in wild-type animals fed with SS (Figure 4C), where
AWC neurons exhibit the AWC^{OFF} state (Figure 3D, E). Therefore, it is possible that
the high expression of *str-130*, regulated by *nsy-1*, alters the AWC state and inhibits
SS digestion.

Firstly, we found that knockdown of *str-130* in wild-type animals promoted SS
digestion, thereby supporting animal growth (Figure 4D), and the proportion of
animals with two AWC^{OFF} neurons decreased (Figure 4E). Secondly, we found that
overexpression of *str-130* in *nsy-1* mutant animals inhibited SS digestion, thereby
slowing animal growth (Figure 4F), and the proportion of animals with two AWC^{OFF}
neurons increased (Figure 4G). These results demonstrate that NSY-1 promotes the
AWC^{OFF} state by inducing *str-130* expression, which in turn inhibits SS digestion in
C. elegans.

NSY-1 Mutation Promotes SS Digestion by Inducing Insulin Signaling

NSY-1 mutation promotes the digestion of unfavorable food, such as SS, and supports
C. elegans growth (Figure 2A). We hypothesize that, in addition to upregulating
certain genes, such as *str-130*, to inhibit SS digestion, NSY-1 may also suppress
certain genes to prevent nematodes from utilizing SS (Figure 5A). One possibility is
that some genes, induced by the *nsy-1* mutation under SS feeding conditions could
facilitate SS digestion in the *nsy-1* mutant (Figure 5A).

Our RNA-seq analysis identified 308+46=354 genes that are induced by the *nsy-1*
mutation under SS feeding conditions (Figure 5B, Table S3). However, among these
354 genes, 46 genes can also be induced in wild-type animals fed with SS, suggesting
that these 46 genes may not be involved in digesting SS in *nsy-1* mutants. Therefore,
the 308 candidate genes induced by the *nsy-1* mutation under SS feeding conditions
could potentially promote animals to digest SS.

Enrichment analysis revealed that genes related to extracellular functions, such as
insulin-related genes, are induced in *nsy-1* mutant animals (Figure S5A, Table S4).

Further analysis of insulin-related genes from the RNA-seq data showed that *ins-23* is predominantly induced in *nsy-1* mutant animals (Figure S5B), suggesting its potential role in promoting SS digestion. We found that knockdown of *ins-23* in *nsy-1* mutants inhibited SS digestion (Figure 5D). These results demonstrate that the *nsy-1* mutation induces the insulin peptide *ins-23*, which promotes SS digestion.

The insulin/insulin-like growth factor signaling (IIS) pathway, particularly through the DAF-2 receptor, integrates nutritional signals to regulate various behavioral and physiological responses related to food (Kodama et al., 2006; Ryu et al., 2018). It has been shown that INS-23 acts as an antagonist for the DAF-2 receptor to promote larval diapause (Matsunaga et al., 2018). To test whether *ins-23* induction in *nsy-1* mutants promotes SS digestion through its receptor, DAF-2, we constructed a *nsy-1; daf-2* double mutant. We found that the SS digestion ability of the *nsy-1* mutant was inhibited by the *daf-2* mutation. This suggests that the *nsy-1* mutation induces the insulin peptide *ins-23*, which promotes SS digestion through its potential receptor, DAF-2.

NSY-1 Mutation Promotes SS Digestion through Regulation of Intestinal BCF-1

In our previous study, we found that heat-killed *E. coli* promotes SS digestion in *C. elegans* (Geng et al., 2022), a process requiring intestinal BCF-1 (Hao et al., 2024). In the absence of BCF-1, the digestive capability of the animals is significantly reduced (Hao et al., 2024). This led us to investigate whether NSY-1 in AWC neurons regulates intestinal *bcf-1* expression.

Firstly, we used a *bcf-1*::GFP reporter to measure *bcf-1* expression in *nsy-1* mutant animals. We found that mutation of *nsy-1* induced *bcf-1* expression in animals fed either SS or OP50 food (Figure 6A). Additionally, we confirmed that *nsy-1* mutation in AWC neurons also induced intestinal *bcf-1* expression under SS feeding conditions (Figure 6B). This data indicates that NSY-1 in AWC neurons inhibits intestinal *bcf-1* expression, implying that *nsy-1* mutation promotes SS digestion through BCF-1.

Next, we constructed a *nsy-1; bcf-1* double mutant and analyzed the growth of these animals on SS. We found that the digestive ability of *nsy-1* mutants was inhibited by the mutation of *bcf-1* (Figure 6C). Together, our data suggest that the increased

digestion ability in *nsy-1* mutant animals is dependent on the intestinal digestion

factor BCF-1.

We then asked how *nsy-1* regulates intestinal *bcf-1* expression. Since *nsy-1* mutation

induces the insulin peptide *ins-23*, which promotes SS digestion, we tested whether

the induction of intestinal *bcf-1* by *nsy-1* mutation is also mediated through INS-23.

We found that the *bcf-1*::GFP level decreased in *nsy-1* mutant animals following

ins-23 RNAi treatment (Figure 6D). This suggests that *nsy-1* mutation activates *bcf-1*

expression in the intestine, which requires INS-23.

It has been reported that DAF-2 acts as the receptor for INS-23 (Matsunaga et al.,

2018). Therefore, we also investigated whether INS-23-induced digestion in

nsy-1(ag3) is mediated through its receptor, DAF-2. Our findings revealed that the

food digestion phenotype of *nsy-1(ag3)* was impaired by mutations in *daf-2* (Figure

6E), indicating that the enhanced digestion observed in *nsy-1(ag3)* mutants also relies

on INS-23's receptor, DAF-2.

Overall, our data indicated that *nsy-1* mutation promotes SS digestion through

inducing intestinal *bcf-1*, which is regulated by INS-23.

Discussion

This study in *Caenorhabditis elegan*s reveals a neural-digestive mechanism for

evaluating harmful food (Figure 7). The olfactory neuron-expressed NSY-1 protein

detects *Staphylococcus saprophyticus* (SS) as unsafe food, triggering a digestive

shutdown via the AWC^{OFF} neural circuit and the NSY-1-dependent STR-130.

Mutations in NSY-1 lead to SS digestion, activating the insulin/IGF-1 signaling (IIS)

pathway and BCF-1 expression. These findings highlight a food quality evaluation

strategy where neurons communicate with the digestive system to assess food safety,

providing insights into how animals adapt to toxic food environments.

The identification of NSY-1 in AWC olfactory neurons as a key player in detecting

Staphylococcus saprophyticus (SS) and initiating digestive shutdown is particularly

intriguing. NSY-1, a MAP kinase (MAPKKK), is known to regulate the asymmetric

expression of odorant receptors, contributing to neuronal asymmetry and diversity

(Chuang and Bargmann, 2005; Chuang et al., 2007; Sagasti et al., 2001; Troemel et al., 1999). Previous research has demonstrated that AWC neurons are pivotal in chemotaxis and sensory processing (Bargmann et al., 1993; Troemel et al., 1997; Wes and Bargmann, 2001) . Our findings extend its function to include food quality assessment, showing that NSY-1 can trigger a digestive shutdown via the AWC^{OFF} neural circuit. This highlights a sophisticated system where olfactory inputs directly influence digestive processes. It suggests that the olfactory system, beyond its primary function of detecting odors, may also play a significant role in monitoring food quality and signaling the digestive system.

This neural circuit appears to be a crucial component of a systemic food quality control mechanism, allowing animals to adapt effectively to harmful food sources. The state of AWC neurons (AWC^{ON} or AWC^{OFF}) directly influences the animal's ability to digest SS, with the AWC^{OFF} state inhibiting digestion and the AWC^{ON} state promoting it. The finding that activation of the AWC^{OFF} neural circuit leads to a systemic digestive shutdown mediated by NSY-1-dependent GPCR(STR-130) is another notable advancement. GPCRs are well-known for their roles in sensory perception (Julius and Nathans, 2012; Troemel et al., 1995). Our results suggested that GPCR STR-130 play a role in shutting down digestive processes though maintaining AWC^{OFF} states for evaluating harmful food.

Our study underscores the critical role of insulin signaling pathways in mediating the effects of neuronal detection on intestinal functions. Upon detection of SS by AWC neurons, NSY-1 inhibits the expression of insulin-like peptides, particularly INS-23. These peptides interact with the DAF-2 receptor in the gut, influencing the expression of BCF-1, a key regulatory factor in digestion (Hao et al., 2024). Once ins-23 was inhibited by neuronal NSY-1, the intestinal BCF-1 level is also reduced, which in turn shutdown digestion. We found that the digestive ability of *nsy-1* mutants was totally inhibited by the mutation of *bcf-1* (Figure 6C), suggest that the increased digestion ability in *nsy-1* mutant animals is mainly dependent on the intestinal digestion factor BCF-1. This regulatory cascade highlights the intricate link between neuronal signals and gut responses, ensuring an adaptive reaction to harmful food. We speculated that except INS-23, there should be other factors as signaling regulated by neuronal NSY-1 to inhibits intestinal digestion factor BCF-1 for digestion shutdown.

Future studies should focus on delineating the precise molecular pathways linking NSY-1 signaling in AWC neurons to digestion regulation in the gut. Identifying the role of other sensory neurons in food quality assessment and their interactions with

the digestive system may uncover new facets of neuron-gut communication and adaptive responses.

In summary, our study reveals a sophisticated mechanism in *C. elegans* that integrates neuronal detection of harmful food sources with systemic digestive responses. This neuron-digestive crosstalk is crucial for maintaining organismal homeostasis and survival in the presence of toxic food sources. The findings suggest that similar pathways may exist in other species, including humans, providing a foundation for future research on food safety, toxin avoidance, and the neural regulation of digestive processes. This has important implications for public health, as it illuminates the biological mechanisms underlying foodborne illness and the body's defenses against such threats.

Author Contributions

Y. L and G.T performed experiments, analyzed data and wrote the paper; Z. W performed phenotype analysis; J. Z performed EMS screen; H. L analyzed EMS sequencing data; S. Z supervised some experiments; Z. S supervised some experiments, wrote and revised this paper; B.Q. supervised this study, and wrote the paper with inputs from G. T and Y. L.

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Declaration of interests

The authors declare no competing interests.

 Main Figure Legends:

Figure 1. *C. elegans* **shuts down its digestion for survival when fed harmful food,**

specifically *Staphylococcus saprophyticus* **(SS).**

(A) Microscopic images showing worms fed with SS arrested at the L1 stage three

days after hatching.

(B) Schematic model illustrating our hypothesis: *C. elegans* can sense or evaluate

inedible food, such as SS, and subsequently shut down their digestion to arrest

development as a protective survival strategy.

(C) Schematic drawing and quantitative data of the food dwelling/avoidance assay.

Yellow circles indicate the food spot for OP50 or SS bacteria, respectively. The

animals were scored at the indicated times after L1 worms were placed on the food

spot. The red point indicates the position of each worm. Data are represented as mean

± SD. Bar = 1000 μm. ***$p < 0.001$; **$p < 0.01$ by Student's t-test.

(D) Schematic drawing, microscopic images, and quantitative data of the food choice

assay. L1 worms were placed at the center spot (origin). OP50 (yellow) and SS (blue)

bacteria were placed on opposite sides of the plate. The red point indicates the

position of each worm. The percentage of worms on each spot was calculated at the

indicated times. Data are represented as mean ± SD. Bar = 1000 μm. ****$p < 0.0001$;

**$p < 0.01$ by Student's t-test.

(E-F) Schematic drawing and quantitative data of the lifespan of animals fed with SS

or OP50. L1 worms were seeded onto OP50 and grown to the L4 stage. L4 worms

were then moved to SS or OP50 food to measure lifespan. **$p < 0.01$ by log-rank test.

All data are representative of at least three independent experiments.

Figure 2. *C. elegans* **senses SS and shuts down digestion through NSY-1.**

(A) Developmental phenotype of wild-type N2 and *nsy-1(ag3)* mutant worms fed

with SS bacteria. Data are represented as mean ± SD. Bar = 200 μm.. ****$p < 0.0001$

by Student's t-test.

(B) Schematic drawing, microscopic images, and quantitative data of the food

dwelling/avoidance assay. Yellow circles indicate the food spot for SS bacteria. The

animals were scored 4 hours after L1 worms were placed on the food spot. The blue

circle indicates the edge of the bacterial lawn, and the red point indicates the position

of each worm. Data are represented as mean ± SD. Bar = 1000 μm. **$p < 0.01$ by

Student's t-test.

(C) Schematic drawing, microscopic images, and quantitative data of the food choice

assay. L1 *nsy-1(ag3)* worms were placed at the center spot (origin). Heat-killed OP50

(yellow) and SS (blue) bacteria were placed on opposite sides of the plate. The red point indicates the position of each worm. The percentage of worms on each spot was calculated at the indicated times. Data are represented as mean ± SD. Bar = 1000 μm. **p < 0.01; ***p < 0.001 by Student's t-test.

(D) Survival curves of wild-type N2 and *nsy-1(ag3)* mutant worms fed with SS bacteria. L4 worms, previously fed OP50 bacteria, were transferred to SS food to measure lifespan. ****p < 0.0001 by log-rank test.

All data are representative of at least three independent experiments.

Figure 3. NSY-1 plays a critical role in AWC neurons to inhibit SS digestion.

(A) Microscopic image showing the expression pattern of *nsy-1*. The head of an adult transgenic animal carrying *Pnsy-1::GFP* and *Podr-1::RFP* shows colocalization of *nsy-1* and *odr-1*. Bar = 20 μm.

(B) Developmental progression of *nsy-1(ag3)* mutant worms carrying *Podr-1::nsy-1::gfp* (AWC neuron-specific expression) grown on SS bacteria. Control animals are labeled with white stars, and animals carrying the transgenes (rescued animals) are labeled with yellow stars. Data are represented as mean ± SD. Bar = 200 μm. ****p < 0.0001 by Student's t-test.

(C) Developmental progression of wild-type N2 and AWC neuron-specific knockout *nsy-1* animals (AWC *nsy-1* KO) grown on SS bacteria. Data are represented as mean ± SD. Bar = 500 μm. ***p < 0.001 by Student's t-test.

(D) Microscopic images show *str-2::GFP*, a marker for AWC neuron states, in L1-staged wild-type and *nsy-1(ky397)* mutant worms grown on OP50 or SS bacteria for 6 hours. AWC neuron positions are highlighted with red and yellow arrows. Bar = 20 μm.

(E-F) Percentage of animals with different AWC neuron states. *nsy-1* mutation promotes an 2AWC^{ON} state under SS feeding conditions (E), with approximately 50% of animals exhibiting 2AWC^{OFF} neurons when feeding on SS (F). Data are represented as mean ± SD. ****p < 0.0001 by Student's t-test.

(G) Developmental progression of wild-type N2, *tir-1(qd4)*, and *nsy-1(ag3)* mutant worms grown on SS bacteria. Data are represented as mean ± SD. Bar = 200 μm. ****p < 0.0001 by Student's t-test.

All data are representative of at least three independent experiments.

Figure 4. NSY-1 inhibits animals from digesting SS by inducing *str-130*.

(A) Schematic illustration showing that "X" genes rely on NSY-1 to shut down SS

digestion. "X" genes induced by SS food are dependent on NSY-1, and their induction aids in shutting down SS digestion.

(B) Venn diagram showing the overlap of genes that respond to SS and rely on NSY-1. The number of genes is indicated in the diagram (also see Table S1).

(C) Transcriptome analysis showing *str-130* mRNA expression, which relies on NSY-1 in response to SS. Data are represented as mean ± SD. ****$p < 0.0001$; **$p < 0.01$; *$p < 0.05$ by Student's t-test.

(D) Developmental progression of wild-type animals treated with control RNAi or *str-130* RNAi grown on SS bacteria. Data are represented as mean ± SD. Bar = 200 μm. ****$p < 0.0001$ by Student's t-test.

(E) Microscopic images and quantitative data of AWC neuron states in L1 animals treated with control RNAi or *str-130* RNAi grown on SS bacteria. Data are represented as mean ± SD. Bar = 20 μm. ***$p < 0.001$ by Student's t-test (1AWC^{ON}/1AWC^{OFF}: control vs *str-130* RNAi).

(F) Developmental progression of *nsy-1(ag3)* mutant worms carrying *Pstr-130::str-130::mCherry* grown on SS bacteria. Control animals are labeled with white stars, and animals carrying transgenes are labeled with yellow stars. Data are represented as mean ± SD. Bar = 400 μm. ***$p < 0.001$ by Student's t-test.

(G) Microscopic images and quantitative data of AWC neuron states in L1 animals carrying *Pstr-130::str-130::mCherry*. Transgenic animals with overexpression of *str-130* (carrying *Pord-1::GFP* as a co-injection marker) show an increased 2AWC^{OFF} state. Data are represented as mean ± SD. Bar = 20 μm. ****$p < 0.001$ by Student's t-test (2AWC^{OFF}: Control vs Transgene).

All data are representative of at least three independent experiments.

Figure 5. NSY-1 mutation activates animals to digest SS by inducing insulin signaling.

(A) Schematic illustration showing that NSY-1 inhibits the expression of "Y" genes, which promote SS digestion. Some genes induced by the *nsy-1* mutation under SS feeding conditions could facilitate SS digestion in the *nsy-1* mutant.

(B) Venn diagram showing the overlap of genes that respond to SS but are limited by NSY-1. A total of 308 candidate genes induced by the *nsy-1* mutation under SS feeding conditions could potentially promote SS digestion.

(C) Transcriptome analysis showing that *ins-23* expression is induced in animals with the *nsy-1* mutation under SS feeding conditions. Data are represented as mean ± SD. **$p < 0.01$; n.s. not significant by Student's t-test.

(D) Developmental progression of *nsy-1(ag3)* mutant animals treated with control

RNAi or *ins-23* RNAi grown on SS bacteria. Data are represented as mean ± SD. Bar

= 500 μm. ****p < 0.0001 by Student's t-test.

(E) Developmental progression of *nsy-1(ag3), daf-2(e1370),* and

nsy-1(ag3);daf-2(e1370) double mutant animals grown on SS bacteria. Data are

represented as mean ± SD. Bar = 500 μm. ****p < 0.0001 by Student's t-test.

All data are representative of at least three independent experiments.

Figure 6. NSY-1 mutation promotes animals to digest SS through inducing

intestinal *bcf-1*.

(A) Microscopic images and quantitative data showing fluorescence of

Pbcf-1::bcf-1::GFP in L1-staged wild-type (WT) and *nsy-1(ag3)* mutant animals fed

with OP50 or SS bacteria for 6 hours. Data are represented as mean ± SD. Bar = 100

μm. ****p < 0.0001 by Student's t-test.

(B) Microscopic images and quantitative data showing fluorescence of

Pbcf-1::bcf-1::GFP in L1-staged wild-type and AWC *nsy-1* KO mutant (AWC

neuron-specific knockout *nsy-1* animals) fed with SS bacteria for 6 hours. Data are

represented as mean ± SD. Bar = 50 μm. ***p < 0.001 by Student's t-test.

(C) Developmental progression of wild-type N2, *nsy-1(ag3), bcf-1(ok2599),* and

nsy-1(ag3);bcf-1(ok2599) double mutant animals grown on SS bacteria. Data are

represented as mean ± SD. Bar = 200 μm. ****p < 0.0001; n.s. not significant by

Student's t-test.

(D) Microscopic images and quantitative data showing fluorescence of

Pbcf-1::bcf-1::GFP in *nsy-1(ag3)* mutant animals treated with control RNAi or *ins-23*

RNAi under normal RNAi feeding conditions. Data are represented as mean ± SD.

Bar = 200 μm. ****p < 0.0001 by Student's t-test.

All data are representative of at least three independent experiments.

Figure 7. A model reveals a neural-digestive mechanism for evaluating harmful

food.

(A) AWC neuron-expressed NSY-1 detects *Staphylococcus saprophyticus* (SS) as

harmful food and shuts down digestion by inducing the AWC^{OFF} neural circuit and

NSY-1-dependent STR-130. This mechanism protects the animals and helps them

avoid harmful food.

(B) Mutations in NSY-1 lead to SS digestion by activating the insulin/IGF-1 signaling

(IIS) pathway and BCF-1 expression, thereby reducing the animals' ability to avoid

harmful food and decreasing their protection.

Supplemental Figure Legends:

Figure S1. SS is harmful food that animals cannot digest. Related to Figure 1.

(A) Schematic drawing, microscopic images, and quantitative data from the food choice assay. L1 worms were placed at the center spot (origin). OP50 (yellow) and heat-killed OP50 (blue) bacteria were positioned on opposite sides of the plate. The red point indicates the position of each worm. The percentage of worms on each spot was calculated at the indicated times. Data are represented as mean ± SD. Bar = 1000 μm. ****$p < 0.0001$; ***$p < 0.001$; **$p < 0.01$ by Student's t-test.

(B) Schematic drawing, microscopic images, and quantitative data from the food choice assay. L1 worms were placed at the center spot (origin). Heat-killed OP50 (blue) and SS (red) bacteria were positioned on opposite sides of the plate. The red point indicates the position of each worm. The percentage of worms on each spot was calculated at the indicated times. Data are represented as mean ± SD. Bar = 1000 μm. ****$p < 0.0001$; n.s. not significant by Student's t-test.

(C) Schematic drawing and quantitative data of the lifespan of animals fed with SS or OP50. L1 worms were seeded on plates with no food (NGM) or SS bacteria to measure lifespan. n.s. not significant by log-rank test.

(D) Schematic drawing and quantitative data of the developmental progression of wild-type N2 under different feeding conditions. L1 animals were seeded onto OP50 plates and grown to the L2 stage. L2 animals were then transferred to OP50, SS, or no food (NGM) plates to measure worm length at the indicated time points.

All data are representative of at least three independent experiments.

Figure S2. EMS screen to identify genes involved in shutting down digestion of SS. Related to Figure 2.

(A) Schematic illustration of the EMS screen strategy to identify "Y" genes involved in shutting down digestion after sensing SS. In mutants with defects in "Y" genes, digestion of SS is restored, allowing the mutants to grow on SS.

(B) Developmental phenotype of wild-type N2 and *ylf6* mutant worms fed with SS bacteria. Bar = 200 μm.

(C) Schematic drawing showing the mutation sites in *nsy-1(ylf6)* and *nsy-1(ag3).*

Figure S3. Construction of *nsy-1* specific knockout in AWC neurons using CRISPR-Cas9. Related to Figure 3.

Representative DNA gels showing NheI digestion of PCR-amplified genomic DNA extracted from wild-type (WT) worms and worms with *nsy-1*-specific knockout in AWC neurons (*odr-1p::Cas9 + u6p::nsy-1-sg*).

Figure S4. *str-130* **is induced in wild-type in response to SS, dependent on NSY-1.**
(A) GO enrichment analysis of 304 NSY-1-dependent candidate genes responding to SS (Figure 4B, Table S2). Genes related to sensory perception (*sra-32, str-87, str-112, str-130, str-160, str-230*) are highlighted as enriched (red arrow).
(B) Relative mRNA expression levels of sensory perception-related genes (*sra-32, str-87, str-112, str-130, str-160, str-230*) extracted from RNA-seq data. These genes are induced in wild-type N2 animals in response to SS, but their expression is reduced in *nsy-1(ag3)* mutant animals under SS feeding conditions, indicating that the induction of these genes in wild-type in response to SS is dependent on NSY-1.

Figure S5. *nsy-1* **mutation induces the expression of insulin-related genes.**
Related to Figure 5.
(A) GO enrichment analysis of 308 genes induced by the nsy-1 mutation under SS feeding conditions (Figure 5B, Table S2).
(B) Relative mRNA expression levels of insulin-related genes (*ins-23, ins-22, ins-27, ins-24*) extracted from RNA-seq data. These genes are upregulated in *nsy-1(ag3)* mutant animals under SS feeding conditions, which may contribute to SS digestion in the *nsy-1* mutant.

Supplemental Table Legends:

Table S1. List of genes induced by SS food that are dependent on NSY-1. Related to Figure 4B.
Table S2. GO enrichment analysis of 304 NSY-1-dependent candidate genes responding to SS. Related to Figure S4A and 4B.
Table S3. List of genes induced in *nsy-1(ag3)* mutant animals feeding on SS. Related to Figure 5B.
Table S4. GO enrichment analysis of 308 genes induced by the nsy-1 mutation under SS feeding conditions. Related to Figure S5A and 5B.

Star Methods

609 **Resource Availability**
610
611 **Lead contact**
612 Further information and requests for reagents may be directed to the Lead contact Bin
613 Qi (qb@yun.edu.cn).
614
615 **Materials availability**
616 All reagents and strains generated by this study are available through request to the
617 lead contact with a completed Material Transfer Agreement.
618
619 **Data and code availability**
620 This paper does not report original code.
621 Any additional information required to reanalyze the data reported in this paper is
622 available from the lead contact upon request (qb@ynu.edu.cn).
623
624 **Experimental model and subject details**
625
626 *C. elegans* **strains and maintenance**
627 Nematode stocks were maintained on nematode growth medium (NGM) plates seeded
628 with bacteria (*E. coli* OP50) at 20˚C.
629 The following strains/alleles were obtained from the Caenorhabditis Genetics Center
630 (CGC) or as indicated:
631
1) The following strains were obtained from CGC:
N2 Bristol (wild-type control strain);
AU3: *nsy-1(ag3)*;
ZD101: *tir-1(qd4)*;
RB1971: *bcf-1(ok2599)*;
KU25: *pmk-1(km25)*;
KU4: *sek-1(km4)*;
CX3695: *str-2::gfp+lin-15(+)*; shared from Huanhu Zhu lab
CX4998: *str-2::gfp+lin-15(+);nsy-1(ky397)*; shared from Hongyun Tang lab
641
642 2) The following strains were obtained from published papers.
643   PHX4067: [*Pbcf-1::bcf-1::gfp::3xflag*](He et al., 2023);
644
3) **The following strains were constructed by this study:**

YNU238: *nsy-1(ylf6)*, EMS mutant;

YNU186: [*Pnsy-1::gfp;Podr-1::rfp*] was constructed by injecting plasmid *P*

nsy-1::nsy-1::gfp with *Podr-1::rfp* in N2 background;

YNU465: [*Podr-1::nsy-1::gfp;Podr-1::rfp;nsy-1(ag3)*] was constructed by inj

ecting plasmid *Podr-1::nsy-1::gfp* with *Podr-1::rfp* in *nsy-1(ag3)* background;

YNU491: AWC neuron specific knock out *nsy-1* strain was constructed by

injecting plasmid pDD162[P*odr-1::Cas9*+P*u6::nsy-1-sg*], *nsy-1* repair template

(synthesis from Tsingke), pDD162[P*eft-3::Cas9*+ P*u6::dpy-10-sg*], dpy-10 repair

template(synthesis from Tsingke) in PHX4067(P*bcf-1::bcf-1::gfp::3xflag*)

background.

YNU488: [*Pstr-130::str-130::mcherry;Podr-1::rfp;nsy-1(ag3)*] was constructe

d by injecting plasmid *Pstr-130::str-130::mcherry* with *Podr-1::rfp* in *nsy-1(ag3)*

background;

YNU189: *Pbcf-1::bcf-1::gfp::3xflag;nsy-1(ag3)* was constructed by crossing

PHX4067[*Pbcf-1::bcf-1::gfp::3xflag*] with AU3[*nsy-1(ag3)*];

YNU501: *nsy-1(ag3);bcf-1(ok2599)* double mutant was constructed by

crossing RB1971[*bcf-1(ok2599)*] with AU3[*nsy-1(ag3)*];

YNU517: *nsy-1(ag3);daf-2(e1370)* double mutant was constructed by crossing

CB1370[*daf-2(e1370)*] with AU3[*nsy-1(ag3)*];

YNU508: [*Pstr130::str-130::mcherry;Podr-1::rfp;nsy-1(ag3)*] was constructed

by injecting plasmid *Pstr130::str-130::mcherry* with *Podr-1::rfp* in

str-2::gfp+lin-15(+) background.

Bacteria Strains

E. coli-OP50 (from Caenorhabditis Genetics Center (CGC)), and *Staphylococcus.*

Saprophyticus (from ATCC) were cultured at 37°C in LB medium. A standard

overnight cultured bacteria was then spread onto each Nematode growth media

(NGM) plate.

Method Details

Generation of transgenic strains

1）To construct the *C. elegans* plasmid for expression of *nsy-1*, 1527bp promoter of

nsy-1 was inserted into the pPD95.77 vector. DNA plasmid mixture containing

P*nsy-1::GFP* (20ng/ul) and P*odr-1p::RFP*(50ng/ul) was injected into the gonads of

adult wild-type N2 animals.

2）To construct the *C. elegans* plasmid for expression of *nsy-1* in AWC neuron,

1348bp promoter of *odr-1* and genomic DNA of *nsy-1* was inserted into the pPD49.26

vector. DNA plasmid mixture containing P*odr-1::nsy-1::GFP* (20ng/ul) and

P*odr-1::RFP* (50ng/ul) was injected into the gonads of adult *nsy-1(ag3)*.

3）To construct the *C. elegans* plasmid for expression of *str-130*, 2000bp promoter of

str-130 and 1324bp genomic DNA of *str-130* was inserted into the pPD49.26-mcherry

vector. DNA plasmid mixture containing P*str-130::str-130::mcherry*(20ng/μl) and

P*odr-1::rfp* (50ng/μl) was injected into the gonads of adult

CX3695[*str-2::gfp+lin-15(+)*].

Generation *nsy-1* AWC neuron specific knock out strain and Genotyping.

To construct the *C. elegans* plasmid for knock out of *nsy-1* in AWC neuron,

600bp promoter of *eft-3* was replaced by 1348bp promoter of *odr-1* and *nsy-1* sgRNA

was also inserted into the same CRISPR-Cas9-sgRNA vector pDD162 (Dickinson et

al., 2013). The Cas9 target sites were designed via CRISPR design tool

(http://crispor.tefor.net/) and the sgRNA sequences was 5'-

GAATTTACGCGTTCGAGAAATGG-3'. Knockout strains were generated by

injecting 25ng/μl Cas9-sgRNA plasmid, 2μM repair template, co-injection markers

include 20ng/μl *dpy-10* Cas9-sgRNA plasmid and 2μM *dpy-10* repair template.

Worms were picked into 10 μl of worm lysis buffer (50 mM KCl,10 mM

Tris-HCl pH 8.0, 2.5 mM $MgCl_2$, 0.45% NP40, 0.45% Tween-20, 0.01% Gelactin, 0.2

mg/mL Proteinase K), quickly freeze-thaw three times using liquid nitrogen,

incubated it at 60°C for 90min and 95 °C for 20min. 1μl supernatant was taken and

performed for PCR analysis with the following primers:

nsy-1: forward 5′-CAAGAGGCAAGTGCAGCATA-3′, reverse

5′-TGACTGTCCCATGCTCTCAC-3′, then digested with NheI endonuclease

overnight and identified by DNA agarose electrophoresis.

Preparation of *Staphylococcus. Saprophyticus* (SS)

711 SS preparation was followed by our published protocol (Geng et al., 2022; Liu and Qi,

712 2023). Briefly, a standard overnight culture of SS (37°C in LB broth) was diluted into

713 fresh LB broth (1:100ratio). SS was then spread onto each NGM plate when the

714 diluted bacteria grew to OD600 = 0.5.

Analysis of worm's growth in SS bacteria

717 The standard overnight cultured SS was then spread onto 60mm NGM plate. Worms

718 were grown on *E. coli*-OP50, and eggs were collected by bleaching and then washing

719 in M9 buffer. Synchronized L1 larvae were obtained by allowing the eggs to hatch in

M9 buffer for 12 hr. Synchronized L1s were seeded to plates prepared for the specific assay and incubated at 20℃ for 4 days. The developmental conditions were determined by body length.

Food behavior assay

1) Food avoidance assay

Food avoidance assay was performed following to our published methods (Qi et al., 2017). Briefly, 5ul of overnight cultured bacteria was seeded on the center of 60mm NGM plates. About 30-50 synchronized L1 animals were seeded onto the bacterial lawns and cultured at 20℃ for 8hr. The aversion index was determined by N(out of lawn)/N(total).

2) Food choice assay

Food choice assay was performed following to our published methods (Qi et al., 2017). Briefly, 5ul of overnight cultured bacteria was seeded on the different side of 60mm NGM plates. About 300 synchronized L1 animals were seeded onto the center of NGM plates and cultured at 20℃ for 8hr. The food trend index was determined by N (selecting food1)/ [N(selecting food1)+N(selecting food2)] and N(selecting food2)/[N(selecting food1)+N(selecting food2)].

Lifespan analysis

Larval Lifespan

Studies of larval lifespan were performed on NGM plates at 20℃ as previously described (Cui et al., 2013). Briefly, L1 staged worms were placed NGM plates or SS seeded NGM plates. Worms were scored every day. Prism8 software was used for statistical analysis.

Adult Lifespan

Studies of lifespan were performed on NGM plates at 20℃ as previously described (Kimura et al., 1997).

Briefly, lifespan was begun on day zero by placing healthy L4 stage hermaphrodites onto OP50 seeded NGM plates. Animals were transferred to a fresh OP50 or SS seeded plates during the reproductive period (approximately the first ten days) to eliminate self-progeny and every 2 days thereafter. Worms were scored every day. Prism8 software was used for statistical analysis.

EMS mutagenesis

Synchronized L1 animals were grown to the L4 stage on OP50 and then subjected to a

4-hour treatment with 0.5% EMS (Ethyl Methanesulfonate). After treatment, the P0 generation animals were thoroughly washed with M9 solution and transferred to OP50 plates to grow and produce the F1 generation. Groups of 3-4 F1 animals were picked and placed onto new OP50 plates (3-4 F1 worms per plate) to generate the F2 generation through self-fertilization. Once the F2 generation reached adulthood, all the F2 animals were bleached to obtain the next generation of eggs. Synchronized L1 larvae were obtained by allowing the eggs to hatch in M9 buffer for 12 hours. The synchronized L1s were then seeded onto SS plates and incubated at 20°C for 4 days. Candidate mutants that could grow on SS plates were identified. To confirm the suspected mutants, each candidate mutant was picked singly onto OP50 for passaging and growth to adulthood. These adult animals were then bleached to obtain synchronized L1 mutants. The synchronized L1 mutants were seeded onto SS plates to confirm their ability to grow on SS.

Identification of EMS mutants

DNA isolation, library construction, and whole genome sequencing with gene identified were carried out according to the published protocol (Joseph et al., 2018).

i) Preparation of samples for Whole-Genome-Sequencing (WGS)

For each backcross, wild-type males were crossed to mutant hermaphrodites, F1 cross-progeny animals were individually cloned and F2 variants and wild-types were isolated under SS feeding conditon. The variant strains and wild-type strains were mixed respectively to constitute the "DNA-pool" used as samples for WGS. Whole-genome sequencing of pooled F2 recombinants, homozygous for the mutant phenotype following two outcrosses to wild-type N2 animals, was performed to identify the mutations.

ii) WGS data processing

For Whole-Genome-Sequencing, paired-end libraries were sequenced on an Illumina HiSeq 2000. Fastqc was used to control the quality of raw data and Trimmomatic was used to filter the data. Bwa was used to construct the index of *C.elegans* genome and align clean reads to the reference gene sequence (Species: *Caenorhabditis_elegans*; Source: UCSC; Reference Genome Version: WBcel235/ce11). The Samtools was used for file format conversion and sorting. Picard was used to remove the duplicate reads and then GATK was used to identify the intervals and realign. The realigned sequence was piled up by Samtools and then inputted to Varscan to call the variants including

SNPs and INDELs. Vcflib was used to perform subtraction between the wild-types

and variants. The file was annotated by Snpeff and the candidate genes was finally

obtained.

Preparation of samples for RNA sequencing

RNA-seq was done with three biological replicates that were independently generated,

collected, and processed. Adult wild type (N2) or *nsy-1* mutant worms were bleached

and then the eggs were incubated in M9 for 18 hours to obtain synchronized L1

worms. Synchronized L1 worms were cultured in the NGM plate seeded with OP50

or SS for 4hrs at 20°C. L1 worms were then collected for sequencing.

Fluorescence microscopy of *C. elegans*

Slides for imaging were prepared by making a fresh flattened 5% agarose pad. Worms

were mounted on 5% agar pads in M9 buffer with 5mM levamisolem then sealed

beneath a 22x22mm coverglass. Imaging was done using an Olympus BX53

microscope with a DP80 camera. *str-2::gfp* or *bcf-1::gfp* expression was measured

through imaging.

Microscopy

The fluorescence photographs were taken by Olympus BX53 microscope with a

DP80 camera. Development statistics were taken by Olympus MVX10 dissecting

microscope with a DP80 camera.

QUANTIFICATION AND STATISTICAL ANALYSIS

Quantification

Animals were randomly selected for fluorescent photography. The size of transgene

worms was photographed by the Nomarski microscope and measured by ImageJ

software. ImageJ software was used for quantifying fluorescence intensity of

indicated animals, which was then normalized with control group.

Statistical analysis

All experiments were performed independently at least three times with similar

results.

All statistical analyses were performed using the unpaired two-tailed Student's test.

Statistical parameters are presented as mean ± SD, statistical significance (P<0.05, *,

P < 0.01, **, P < 0.001, ***), and "n" (the number of worms counted).

The Log rank (Mantel-Cox) test was used for lifespan assay and the exact p values of

statistics for all survival assays are listed in the Figure.

Reference:

Avery, J.A., Liu, A.G., Ingeholm, J.E., Gotts, S.J., and Martin, A. (2021). Viewing images of foods evokes
taste quality-specific activity in gustatory insular cortex. Proc Natl Acad Sci U S A *118*.

Bargmann, C.I. (2006). Chemosensation in C. elegans. WormBook, 1-29.

Bargmann, C.I., Hartwieg, E., and Horvitz, H.R. (1993). Odorant-selective genes and neurons mediate
olfaction in C. elegans. Cell *74*, 515-527.

Baugh, L.R., and Sternberg, P.W. (2006). DAF-16/FOXO regulates transcription of cki-1/Cip/Kip and
repression of lin-4 during C. elegans L1 arrest. Curr Biol *16*, 780-785.

Buck, L., and Axel, R. (1991). A novel multigene family may encode odorant receptors: a molecular
basis for odor recognition. Cell *65*, 175-187.

Chuang, C.F., and Bargmann, C.I. (2005). A Toll-interleukin 1 repeat protein at the synapse specifies
asymmetric odorant receptor expression via ASK1 MAPKKK signaling. Gene Dev *19*, 270-281.

Chuang, C.F., VanHoven, M.K., Fetter, R.D., Verselis, V.K., and Bargmann, C.I. (2007). An
innexin-dependent cell network establishes left-right neuronal asymmetry in
. Cell *129*, 787-799.

Cui, M., Cohen, M.L., Teng, C., and Han, M. (2013). The tumor suppressor Rb critically regulates
starvation-induced stress response in C. elegans. Curr Biol *23*, 975-980.

Dickinson, D.J., Ward, J.D., Reiner, D.J., and Goldstein, B. (2013). Engineering the   genome using
Cas9-triggered homologous recombination. Nat Methods *10*, 1028-+.

Felix, M.A., and Braendle, C. (2010). The natural history of Caenorhabditis elegans. Curr Biol *20*,
R965-R969.

Fiala, A. (2007). Olfaction and olfactory learning in Drosophila: recent progress. Curr Opin Neurobiol
17, 720-726.

Florsheim, E.B., Bachtel, N.D., Cullen, J.L., Lima, B.G.C., Godazgar, M., Carvalho, F., Chatain, C.P.,
Zimmer, M.R., Zhang, C.L., Gautier, G.*, et al.* (2023). Immune sensing of food allergens promotes
avoidance behaviour. Nature *620*, 643-+.

Florsheim, E.B., Sullivan, Z.A., Khoury-Hanold, W., and Medzhitov, R. (2021). Food allergy as a
biological food quality control system. Cell *184*, 1440-1454.

Geng, S., Li, Q., Zhou, X., Zheng, J., Liu, H., Zeng, J., Yang, R., Fu, H., Hao, F., Feng, Q.*, et al.* (2022). Gut
commensal E. coli outer membrane proteins activate the host food digestive system through
neural-immune communication. Cell Host Microbe.

Hao, F.R., Liu, H.M., and Qi, B. (2024). Bacterial peptidoglycan acts as a digestive signal mediating host
adaptation to diverse food resources in. Nat Commun *15*.

He, Y., Hao, F., Fu, H., Tian, G., Zhang, Y., Fu, K., and Qi, B. (2023). N-glycosylated intestinal protein
BCF-1 shapes microbial colonization by binding bacteria via its fimbrial protein. Cell Rep *42*, 111993.

Hukema, R.K., Rademakers, S., Dekkers, M.P., Burghoorn, J., and Jansen, G. (2006). Antagonistic
sensory cues generate gustatory plasticity in Caenorhabditis elegans. Embo J *25*, 312-322.
Joseph, B.B., Blouin, N.A., and Fay, D.S. (2018). Use of a Sibling Subtraction Method for Identifying
Causal Mutations in Caenorhabditis elegans by Whole-Genome Sequencing. G3 (Bethesda) *8*,
669-678.
Julius, D., and Nathans, J. (2012). Signaling by sensory receptors. Cold Spring Harbor perspectives in
biology *4*, a005991.
Kim, D.H., Feinbaum, R., Alloing, G., Emerson, F.E., Garsin, D.A., Inoue, H., Tanaka-Hino, M., Hisamoto,
N., Matsumoto, K., Tan, M.W.*, et al.* (2002). A conserved p38 MAP kinase pathway in Caenorhabditis
elegans innate immunity. Science *297*, 623-626.
Kimura, K.D., Tissenbaum, H.A., Liu, Y.X., and Ruvkun, G. (1997). daf-2, an insulin receptor-like gene
that regulates longevity and diapause in Caenorhabditis elegans. Science *277*, 942-946.
Kodama, E., Kuhara, A., Mohri-Shiomi, A., Kimura, K.D., Okumura, M., Tomioka, M., Iino, Y., and Mori, I.
(2006). Insulin-like signaling and the neural circuit for integrative behavior in C. elegans. Genes Dev *20*,
2955-2960.
Liu, H., and Qi, B. (2023). Protocol for investigating the effect of food digestion in C. elegans on
development by feeding the inedible bacteria Staphylococcus saprophyticus. STAR Protoc *4*, 101990.
Liu, P., Liu, X., and Qi, B. (2024). UPRER–immunity axis acts as physiological food evaluation system
that promotes aversion behavior in sensing low-quality food. Elife *13:RP94181*.
Matsunaga, Y., Matsukawa, T., Iwasaki, T., Nagata, K., and Kawano, T. (2018). Comparison of
physiological functions of antagonistic insulin-like peptides, INS-23 and INS-18, in. Biosci Biotech Bioch
82, 90-96.
McLachlan, I.G., Kramer, T.S., Dua, M., DiLoreto, E.M., Gomes, M.A., Dag, U., Srinivasan, J., and Flavell,
S.W. (2022). Diverse states and stimuli tune olfactory receptor expression levels to modulate
food-seeking behavior. Elife *11*.
Plum, T., Binzberger, R., Thiele, R., Shang, F.W., Postrach, D., Fung, C., Fortea, M., Stakenborg, N., Wang,
Z., Tappe-Theodor, A.*, et al.* (2023). Mast cells link immune sensing to antigen-avoidance behaviour.
Nature *620*, 634-+.
Qi, B., Kniazeva, M., and Han, M. (2017). A vitamin-B2-sensing mechanism that regulates gut protease
activity to impact animal's food behavior and growth. Elife *6*.
Ryu, L., Cheon, Y., Huh, Y.H., Pyo, S., Chinta, S., Choi, H., Butcher, R.A., and Kim, K. (2018). Feeding state
regulates pheromone-mediated avoidance behavior via the insulin signaling pathway in. Embo J *37*.
Sagasti, A., Hisamoto, N., Hyodo, J., Tanaka-Hino, M., Matsumoto, K., and Bargmann, C.I. (2001). The
CaMKII UNC-43 activates the MAPKKK NSY-1 to execute a lateral signaling decision required for
asymmetric olfactory neuron fates. Cell *105*, 221-232.
Samuel, B.S., Rowedder, H., Braendle, C., Felix, M.A., and Ruvkun, G. (2016). Caenorhabditis elegans
responses to bacteria from its natural habitats. P Natl Acad Sci USA *113*, E3941-E3949.
Schulenburg, H., and Felix, M.A. (2017). The Natural Biotic Environment of Caenorhabditis elegans.
Genetics *206*, 55-86.
Scott, K. (2018). Gustatory Processing in Drosophila melanogaster. Annu Rev Entomol *63*, 15-30.
Sengupta, P., Chou, J.H., and Bargmann, C.I. (1996). odr-10 encodes a seven transmembrane domain
olfactory receptor required for responses to the odorant diacetyl. Cell *84*, 899-909.
Troemel, E.R., Chou, J.H., Dwyer, N.D., Colbert, H.A., and Bargmann, C.I. (1995). Divergent seven
transmembrane receptors are candidate chemosensory receptors in C. elegans. Cell *83*, 207-218.

Troemel, E.R., Kimmel, B.E., and Bargmann, C.I. (1997). Reprogramming chemotaxis responses:

sensory neurons define olfactory preferences in C. elegans. Cell *91*, 161-169.

Troemel, E.R., Sagasti, A., and Bargmann, C.I. (1999). Lateral signaling mediated by axon contact and

calcium entry regulates asymmetric odorant receptor expression in C. elegans. Cell *99*, 387-398.

Vidal, B., Aghayeva, U., Sun, H., Wang, C., Glenwinkel, L., Bayer, E.A., and Hobert, O. (2018). An atlas of

Caenorhabditis elegans chemoreceptor expression. Plos Biol *16*, e2004218.

Wes, P.D., and Bargmann, C.I. (2001). odour discrimination requires asymmetric diversity in olfactory

neurons. Nature *410*, 698-701.

Figure 1

Figure 2

Figure 3

A *Pnsy-1::gfp* *Podr-1::rfp* *Merge*

B *nsy-1(ag3); Podr-1::nsy-1::gfp;Podr-1::rfp*

Control Transgene

Bacteria: SS

Relative worm lenth ****

Control Transgene

C WT AWC *nsy-1* KO

Bacteria: SS

Relative worm lenth ****

WT AWC *nsy-1* KO

D P*str-2*::GFP

OP50 WT AWC AWC Dendrite SS WT

OP50 *nsy-1(ky397)* SS *nsy-1(ky397)*

E

■ 2AWC OFF
■ 1AWC ON/1AWC OFF
■ 2AWC ON

% of animals

WT-OP50 WT-SS *nsy-1(ky397)*-OP50 *nsy-1(ky397)*-SS

F Percentage of 2AWC OFF worms

% of animals ** ns

WT OP50 WT SS *nsy-1(ag3)* OP50 *nsy-1(ag3)* SS

G N2 *tir-1(qd4)* *nsy-1(ag3)*

Relative worm lenth **** ****

N2 *nsy-1(ag3)* *tir-1(qd4)*

Figure 4

Figure 5

Figure 6

Figure 7