An intestinally secreted host factor promotes microsporidia invasion of *C. elegans*

Hala Tamim El Jarkass¹, Calvin Mok¹, Michael R Schertzberg², Andrew G Fraser¹, Emily R Troemel³, Aaron W Reinke¹*

¹Department of Molecular Genetics, University of Toronto, Toronto, Canada; ²The Donnelly Centre, University of Toronto, Toronto, Canada; ³Division of Biological Sciences, University of California, San Diego, La Jolla, United States

Abstract

Microsporidia are ubiquitous obligate intracellular pathogens of animals. These parasites often infect hosts through an oral route, but little is known about the function of host intestinal proteins that facilitate microsporidia invasion. To identify such factors necessary for infection by *Nematocida parisii*, a natural microsporidian pathogen of *Caenorhabditis elegans*, we performed a forward genetic screen to identify mutant animals that have a Fitness Advantage with *Nematocida* (Fawn). We isolated four fawn mutants that are resistant to *Nematocida* infection and contain mutations in T14E8.4, which we renamed aaim-1 (Antibacterial and Aids invasion by Microsporidia). Expression of AAIM-1 in the intestine of aaim-1 animals restores *N. parisii* infectivity and this rescue of infectivity is dependent upon AAIM-1 secretion. *N. parisii* spores in aaim-1 animals are improperly oriented in the intestinal lumen, leading to reduced levels of parasite invasion. Conversely, aaim-1 mutants display both increased colonization and susceptibility to the bacterial pathogen *Pseudomonas aeruginosa* and overexpression ofaaim-1 reduces *P. aeruginosa* colonization. Competitive fitness assays show that aaim-1 mutants are favored in the presence of *N. parisii* but disadvantaged on *P. aeruginosa* compared to wild-type animals. Together, this work demonstrates how microsporidia exploits a secreted protein to promote host invasion. Our results also suggest evolutionary trade-offs may exist to optimizing host defense against multiple classes of pathogens.

Editor’s evaluation

Host factors involved in microsporidia infection have not been characterized in any detail, despite their ubiquitous distribution as infectious agents of animals. Through genetics screens, this study identifies a gene required for microsporidia invasion of the *C. elegans* intestine. Decreased susceptibility to microsporidia comes at the cost of increased colonization and infection by certain bacterial species, suggesting a tradeoff between resistance to different classes of pathogens.

Introduction

Microsporidia are a large group of obligate intracellular parasites that infect most types of animals (*Murareanu et al., 2021b*). These ubiquitous parasites possess the smallest known eukaryotic genomes and are extremely reliant on their host as a result of the loss of many genes involved in metabolism and energy production (*Corradi, 2015; Wadi and Reinke, 2020*). Microsporidia can have a large impact on the evolution of their hosts, as infection often leads to a reduction in host offspring and the effect of this selective pressure has resulted in resistant animals within a population (*Balla et al., 2015; Routtu and Ebert, 2015*). Microsporidia are currently a major threat to many commercially
important species such as honeybees and shrimp (Martín-Hernández et al., 2018; Jaroenlak et al., 2018). Many species also infect humans and infections in immunocompromised individuals can result in lethality (Stentiford et al., 2016). Despite their ubiquitous nature, effective treatment strategies are currently lacking for these poorly understood parasites (Han and Weiss, 2018).

Microsporidia infection begins with invasion of host cells. Microsporidia possess fascinating invasion machinery, a unique structure known as the polar tube (Han et al., 2020). This apparatus, resembling a long thread, is often coiled within a dormant spore. However, once inside of a host, and in proximity to the tissue of interest, the polar tube rapidly emerges or ‘fires’, releasing the infectious material (the sporoplasm) which is deposited intracellularly either through direct injection, or through the internalization of the sporoplasm (Han et al., 2020; Tamim El Jarkass and Reinke, 2020).

A number of microsporidia proteins have been demonstrated to play important roles during invasion by insect- and human-infecting species of microsporidia (Han et al., 2020). For example, spore wall proteins can interact with host cells through the recognition of sulfated glycosaminoglycans, heparin binding motifs, integrins, and proteins on the cell surface (Hayman et al., 2001; Hayman et al., 2005; Southern et al., 2007; Li et al., 2009; Wu et al., 2008; Chen et al., 2017). In Encephalitozoon species, polar tube proteins (PTP) can mediate interactions with the host. For instance, O-linked mannosylation on PTP1 has been demonstrated to bind mannose binding receptors, whereas PTP4 interacts with the transferrin receptor (Trf1) (Tamim El Jarkass and Reinke, 2020; Xu et al., 2003; Xu et al., 2004; Han et al., 2017). Additionally, the sporoplasm surface protein, EhSSP1, binds to an unknown receptor on the cell surface (Han et al., 2019). These proteins on the spore, polar tube, and sporoplasm have all been shown to promote microsporidia adhesion or invasion of host cells in culture systems, but the role of these proteins during animal infection is unclear.

The nematode Caenorhabditis elegans is infected in its natural habitat by several species of microsporidia, and frequently by Nematocida parisii (Luallen et al., 2016; Zhang et al., 2016; Troemel et al., 2008). This species infects the intestinal cells of C. elegans, which possess similarity to those of mammalian cells, making this animal both a relevant tissue and model to study these infections in vivo (Troemel et al., 2008; Troemel, 2011). Infection of C. elegans by N. parisii begins when spores are consumed by the worm, where they then pass through the pharynx into the intestinal lumen and fire, depositing sporosomes inside of intestinal cells. Within 72 hr, the sporoplasm will divide into meronts, which differentiate into spores, that then exit the animal, completing the parasite’s life cycle (Balla et al., 2016; Willis et al., 2021). Infection with N. parisii leads to reduced fecundity and premature mortality in C. elegans (Troemel et al., 2008; Balla et al., 2016). Several mutants have been shown to affect proliferation and spore exit (Botts et al., 2016; Szumowski et al., 2014). Immunity that can either prevent infection or clear the pathogen once infected has also been described (Balla et al., 2015; Willis et al., 2021; Balla et al., 2019; Reddy et al., 2019; Tecle et al., 2021). In contrast, very little is known about how N. parisii invades C. elegans intestinal cells. Almost all the microsporidia proteins known to facilitate invasion of host cells are not conserved in N. parisii and although host invasion factors described in other species are present in C. elegans, there is no evidence that they are being used by microsporidia during invasion of C. elegans (Tamim El Jarkass and Reinke, 2020).

To understand how microsporidia invade animal cells, we performed a forward genetic screen to identify host factors that promote infection. We identified a novel, nematode-specific protein, AAIM-1, whose loss of function confers resistance to N. parisii infection. This protein is expressed in intestinal cells, secreted into the intestinal lumen, and is necessary to ensure proper spore orientation during intestinal cell invasion. In addition, we show that AAIM-1 limits bacterial colonization of pathogenic Pseudomonas aeruginosa. Strikingly, AAIM-1 plays opposing roles on host fitness in the face of pathogenesis. The utilization of a host factor critical for bacterial defense reflects a clever strategy to ensuring microsporidia’s reproductive success.

**Results**

**A forward genetic screen identifies aaim-1 as being necessary for N. parisii infection**

To identify host factors needed for infection by microsporidia, we carried out a forward genetic screen using a C. elegans model of N. parisii infection. We took advantage of the previously described phenotypes of C. elegans displaying reduced fitness when infected with N. parisii, including reduced
progeny production and stunted development (Balla et al., 2016; Willis et al., 2021; Luallen et al., 2015; Murareanu et al., 2021a). We mutagenized animals and subjected their F2 progeny to N. parisii infection. After infecting populations for five subsequent generations, we selected individual worms containing embryos, indicating increased fitness in the presence of infection (see Materials and methods). We identified four independent isolates that when exposed to N. parisii reproducibly had higher fractions of animals containing embryos compared to wild type (N2). We named these isolates Fitness Advantage With Nematocida (fawn 1–4) (Figure 1—figure supplement 1a).

As C. elegans that are less infected with N. parisii produce more progeny, we hypothesized that these fawn mutants would be resistant to N. parisii infection (Willis et al., 2021). To determine this, we grew the three isolates with the strongest phenotype, fawn 1–3, in the presence and absence of N. parisii, and stained each population of worms with the chitin binding dye, Direct-yellow 96 (DY96), at 72 hr post infection (hpi). DY96 allows for the visualization of chitinous microsporidia spores as well as worm embryos (Figure 1a). In the absence of infection, there is no difference in the fraction of fawn-2 and fawn-3 animals developing into adults containing embryos (gravid adults), although fawn-1 has a modest defect. In comparison, all three fawn isolates generate significantly more gravid adults than N2 animals in the presence of infection (Figure 1b). We next examined the fraction of animals in each strain containing intracellular microsporidia spores and observed that all three fawn isolates display significantly fewer numbers of spore-containing worms (Figure 1c). These results suggest that fawn mutants are missing an important factor for efficient microsporidia infection.

To identify the causal mutations underlying the Fawn phenotype, we used a combination of whole-genome sequencing and genetic mapping. We generated F2 recombinants and performed two rounds of infection with microsporidia, selecting for gravid animals. After each round, we used molecular inversion probes to determine the region of the genome linked to the causal mutation (Mok et al., 2017). This revealed strong signatures of selection on the left arm of chromosome X in all three fawn isolates and absent in N2 (Figure 1—figure supplement 1b). Analysis of whole genome sequencing showed that all four fawn isolates contained different alleles of T14E8.4, which we named aaim-1 (Antibacterial and Aids Invasion by Microsporidia-1) for reasons described below (Figure 1d). We validated the role of aaim-1 in resistance to infection using several additional alleles: an independent allele aaim-1 (ok295), carrying a large gene deletion in both aaim-1 and dop-3, and a CRISPR-Cas9 derived allele, aaim-1 (kea22), that contains a large gene deletion. Both of these alleles displayed a fitness advantage when infected with N. parisii (Figure 1d and e and Figure 1—figure supplement 1c, d). These data demonstrate that aaim-1 is the causative gene underlying the fawn 1–4 infection phenotypes. In subsequent experiments we utilized both aaim-1 (kea22), and fawn-3 (kea28), carrying a 2.2 kb deletion in aaim-1, which was outcrossed to N2 six times [hereafter referred to as aaim-1 (kea28)].

aaim-1 is expressed in the pharynx and intestine, and secretion is important for function

AAIM-1 is a poorly characterized protein that does not possess any known or conserved domains. Homologs of the protein exist in both free-living and parasitic nematodes (Figure 2—figure supplement 1). To further characterize the role of AAIM-1 during N. parisii infection, we generated transgenic extrachromosomal lines of C. elegans carrying a reporter transgene of GFP under control of the aaim-1 promoter. GFP fluorescence was observed in the terminal bulb of the pharynx as well as the posterior of the intestine throughout development (Figure 2a). Embryos and L1 animals display additional expression in the arcade cells of the pharynx (Figure 2a and Figure 2—figure supplement 2a).

The first 17 amino acids of AAIM-1 are predicted to encode a signal peptide (Almagro Armenteros et al., 2019). This suggests that AAIM-1 may be secreted into the pharyngeal and intestinal lumen, the extracellular space through which N. parisii spores pass before invading intestinal cells. To test which tissues AAIM-1 functions in and if secretion is important for function, we generated a series of transgenic worms expressing extrachromosomal arrays (Key resources table, Appendix 1). First, we generated transgenic aaim-1 (kea22) animals expressing AAIM-1 tagged on the C-terminus with a 3x Flag epitope. Transgenic animals expressing AAIM-1 under its native promoter complement the ability of aaim-1 (kea22) animals to develop into adults in the presence of a high amount of N. parisii spores (Figure 2b). A construct expressing GFP or GFP::3xFlag does not influence this phenotype nor does the presence of the epitope tag impair the ability of AAIM-1 to rescue the mutant...
Figure 1. Mutations in aaim-1 result in resistance to N. parisii infection. (a-c, and e) L1 stage wild-type (N2) and aaim-1 mutant animals were infected with either a high dose (a, b, and e) or a very lose dose (c) of N. parisii, fixed at 72 hr, and stained with direct-yellow 96 (DY96). (a) Representative images stained with DY96, which stains C. elegans embryos and microsporidia spores. Scale bars, 100 μm. (b and e) Graph displays percentage of gravid worms. (c) Percentage of worms that contain newly formed N. parisii spores. (d) Schematic depicting the nature and location of the different aaim-1 alleles. Boxes represent exons, and connecting lines represent introns. Arrows depict point mutations, and the solid red lines depict deletions. fawn-2 (kea28) has a 2.2 kb deletion and aaim-1 (kea22) has a 2.3 kb deletion. fawn-1 (kea89) carries a C127T, Q43Stop mutation, fawn-3 (kea91) carries a G221A splice site mutation and fawn-4 (kea103) carries a C1286T, A429V mutation in aaim-1. (b, c, and e) Data is from three independent replicates of at least 90 worms each. Mean ± SEM represented by horizontal bars. p-Values determined via one-way ANOVA with post hoc. Significance defined as: * p < 0.05, ** p < 0.01, *** p < 0.001, **** p < 0.0001.

The online version of this article includes the following source data and figure supplement(s) for figure 1:

Source data 1. Mutations in aaim-1 result in resistance to N. parisii infection.

Figure supplement 1. Mapping and validation of aaim-1 as the gene associated with resistance to N. parisii.

Figure supplement 1—source data 1. Mapping and validation of aaim-1 as the gene associated with resistance to N. parisii.
Figure 2. AAIM-1 is secreted from intestinal cells. (a) Wild-type worms containing an extrachromosomal array expressing GFP from the aaim-1 promoter and mCherry (labelled in magenta) in the pharyngeal muscles were imaged at the embryo, L1, L3, L4, and adult stage. Embryo, L1, and L3 animals were imaged at 40 x, scale bar 20 μm and L4 and adult animals were imaged at 20 x, scale bar 50 μm. L1 to L4 animals are oriented anterior to posterior and the adult animal is oriented posterior to anterior from left to right. Schematic made with Biorender.com. (b) N2, aaim-1, and aaim-1 expressing
extrachromosomal arrays were infected with a medium-dose of *N. parisii*. Graph displays percentage of gravid worms. Data is from three independent replicates of at least 90 worms each. Mean ± SEM represented by horizontal bars. *p*-Values determined via one-way ANOVA with post hoc. Significance defined as **** *p* < 0.0001 (c) intestines (denoted by dashed lines) of 72 hr post-L1 adults were dissected and stained using anti-Flag (magenta) and DAPI (blue). Images taken at 40 x, scale bar 20 μm.

The online version of this article includes the following source data and figure supplement(s) for figure 2:

Source data 1. AAIM-1 is secreted from intestinal cells.

**Figure supplement 1.** AAIM-1 is conserved in both free-living and parasitic nematodes.

**Figure supplement 2.** aaim-1 is expressed in arcade cells and presence of C-terminal 3 x Flag tag does not disrupt AAIM-1 function.

**Figure supplement 2—source data 1.** aaim-1 is expressed in arcade cells and presence of C-terminal 3 x Flag tag does not disrupt AAIM-1 function.

AAIM-1 is only necessary for microsporidia infection at the earliest larval stage

*N. parisii* infection of *C. elegans* can occur throughout development, but several forms of immunity toward microsporidia have been shown to be developmentally regulated (Balla et al., 2015; Willis et al., 2021). To determine if *aaim*-1 mutant animals display developmentally restricted resistance to infection, we infected *fawn* 1–3 at the L1 and L3 stage. For these experiments, we took advantage of another intestinal-infecting species of microsporidia, *Nematocida ausubeli*, which has a more severe effect on *C. elegans* fecundity, and performed immunofluorescence using anti-Flag antibodies. We were unable to detect expression of AAIM-1::3xFlag when expressed from its endogenous promoter. However, we observed protein expression in the intestinal cells of animals expressing AAIM-1::3xFlag from a strong, intestinal specific-promoter or when the signal peptide was removed (Figure 2c). We did not observe AAIM-1::3xFlag localized in the extracellular space of the intestinal lumen, possibly due to rapid turnover of intestinal contents or due to loss from dissection of the intestines (McGhee and Ghafouri, 2007). The increased expression in the signal peptide mutant suggests an accumulation of protein that is unable to be secreted. Taken together, these data demonstrate that AAIM-1 is secreted and acts within the intestinal lumen to promote *N. parisii* infection.

AAIM-1 is needed for efficient invasion of intestinal cells

Resistance to infection could be the result of a block in invasion, proliferation, or through the destruction of the parasite. To test the mechanism of resistance in *aaim*-1 mutants, we performed pulse-chase infection assays at the L1 and L3 stage of development (Balla et al., 2015; Willis et al., 2021). Here, we treated animals with a medium-dose (as defined in *Supplementary file 1*) of *N. parisii* for 3 hr, washed away any un-ingested spores, and then replated the animals in the absence of spores for an additional 21 hr. We then used an 18 S RNA Fluorescent In Situ Hybridization (FISH) probe to detect *N. parisii* sporoplasts, which is the earliest stage of microsporidia invasion. In our *fawn* 1–3 isolates, we detect less invasion at 3 hpi compared to N2 (Figure 3—*figure supplement 1c*). However, there was no reduction in the number of infected animals between 3 hpi and 21
Figure 3. aaim-1 mutants are resistant to microsporidia at the earliest larval stage due to spore misfiring. (a–b) N2 and aaim-1 mutants were infected with a medium dose of N. ausubeli at either the L1 stage for 72 hr (a) or a high dose of N. ausubeli at the L3 stage for 48 hr (b). Graph displays percentage of gravid worms. (c–f) N2 and aaim-1 animals were infected with a medium-3 dose of N. parisii for 45 min at L1 (c–e) or L3 (f–h), fixed, and then stained with DY96 and an N. parisii 18 S RNA fish probe. The number of spores per animal (c,f), the percentage of spores fired (d,g), and the number of sporoplasm per worm (e,h) are displayed. Data is from three independent replicates of at least 100 worms each (a–b) or 20–30 worms each (c–h). (a–h) Mean ± SEM represented by horizontal bars. p-values determined via one-way ANOVA with post hoc. Significance defined as: * p < 0.05, ** p < 0.01, *** p < 0.001, **** p < 0.0001.

Figure 3 continued on next page
AAIM-1 plays a role in promoting proper spore orientation

To determine how AAIM-1 promotes N. parisii invasion, we further examined the invasion process. We pre-stained spores with calcofluor white (CFW) and assessed their orientation relative to the intestinal apical membrane using the apical membrane marker PGP-1::GFP in L1 worms infected for 45 min (Figure 4a). In N2 animals, 32.4% of spores are angled relative to the apical membrane. In contrast, spores in an aaim-1 mutant were angled 14.3% of the time (Figure 4b). Several host factors that promote microsporidia invasion cause adherence to host cells (Tamim El Jarkass and Reinke, 2020). To determine if AAIM-1 influences the location of spores relative to intestinal cells in aaim-1 mutants, we measured the perpendicular distance from the center of a parallel spore to the apical membrane of the intestine. Surprisingly, parallel spores in aaim-1 alleles were significantly closer to the apical membrane (0.29 μm) than those in N2 (0.34 μm) (Figure 4c). In agreement with resistance being developmentally restricted, aaim-1 mutants display wild-type spore orientations and distances from the membrane when infections were initiated at the L3 stage (Figure 4d and e). The width of the intestinal lumen at the L1 stage does not differ significantly between N2 and aaim-1 mutants, however, L3 animals generally possess wider intestinal lumens (Figure 3—figure supplement 2g,h). Thus, taken together these results suggest that AAIM-1 plays a distinct role in the intestinal lumen at L1 to promote proper spore orientation, through maintaining an appropriate distance and angle to the apical membrane, resulting in successful invasion.
AAIM-1 inhibits intestinal colonization by *Pseudomonas aeruginosa*

Interestingly, *aaim-1* has been shown to be upregulated by a variety of different fungal and bacterial pathogens, including *P. aeruginosa* (Engelmann et al., 2011; Head et al., 2017). Using our transcriptional reporter strain, we sought to confirm this and determine if microsporidia infection could also induce *aaim-1* transcription. N2 animals carrying a transcriptional reporter (paaim-1::GFP::3xFlag)
were exposed to *N. parisiis*, *P. aeruginosa* PA14, or E. coli OP50-1, and the levels of GFP quantified when grown on these pathogens for 72 hr from the L1 stage, or for 24 hr from the L4 stage. Infection by either *N. parisiis* or *P. aeruginosa* PA14 resulted in the upregulation of *aaim-1* as detected by an increase in the GFP signal (Figure 5a and Figure 5—figure supplement 1f).

Previously, an *aaim-1* deletion strain, RB563 (ok295), was shown to display reduced survival on lawns of *P. aeruginosa* PA14 (Styer et al., 2008). The enhanced susceptibility previously reported was attributed to dop-3, which is also partially deleted in RB563 (ok295) (Styer et al., 2008). To determine

---

**Figure 5.** *aaim-1* is upregulated by *N. parisiis* and *P. aeruginosa* and *aaim-1* animals are susceptible to infection by *P. aeruginosa*. (a) Expression of paaim-1::GFP::3xFlag in response to infection with either PA14 or *N. parisiis* for either 72 hr from L1 or 24 hr from L4. Data is from three independent replicates of at least 18–25 worms each. Every point represents a single worm. Percentage GFP was measured as the percentage of the animal containing GFP via FIJI. (b) L4 stage N2, *aaim-1*, and *pmk-1* (km25) animals were plated on full lawns of *P. aeruginosa* PA14::DsRed and the percentage of animals alive was counted over the course of 96 hr. TD50: N2 48 hr, *aaim-1* (kea28) 44 hr, *aaim-1* (kea22) 33 hr, and *pmk-1* (km25) 28 hr. Three independent replicates were carried out, and a representative replicate is displayed. At least 37 worms were quantified per strain. p-Values determined via Log-rank (Mantel-Cox) test. Significance defined as * p < 0.05, ** p < 0.01. (c–e) *N2*, *aaim-1*, or *aaim-1* animals with different extrachromosomal arrays were plated on PA14::DsRed at either the L1 stage (d) or L4 stage (c,e) for 48 hr. Bacterial burden was measured as the percentage of the animal containing PA14::DsRed. Data is from three independent replicates of 20–30 worms each. Every point represents a single worm. Mean ± SEM represented by horizontal bars. p-Values determined via two-way (a) or one-way ANOVA (c–e) with post hoc. Significance defined as * p < 0.05, ** p < 0.01, *** p < 0.001, **** p < 0.0001.

The online version of this article includes the following source data and figure supplement(s) for figure 5:

**Source data 1.** *aaim-1* is upregulated by *N. parisiis* and *P. aeruginosa* and *aaim-1* animals are susceptible to infection by *P. aeruginosa*.

**Figure supplement 1.** Susceptibility to *P. aeruginosa* PA14 appears at L4.

**Figure supplement 1—source data 1.** Susceptibility to *P. aeruginosa* PA14 appears at L4.

**Figure supplement 2.** A mutation in *aaim-1* does not influence *C. elegans* defense against *S. aureus* or lifespan.

**Figure supplement 2—source data 1.** A mutation in *aaim-1* does not influence *C. elegans* defense against *S. aureus* or lifespan.
if aaim-1 mutants are susceptible to pathogenic bacterial infection, we assayed the survival of L4 stage worms in P. aeruginosa PA14 slow killing assays. A mutant in the p38 MAPK pathway (pmk-1) was used as control for susceptibility to PA14 (Kim et al., 2002). We observed reduced survival in aaim-1 alleles, although not to the same extent as the pmk-1 mutant (Figure 5b and Figure 5—figure supplement 1a-c). In contrast to significant susceptibility to the Gram-negative P. aeruginosa, aaim-1 mutants do not display enhanced susceptibility to the Gram-positive bacterium Staphylococcus aureus NCTC8325, suggesting specificity of AAIM-1 to PA14 infection (Figure 5—figure supplement 2a).

Lethality in slow killing assays is a result of P. aeruginosa accumulation within the intestinal lumen (Tan et al., 1999; Kirienko et al., 2014). To investigate if aaim-1 alleles displayed higher levels of bacterial burden, animals were grown on lawns of PA14::DsRed at the L1 or L4 stage for 48 hr. aaim-1 mutant alleles exposed as L4s, but not L1s, displayed higher bacterial burden relative to N2 (Figure 5c and Figure 5—figure supplement 1d,e). To test if intestinal expression of aaim-1 was sufficient to limit bacterial colonization, transgenic aaim-1 (kea22) overexpressing AAIM-1::3xFlag from the endogenous or an intestinal-specific promoter were exposed to lawns of PA14::DsRed. When grown for 48 hr at the L1 or L4 stage, bacterial burden was significantly reduced, relative to N2 (Figure 5d and e). These results indicate that AAIM-1 plays a role in limiting bacterial colonization, and its loss results in reduced survival due to hyper-colonization of the intestinal lumen.

Fitness of aaim-1 animals is dependent upon microbial environment

To investigate how aaim-1 alleles can influence population structure, we set up competitive fitness assays. A C. elegans strain with a fluorescent marker (RFP::ZNFX-1) was co-plated with N2 or aaim-1 mutants on E. coli OP50-1, N. parisii or P. aeruginosa PA14. Animals were grown for 8 days, such that the population was composed of adult F1s and developing F2s. On E. coli OP50-1, there is equal representation of N2 and aaim-1 mutants in the population (Figure 6a). This is consistent with aaim-1 mutants not having a developmental delay (Figure 1b) or a decrease in longevity (Figure 5—figure supplement 2b). In contrast, growth on N. parisii resulted in aaim-1 alleles outcompeting the N2 strain. Conversely, aaim-1 mutants on P. aeruginosa PA14 did significantly worse, being underrepresented in the population compared to N2 (Figure 6a). Interestingly, wild isolates of C. elegans do not carry any obvious loss of function alleles of aaim-1 suggesting that natural conditions have selected for its retention (Figure 6—figure supplement 1; Cook et al., 2017).

Given the opposing fates of aaim-1 mutants on N. parisii and P. aeruginosa, we investigated the effects of co-infection. Animals were infected with a maximal dose of N. parisii for 3 hr, prior to placement on lawns of PA14. For infections with a single pathogen, we observed similar results as before whereby aaim-1 mutants have increased fitness in the presence of N. parisii and display lower levels of parasite burden but have increased bacterial accumulation when grown on PA14. In the presence of both pathogens, populations of aaim-1 mutants display fewer gravid adults and increased amounts of N. parisii spores. (Figure 6b and c). These results suggests that coinfection with N. parisii and P. aeruginosa has synergistically negative effects on the fitness of C. elegans.

Discussion

To identify host factors needed for microsporidia infection, we isolated mutants from a forward genetic screen that have a fitness advantage when challenged with N. parisii infection. This screen identified mutants in the poorly understood protein AAIM-1 (previously T14E8.4). Here, we demonstrate that this protein both promotes microsporidia invasion and limits colonization by pathogenic bacteria. Although we were unable to visualize the localization of secreted AAIM-1, our genetic and infection experiments strongly suggest that this protein acts in the intestinal lumen where both microsporidia invasion and bacterial colonization take place. The key role that AAIM-1 plays in immunity is further exemplified by its transcriptional regulation in response to infection (Figure 7).

The processes by which microsporidia invade host cells are poorly understood. We show that N. parisii spores are often angled in wild-type C. elegans, suggesting that successful invasion requires a particular spore orientation. In the absence of AAAM-1, spores are more often parallel to the intestinal lumen, where spores may fire without the successful deposition of the sporoplasm inside an intestinal cell. In contrast to previously described host and microsporidia proteins involved in invasion, AAIM-1 does not appear to be involved in promoting adhesion to the surface of host cells (Han et al., 2020;
N. parisii spores are ~2.2 μm long by ~0.8 μm wide and the average width of the intestinal lumen at the L1 stage is ~0.6 μm (Zhang et al., 2016). Therefore, at the L1 stage spores may not be able to move freely, but at the L3 stage, where AAIM-1 is not needed for...
invasion, there is less of a constraint on spore movement as the luminal width increases to \( \sim 1.3 \mu m \). Alternatively, the developmentally restricted role of AAIM-1 could be due stage-specific expression of other factors that work along with AAIM-1 to promote microsporidia invasion. Together, our results highlight the power of studying microsporidia invasion in the context of a whole animal model.

Several lines of evidence suggest that AAIM-1 plays a role in protecting animals against \( P. \) aeruginosa. First, \( aaim-1 \) is upregulated in the intestine in response to PA14 exposure. Second, overexpression of AAIM-1 significantly decreases PA14 burden in the intestine. Third, loss of \( aaim-1 \) leads to enhanced susceptibility and increased PA14 colonization. Fourth, competition assays show reduced reproductive fitness of \( aaim-1 \) mutants on PA14. The survival phenotype of \( aaim-1 \) mutants (~78% survival compared to wild type) is modest compared to loss of the p38 MAPK pathway (~51% survival compared to wild type). However, in competitive fitness assays, \( aaim-1 \) mutants are ~60% less represented than wild type in the F2 generation. Taken together, our data suggests that in addition to promoting microsporidia invasion, AAIM-1, at least in part, limits bacterial colonization and decreases susceptibility to \( P. \) aeruginosa.

\( C. \) elegans employs a variety of proteins to protect against bacterial infection. Many of these proteins belong to several classes of antimicrobial effectors used to eliminate and prevent colonization by pathogenic bacteria (Dierking et al., 2016), are upregulated upon infection, and predicted to be secreted (Suh and Hutter, 2012; Gallotta et al., 2020). One class of secreted proteins that is known to have immune functions and prevent bacterial adherence are the mucins. These large,
glycosylated secreted proteins are upregulated during *C. elegans* infection and their knockdown alters susceptibility to *P. aeruginosa* infection. (Strzyz, 2019; Hoffman et al., 2020) AAIM-1 has many predicted mucin-like O-glycosylation sites on serine and threonine residues (Steentoft et al., 2013; Jensen et al., 2010; Tran and Ten Hagen, 2013). Thus, one possibility is that AAIM-1 may be functionally analogous to mucins, preventing the adhesion of microbes to the surface of intestinal cells. As AAIM-1 does not contain any known or conserved domains, further work will be necessary to determine its exact biochemical function.

*C. elegans* lives in a microbially dense environment containing a wide variety of pathogens that *C. elegans* has evolved immunity towards (Zhang et al., 2016; Schulenburg and Félix, 2017; Samuel et al., 2016; Sinha et al., 2012; Ashe et al., 2013). Although loss of aaim-1 provides a fitness advantage to *C. elegans* when grown in the presence of microsporidia, obvious loss of function alleles are not present in wild isolates sequenced thus far. Additionally, aaim-1 mutants do not have observable defects when grown on non-pathogenic *E. coli*. This is in contrast to mutations in *pals-22* or *lin-35*, which negatively regulate the transcriptional response to infection and provide resistance to microsporidia infection when mutated, but at the cost of reduced reproductive fitness (Willis et al., 2021; Reddy et al., 2017). Loss of aaim-1 disadvantages *C. elegans* when grown on *P. aeruginosa*, but not *S. aureus*, suggesting AAIM-1 does not broadly promote resistance to all bacterial pathogens. These findings demonstrate that there is a trade-off in host defense between microsporidia and some pathogenic bacteria. The opposing functions of aaim-1 with different pathogens adds to the limited set of known examples of trade-offs that constrain the evolution of host defense to multiple biotic threats (Toor and Best, 2016; Thaler et al., 1999).

### Materials and methods

#### Strain maintenance

*C. elegans* strains were grown at 21°C on nematode growth media (NGM) plates seeded with 10 x saturated *Escherichia coli* OP50-1 (Willis et al., 2021). Strains used in this study are listed in the key resources table (Appendix 1). For all infection assays, 15–20 L4 staged animals were picked onto 10-cm seeded NGM plates 4 days prior to sodium hypochlorite/1 M NaOH treatment. After 4 days, heavily populated non-starved plates were washed off with 1 ml M9, treated twice with 1 ml of sodium hypochlorite/1 M NaOH solution, and washed three times in 1 ml M9. Embryos were then resuspended in 5 ml of M9 and left to rock overnight at 21 °C. L1s were used in subsequent experiments no later than 20 hr after bleach treatment. All centrifugation steps with live animals/embryos were performed in microcentrifuge tubes at 845 x g for 30 s.

Throughout the paper, L1 refers to the stage immediately post hatching or bleach synchronization, L3 refers to 24 hr and L4 refers to 48 hr post plating of bleach synchronized L1s at 21 °C. L3 and L4 stage animals were washed off plates in M9 +0.1% Tween-20, followed by an additional wash to remove residual bacteria before infection with microsporidia, or plating on PA14.

#### Forward genetic screen

6,000 L4 N2 hermaphrodites were mutagenized with a combination of 50 mM EMS and 85.4 mM ENU for 4 hr to achieve a large diversity of mutations within the genome (Thompson et al., 2013) P0 animals were then split and placed onto 48 10-cm NGM plates, F1s bleached and resulting F2s pooled onto five separate plates. 180,000 L1 F2 animals were plated onto a 10-cm plate with 10 million *N. parisii* spores and 1 ml 10 x saturated OP50-1. Animals were grown for 72 hr, to select for animals that display a fitness advantage phenotype with respect to N2. Each population was bleached and grown in the absence of infection for one generation, in order to prevent the effects of intergenerational immunity (Willis et al., 2021). Two more cycles of infection followed by growing worms in the absence of infection was performed. Populations of bleached L1s were then infected with either 20 or 40 million spores and grown for 76 hr. Worms were then washed into 1.5 ml microcentrifuge tubes and 1 ml of stain solution (1 x PBS/0.1% Tween-20/2.5 mg/ml DY96/1% SDS) was added. Samples were incubated with rotation for 3.5 hr and then washed three times with M9 +0.1% Tween-20. Individual worms that had embryos, but not spores, were picked to individual plates. Each of the four fawn strains was isolated from a different mutant pool.
Whole genome sequencing

N2 and fawn isolates were each grown on a 10-cm plate until all *E. coli* was consumed. Each strain was washed off with M9 and frozen at −80 °C. DNA was extracted using Gentra puregene Tissue Kit (QiAGEN). Samples were sequenced on an Illumina HiSeq 4000, using 100 base paired end reads.

MIP-map

Molecular inversion probes were used to map the underlying causal mutations in fawn isolates as previously described (Mok et al., 2017). Briefly, fawn hermaphrodites were crossed to males of the mapping strain DM7448 (VC20019 Ex[pmyo3::YFP]) hereafter referred to as VC20019 (Mok et al., 2020). Next, 20 F1 hermaphrodite cross progeny, identified as those carrying pmyo3::YFP, were isolated and allowed to self. F2s were then bleached, and 2500 L1s were exposed to a medium-2 dose of *N. parisii* spores representing the first round of selection. Two plates of 2500 F3 L1s were set up. The experimental plate was grown in the absence of infection for one generation, to negate intergenerational immunity (Willis et al., 2021). A second plate of 2500 L1s was allowed to grow for 72 hr and then frozen in H2O at −80 °C, until used for genomic preparation. The selection and rest steps were repeated once more, and a second frozen sample of worms was taken at the end of the mapping experiment. This process was also performed for a cross between N2 hermaphrodites and males of the mapping strain VC20019, as a negative control to identify non-causal loci that may be selected for reasons other than resistance to infection. Two genomic preparations, corresponding to the two rounds of selection, were used as template for MIP capture, to generate multiplexed libraries for sequencing. An Illumina Mini-seq was used to generate sequencing data that was subjected to demultiplexing via R, and selection intervals were defined as those immediately adjacent to the region on the chromosome carrying the fewest proportion of reads corresponding to the mapping strain, VC20019. This interval was then used to scan for putative causal alleles, resulting in the identification of the four *aaim-1* alleles in the four fawn isolates.

Identification of causal gene

Variants were identified using a BWA-GATK pipeline. Briefly, sequencing reads were checked for sequence quality using FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/) and bases lower than a quality threshold of 30 were trimmed off with Trimmomatic using a sliding window of 4 bases and minimum length of 36 bases (Bolger et al., 2014). Reads were aligned to the *C. elegans* N2 reference genome (release W220) using BWA-mem (Li and Durbin, 2009). Alignments were sorted by coordinate order and duplicate reads removed using Picard (Broad Institute, 2019). Prior to variant calling, reads were processed in Genome Analysis Tool Kit (GATK) v3.8.1 (DePristo et al., 2011), to perform indel realignment and base quality score recalibration using known *C. elegans* variants from dbSNP, build 138 (http://www.ncbi.nlm.nih.gov/SNP/). GATK HaplotypeCaller was used to call variants, and results were filtered for a phred-scaled Qscore >30 and to remove common variants found previously in multiple independent studies. Finally, Annovar (Wang et al., 2010) was used to obtain a list of annotated exonic variants for each sequenced strain.

Microsporidia infection assays

*N. parisii* (ERTm1) and *N. aususbeli* (ERTm2) spores were prepared as described previously (Willis et al., 2021). All infections were carried out on 6-cm NGM plates, unless otherwise specified by spore dose (see Supplementary file 1), or experimental method. 1000 bleach-synchronized L1s were added into a microcentrifuge tube containing 400 μl of 10 X *E. coli* OP50-1, and spores. After pipetting up and down, this mixture was top plated onto an unseeded 6-cm NGM plate, and left to dry in a clean cabinet, prior to incubation at 21 °C for 72 hr. Infections set up on 3.5-cm plates used 160 μl of 10 x *E. coli* OP50-1 and 400 L1s.

Infection of embryos hatched on plates

Twenty-five 72-hr-old synchronized animals of each strain were picked onto 3.5-cm unseeded NGM plates seeded with 16 μl of 10 x *E. coli* OP50-1. Plates were incubated at 21 °C for 2 hr. Adults were then picked off, and a mixture of 144 μl of 10 x *E. coli* OP50-1 and a low dose of *N. parisii* spores were added to each plate. Animals were fixed and stained after 72 hr.
Pulse-chase infection assay
A total of 6000 bleach synchronized animals were exposed to a medium-1 (Figure 3—figure supplement 1) or medium-3 (Figure 3) dose of spores, 10 μl of 10 x E. coli OP50-1 in a total volume of 400 μl made up with M9. To assay pathogen clearance 3 hpi, animals were washed off in 1 ml M9 +0.1% Tween-20, and split into two populations. The first half was fixed with acetone to represent initial infectious load, while the other half was washed twice in M9 +0.1% Tween-20 to remove residual spores in the supernatant and prevent additional infection from occurring. These washed worms were then plated on 6-cm unseeded NGM plates with 40 μl 10 x OP50-1, and 360 μl M9 and left to incubate at 21 °C for 21 additional hours before fixation.

Spore localization and firing assays
Strains were infected as described for the pulse infection assays for either 45 min or 3 hr. Animals were then washed off plates, fixed, and stained with DY96 and an N. parisii 18 S RNA FISH probe. FISH+ DY96+ events represent unfired spores, FISH+ DY96+ events represent fired spores, and FISH+ DY96- events represent sporoplasms. Percentage of fired spores is defined as the number of FISH− DY96+ events over the total number of spores (DY96+).

To assess spore orientation, the localization of calcofluor white spores relative to the apical membrane of the intestine was measured in live anaesthetized animals using differential interference contrast microscopy. To determine if a spore was angled, straight lines were extended from both ends of the spore independently. If either of these two lines crossed the apical membrane, a spore was considered angled. If not, the spore was considered parallel. Distance of spores from the apical membrane was assessed by measuring perpendicular distance from the central edge of a parallel spore to the apical membrane. All measurements were performed with FIJI (Schindelin et al., 2012) using the angle tool or the straight line tool respectively, followed by the Analyze → measure option. Images in Figure 4a were taken in N2 and aaim-1 (kea22) animals carrying PGP-1::GFP (Sato et al., 2007) to label the apical intestinal membrane, thus outlining the lumen.

Intestinal lumen measurements
Measurements were performed on live anaesthetized worms used for spore localization assays (see above). The width of the lumen was determined by extending a straight line from the apical membrane on one end of the worm to that directly across on the other end, at the midpoint of the intestine, and the distance measured in FIJI, via the straight line tool followed by the Analyze → measure option.

Fixation
Worms were washed off infection plates with 700 μl M9 +0.1% Tween-20 and washed once in 1 ml M9 +0.1% Tween-20. All microsporidia infected samples were fixed in 700 μl of aceton for 2 min at room temperature prior to staining. All P. aeruginosa PA14::DsRed infected samples, as well as competitive fitness assays involving RFP::ZNFX-1 were fixed in 500 μl of 4% paraformaldehyde (PFA) for 30 min at room temperature prior to mounting on slides.

Live imaging
Animals were mounted on 2% Agarose pads in 10 μl of 10–25 mM Sodium Azide. This technique was used for spore localization assays, transcriptional reporter imaging, and assessing PA14::DsRed colonization in transgenic animals.

Chitin staining
The chitin binding dye Direct yellow 96 (DY96) was used to assess host fitness ( gravidity) as well as parasite burden. A total of 500 μl of DY96 solution (1 x PBST, 0.1% SDS, 20 μg/ml DY96) was added to washed worm pellets and left to rock for 20–30 min at room temperature. Worms were then resuspended in 20 μl of EverBrite Mounting Medium (Biotium), and 10 μl mounted on glass slides for imaging.

To pre-stain spores prior to infection, 0.5 μl of calcofluor white solution (CFW) (Sigma- Aldrich 18909) was added per 50 μl of spores, pipetted up and down gently and left for 2 min at room temperature prior to infection.
**FISH staining**

To quantify the number of sporoplasts in *N. parisii* infected animals, the MicroB FISH probe (ctct cgccactctttctctgt) labelling *N. parisii* 18 S RNA was used. Animals were fixed in acetone, washed twice in 1 ml PBST, and once in 1 ml of hybridization buffer (0.01% SDS, 900 mM NaCl, 20 mM TRIS pH 8.0). Samples were then incubated overnight in the dark at 46 °C with 100 μl of hybridization buffer containing 5 ng/μl of the MicroB FISH probe conjugated to Cal Fluor 610 (LGC Biosearch Technologies). Samples were then washed in 1 ml of wash buffer (Hybridization buffer + 5 mM EDTA), followed by incubation with 500 μl wash buffer at 46 °C in the dark. To visualize sporoplasts and spores simultaneously, the final incubation was replaced with 500 μl DY96 solution and incubated in the dark at room temperature prior to resuspension in 20 μl of EverBrite Mounting Medium (Biotium).

**Microscopy and image quantification**

All imaging was performed using an Axio Imager.M2 (Zeiss), except for images of the transcriptional reporter in Figure 5—figure supplement 1, which were generated using an Axio Zoom V.16 (Zeiss) at a magnification of 45.5 x. Images were captured via Zen software and quantified under identical exposure times per experiment. Gravidity is defined as the presence of at least one embryo per worm, and animals were considered infected by 72 hr if clumps of spores were visible in the body of animals as seen by DY96. FISH-stained animals were considered infected if at least one sporoplasm was visible in intestinal cells.

To quantify fluorescence within animals (pathogen burden, bead accumulation, and GFP), regions of interest were used to outline every individual worm from anterior to posterior, unless otherwise specified in the methods. Individual worm fluorescence from variable assays (GFP or DsRed) were subjected to the ‘threshold’ followed by ‘measure’ tools in FIJI (Schindelin et al., 2012). To assess PA14::DsRed burden in transgenic animals, regions of interest were generated from the beginning of the intestines (int1) to the posterior end of the worm to prevent the pmyo2::mCherry co-injection marker signal from interfering with quantifications. When assessing pathogen burden in gravid animals stained with DY96, thresholding was used to quantify spore signal without including signal from embryos.

**Pseudomonas aeruginosa infection experiments**

For all *Pseudomonas* assays, a single colony was picked into 3 ml of LB and grown overnight at 37 °C, 220 rpm for 16–18 hr. 10 μl (for 3.5- cm plate) or 50 μl (for 6- cm plate) of culture was spread onto slow killing (SK) plates to form a full lawn, except in the case of competitive fitness assays (see below). Seeded plates were placed at 37 °C for 24 hr, followed by 25 °C for 24 hr prior to use. Plates were seeded fresh prior to each experiment. To assess colonization, 1000 synchronized animals were grown on PA14::DsRed for either 24 or 48 hr at 25 °C. Animals were washed off with 1 ml M9 +0.1% Tween-20, and washed twice thereafter, prior to fixation.

To quantify survival of individual strains on PA14, 3.5-cm SK plates were seeded with 10 μl of PA14::DsRed,(Dunn et al., 2006) to form full lawns. 60 L4s were picked onto each of three, 3.5- cm plates per strain, and 24 hr later, 30 animals from each were picked onto a new 3.5-cm plate. Survival was monitored from 24 hr post L4, three times per day. Survival was assessed based on response to touch. Carcasses were removed, and surviving animals were placed onto fresh 3.5-cm plates every 24 hr. Animals were grown at 25 °C for the duration of the experiment. Technical triplicate data was pooled to represent a single biological replicate. The experiment was carried out until no more worms had survived. Survival curves were generated via GraphPad Prism 9.0, and the Log rank (mantel-cox) test was used to generate P-values. TD_{50} values were calculated as previously described,(Styer et al., 2008) utilizing GraphPad Prism 9.0 and applying a non-linear regression analysis on survival curves.

**Staphylococcus aureus infection experiments**

3.5-cm tryptic soy agar (TSA) plates supplemented with 10 μg/ml nalidixic acid (Nal) and seeded with *S. aureus* NCTC8325 (Sifri et al., 2003) were utilized and survival quantified as described previously (Powell and Ausubel, 2008). Briefly, a 1:10 dilution of an overnight *S. aureus* culture was utilized to seed 3.5-cm TSA + Nal plates, incubated at 37 °C for 3 hr and stored at 4 °C overnight. Thirty L4s were picked onto three TSA + Nal plates per strain, and survival quantified three times a day until all animals were dead. Animals were transferred to new seeded TSA + Nal plates every 24 hr. Survival was
assessed based on response to touch. Technical triplicate data was pooled to represent a single biological replicate. Survival curves were generated via GraphPad Prism 9.0, and the Log rank (mantel-cox) test was used to generate p-values.

**Transgenic strain construction**

N2 or aaim-1 (kea22) animals were injected with a 100 ng/μl injection mix composed of 50 ng/μl of template, 5 ng/μl of pmyo2::mCherry, and 45 ng/μl of pBSK (Ponchon et al., 2009). Three independent lines were generated for each injected construct.

Gateway BP cloning (Walhout et al., 2000; Hartley et al., 2000) was performed to insert AAIM-1 and GFP into pDONR221. Around the horn PCR, (Moore and Prevelige, 2002) was used to insert a 3 x Flag sequence at the C-terminus of this construct. Gibson assembly was used to generate different tissue specific clones driving aaim-1 expression. Paaim-1, aaim-1 and pssp-5 were cloned from N2 genomic DNA, pmyo2 was cloned from pCFJ90 (Frejaer-Jensen et al., 2008). GFP and 3 x Flag sequences were cloned from pDD282 (Frejaer-Jensen et al, 2008). SPΔaaim-1 was amplified from aaim-1::3xFlag in pDONR221 by omitting the first 17 amino acids, the putative secretion signal as predicted via SignalP 5.0 (Almagro Armenteros et al., 2019). All clones possessed an unc-54 3’ UTR. See key resources table for primer sequences (Appendix 1).

**CRISPR-Cas9 mutagenesis**

To generate a deletion allele of aaim-1 via CRISPR-Cas9 mutagenesis, steps were taken as described here (Dickinson et al., 2015). Briefly, 2 crRNA’s were designed using CRISPOR (Concordet and Haeussler, 2018), (Dokshin et al., 2018), near the start and stop sites of aaim-1 and generated via IDT. A repair template was designed to contain 35 base pairs of homology upstream and downstream of the cut sites. Streptococcus pyogenes Cas9 3NLS (10 µg/µl) IDT and tracrRNA (IDT #1072532) were utilized. Reaction mixes were prepared as described previously. pRF4 (Mello et al., 1991) was co-injected with the Cas9 ribonucleoprotein, and F1 rollers picked. Deletions were identified via PCR primers situated outside the cut sites.

**Bead-feeding assays**

1,000 synchronized L1 animals were mixed with 0.2 μm green fluorescent polystyrene beads (Degradex Phosphorex) at a ratio of 25:1 in a final volume of 400 μl containing 10 μl of 10 x E. coli OP50-1, 16 μl of beads and up to 400 μl with M9. Animals were incubated with beads for 3 hr, washed off with M9 +0.1% Tween-20 and fixed with 4% PFA for 30 min at room temperature. Bead accumulation was measured as a percentage of the total animal exhibiting fluorescent signal, using FIJI.

**Lifespan assays**

Lifespan assays were performed as described previously (Amrit et al., 2014). In brief, 120 synchronized L4 animals were utilized per strain, with every 15 animals placed on a single 3.5-cm NGM plate (A total of 8 plates, with 15 animals each per strain). Animals were transferred to a new seeded 3.5-cm NGM plate every 2 days, for a total of 8 days (four transfers), ensuring no progeny were transferred alongside adults. After day 8, survival was quantified daily, on the same plate, via response to touch. Any animals that exhibited internal hatching, protruding intestines, or were found desiccated on the edges of the plate were censored. Survival curves were generated via GraphPad Prism 9, and the Log rank (mantel-cox) test was used to generate p values.

**Immunofluorescence (IF)**

IF was performed as described previously (Crittenden and Kimble, 2009); however, all steps post-dissection were performed in microcentrifuge tubes, and intestines were pelleted on a mini tabletop microcentrifuge for a few seconds. Briefly, animals were dissected to extrude intestinal tissue. Two 25-mm gauge needles on syringes were used to create an incision near the head and/or tail of the animals. Dissections were performed in 5 μl of 10 mM levamisole on glass slides to encourage intestinal protrusion. Fixation, permeabilization and blocking was performed as described previously (Crittenden and Kimble, 2009). Primary M2 anti-Flag antibody (Sigma F1804) was used at 1:250 overnight at 4 °C, and secondary goat anti-mouse Alexa fluor 594 (Thermo Fisher A32742) at 1:300 for 1 hr.
at room temperature. Animals were mounted in 20 μl of EverBrite Mounting Medium (Biotium) and placed on glass slides for imaging.

**Competitive fitness assays**

N2 or aaim-1 mutants were grown together with RFP::Znf1 YY1446 (gg634), which labels the germ granules and can be observed in all developmental stages (Wan et al., 2018). For N. parisii infections, 10-cm NGM plates were seeded with 1 ml of 10 x OP50-1 and a medium-2 dose of spores (no spores were used for uninfected plates). 10 L1s from each strain were picked onto lawns of spores and E. coli OP50-1 immediately after drying, and grown for 8 days at 21 °C, washed off with M9 +0.1% Tween-20, and fixed. For P. aeruginosa infections, 3.5-cm SK plates were seeded with a single spot of 20 μl of PA14 in the center of the plate. 10 L1s of each strain were placed on plates and grown at 21 °C for 8 days and then washed off with M9 +0.1% Tween-20. The percentage of animals that did not display RFP germ granules (i.e. N2 or aaim-1 mutants) was determined by quantifying all animals on the plate, including F1 adults and L1/L2 stage F2 animals.

**Co- infections with N. parisii and P. aeruginosa**

Co-infection assays were performed by first pulse infecting co-infection and N. parisii single infection groups with a maximal dose of spores for 3 hr on unseeded 6-cm NGM plates as described above. PA14::DsRed single infections were pulsed with a volume of M9 to match that of the spores. Animals were then washed off in 1 ml of M9 +0.1% Tween-20, followed by two more washes, prior to placement on full lawns of PA14::DsRed on a 6-cm SK plates prepared as described above. N. parisii single infections were placed on a 6-cm NGM plate pre-seeded with 200 μl of 10 x OP50-1. Plates were incubated at 21 °C.

**Phylogenetic analysis**

Homology between AAIM-1 and other proteins was determined with protein BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi) using default parameters. Sequences with an E-value of at least 10−5 were aligned using MUSCLE (https://www.ebi.ac.uk/Tools/msa/muscle/) using default parameters. Phylogenetic tree of homologs was generated using RAxML BlackBox (https://raxml-ng.vital-it.ch/) using default parameters and 100 boot straps. Tree was visualized using FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).

**Statistical analysis**

All data analysis was performed using GraphPad Prism 9.0. One-way Anova with post hoc (Tukey test) was used for all experiments unless otherwise specified in figure legends. Statistical significance was defined as p < 0.05.

**Acknowledgements**

We thank Ashley M Campbell, Alexandra R Willis, and Kristina Sztanko for providing helpful comments on the manuscript. This work was supported by the Canadian Institutes of Health Research grant no. 400,784 and an Alfred P Sloan Research Fellowship FG2019-12040 (to AWR). This work was supported by National Institutes of Health (http://www.nih.gov/) under R01 AG052622 and GM114139 to ERT. Some strains were provided by the CGC, which is funded by NIH Office of Research Infrastructure Programs (P40 OD010440) and we thank WormBase.

**Additional information**

| Funding                          | Grant reference number | Author         |
|---------------------------------|------------------------|----------------|
| Canadian Institutes of Health Research | 400784                | Aaron W Reinke |
| Alfred P. Sloan Foundation | FG2019-12040            | Aaron W Reinke |
The funders had no role in study design, data collection and interpretation, or the decision to submit the work for publication.

Author contributions
Hala Tamim El Jarkass, Conceptualization, Data curation, Formal analysis, Investigation, Methodology, Validation, Visualization, Writing – original draft, Writing – review and editing; Calvin Mok, Michael R Schertzberg, Formal analysis, Writing – review and editing; Andrew G Fraser, Funding acquisition, Supervision; Emily R Troemel, Funding acquisition, Resources, Supervision, Writing – review and editing; Aaron W Reinke, Conceptualization, Data curation, Funding acquisition, Investigation, Methodology, Project administration, Resources, Supervision, Writing – original draft, Writing – review and editing

Author ORCIDs
Hala Tamim El Jarkass http://orcid.org/0000-0003-0118-5978
Andrew G Fraser http://orcid.org/0000-0001-9939-6014
Emily R Troemel http://orcid.org/0000-0003-2422-0473
Aaron W Reinke http://orcid.org/0000-0001-7612-5342

Decision letter and Author response
Decision letter https://doi.org/10.7554/eLife.72458.sa1
Author response https://doi.org/10.7554/eLife.72458.sa2

Additional files

Supplementary files
• Supplementary file 1. Spore doses utilized in this study. The different species of microsporidia used in the study, and the varying doses (as defined in figure legends) are listed. Plate concentration refers to the number of spores occupied per cm² of either 3.5, 6, or 10 cm NGM plates (indicated by *, ** or *** in the ‘total spores on assay plate’ column). The total number of spores present on a single assay plate are listed for the various doses in millions of spores.
• Transparent reporting form

Data availability
All data generated during this study have been uploaded as source data files for each figure.

References
Almagro Armenteros JJ, Tsirigos KD, Senderby CK, Petersen TN, Winther O, Brunak S, von Heijne G, Nielsen H. 2019. SignalP 5.0 improves signal peptide predictions using deep neural networks. Nature Biotechnology 37:420–423. DOI: https://doi.org/10.1038/s41587-019-0036-z, PMID: 30778233
Amrit FRG, Ratnappan R, Keith SA, Ghazi A. 2014. The C. elegans lifespan assay toolkit. Methods 68:465–475. DOI: https://doi.org/10.1016/j.ymeth.2014.04.002, PMID: 24727064
Ashe A, Bélicard T, Le Pen J, Sarkies P, Frézal L, Lehrbach NJ, Félix MA, Miska EA. 2013. A deletion polymorphism in the Caenorhabditis elegans RIG-I homolog disables viral RNA dicing and antiviral immunity. eLife 2:e00994. DOI: https://doi.org/10.7554/eLife.00994, PMID: 24137537
Balla KM, Andersen EC, Kruglyak L, Troemel E. 2015. A wild C. elegans strain has enhanced epithelial immunity to a natural microsporidian parasite. PLOS Pathogens 11:e1004583. DOI: https://doi.org/10.1371/journal.ppat.1004583, PMID: 25680197
Balla KM, Luallen RJ, Bakowski MA, Troemel ER. 2016. Cell-to-cell spread of microsporidia causes Caenorhabditis elegans organs to form syncytia. Nature Microbiology 1:16144. DOI: https://doi.org/10.1038/nmicrobiol.2016.144, PMID: 27782144
Balla KM, Lažetić V, Troemel ER. 2019. Natural variation in the roles of C. elegans autophagy components during microsporidia infection. PLOS ONE 14:e0216011. DOI: https://doi.org/10.1371/journal.pone.0216011, PMID: 31013330
Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. DOI: https://doi.org/10.1093/bioinformatics/btu170, PMID: 24695404

Botts MR, Cohen LB, Probert CS, Wu F, Troemel ER. 2016. Microsporidia intracellular development relies on myc interaction network transcription factors in the host. G3: Genes, Genomes, Genetics 6:2707–2716. DOI: https://doi.org/10.1534/g3.116.029983, PMID: 27402359

Broad Institute. 2019. Picard Toolkit. GitHub. https://broadinstitute.github.io/picard

Crittenden S, Kimble J. 2009. Preparation and immunolabeling of Caenorhabditis elegans. Cold Spring Harbor.

Corradi NM, Zdraljevic S, Roberts JP, Andersen EC. 2017. CeNDR, the natural diversity, Haeussler M. 2018. CRISPOR: intuitive guide selection for CRISPR/Cas9 genome editing

Concordet JP, Li R, You Y, Zhang K, Zhang L. 2017. A novel spore wall protein from antonospora locustae

Chen L. 2019. Picard Toolkit. GitHub. https://broadinstitute.github.io/picard

Broad Institute, Cohen LB, Probert CS, Wu F, Troemel ER. 2016. Microsporidia intracellular development relies on myc interaction network transcription factors in the host. G3: Genes, Genomes, Genetics 6:2707–2716. DOI: https://doi.org/10.1534/g3.116.029983, PMID: 27402359

Dokshin GA, Dierking K, Yang W, Schulenburg H. 2016. Antimicrobial effectors in the nematode Caenorhabditis elegans: an outgroup to the Arthropoda. Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences 371:20150299. DOI: https://doi.org/10.1098/rstb.2015.0299, PMID: 27166001

Dokshin GA, Ghanta KS, Piscopo KM, Mello CC. 2018. Robust genome editing with short single-stranded and long, partially single-stranded DNA donors in Caenorhabditis elegans. Genetics 210:781–787. DOI: https://doi.org/10.1354 genetic.210.1.0216

Dunn AK, Millikan DS, Adin DM, Bose JL, Stabb EV. 2006. New rfp- and pES213-derived tools for analyzing symbiotic Vibrio fisheri reveal patterns of infection and lux expression in situ. Applied and Environmental Microbiology 72:802–810. DOI: https://doi.org/10.1128/AEM.72.1.802-810.2006, PMID: 16391121

Engelmann I, Grifon A, Tichit L, Montañana-Sanchis F, Wang G, Reinke V, Waterston RH, Hillier LW, Ewbank JJ. 2011. A comprehensive analysis of gene expression changes provoked by bacterial and fungal infection in C. elegans. PLOS ONE 6:e19055. DOI: https://doi.org/10.1371/journal.pone.0019055, PMID: 21602919

Engelmann I, Grifon A, Tichit L, Montañana-Sanchis F, Wang G, Reinke V, Waterston RH, Hillier LW, Ewbank JJ. 2011. A comprehensive analysis of gene expression changes provoked by bacterial and fungal infection in C. elegans. PLOS ONE 6:e19055. DOI: https://doi.org/10.1371/journal.pone.0019055, PMID: 21602919

Frejaer-Jensen C, Davis MW, Hopkins CE, Newman BJ, Thummel JM, Oleasn SP, Grunnet M, Jorgensen EM. 2008. Single-copy insertion of transgenes in Caenorhabditis elegans. Nature Genetics 40:1375–1383. DOI: https://doi.org/10.1038/ng.248, PMID: 18953339

Gallotta I, Sandhu A, Peters M, Haslbeck M, Jung R, Agilkaya S, Blersch JL, Rodelsperger C, Röseler W, Huang C, Sommer RJ, David DC. 2020. Extracellular proteostasis prevents aggregation during pathogenic attack. Nature 584:410–414. DOI: https://doi.org/10.1038/s41586-020-2461-z, PMID: 32641833

Han B, Polonais V, Sugita T, Yakubu R, Takvoriam PM, Cali A, Maier K, Long M, Levy M, Tanowitz HB, Pan G, Delbac F, Zhou Z, Weiss LM. 2017. The role of microsporidian polar tube protein 4 (PTP4) in host cell infection. PLOS Pathogens 13:e1006341. DOI: https://doi.org/10.1371/journal.ppat.1006341, PMID: 28426751

Han B, Weiss LM. 2018. Therapeutic targets for the treatment of microsporidiosis in humans. Expert Opinion on Therapeutic Targets 22:903–915. DOI: https://doi.org/10.1080/14780222.2018.1538360, PMID: 30336698

Han B, Ma Y, Tu V, Tomita T, Mayoral J, Williams T, Horta A, Huang H, Weiss LM. 2019. Microsporidia interact with host cell mitochondria via voltage-dependent anion channels using sporoplasm surface protein 1. MBio 10:e01944-19. DOI: https://doi.org/10.1128/mBio.01944-19, PMID: 31431557

Han B, Takvoriam PM, Weiss LM. 2020. Invasion of host cells by microsporidia. Frontiers in Microbiology 11:172. DOI: https://doi.org/10.3389/fmicb.2020.00172, PMID: 32132983

Hartley JL, Temple GF, Brasch MA. 2000. DNA cloning using in vitro site-specific recombination. Genome Research 10:1788–1795. DOI: https://doi.org/10.1101/gr.143000, PMID: 11076863

Hayman JR, Hayes SF, Amon J, Nash TE. 2001. Developmental expression of two spore wall proteins during maturation of the microsporidian Encephalitozoon intestinalis. Infection and Immunity 69:7057–7066. DOI: https://doi.org/10.1128/IAI.69.11.7057-7066.2001, PMID: 11598081

Hayman JR, Southern TR, Nash TE. 2005. Role of sulfated glycans in adherence of the microsporidian Encephalitozoon intestinalis to host cells in vitro. Infection and Immunity 73:841–848. DOI: https://doi.org/10.1128/IAI.73.3.841-848.2005, PMID: 15664924
Head BP, Olatan AO, Aballay A. 2017. Role of GATA transcription factor ELT-2 and p38 MAPK PMK-1 in recovery from acute P. aeruginosa infection in C. elegans. Virulence 8:261–274. DOI: https://doi.org/10.1080/21505594.2016.1222334, PMID: 27600703

Hoffman CL, Lalsiamthara J, Aballay A. 2020. Host mucin is exploited by Pseudomonas aeruginosa to provide monosaccharides required for a successful infection. MBio 11:e00660-20. DOI: https://doi.org/10.1128/mBio.00660-20, PMID: 32127446

Jaklenik P, Boakyew DW, Vanichviriyakit R, Williams BRP, Sritunyalucksana K, Itsathiphasarn O. 2018. Identification, characterization and heparin binding capacity of a spore-wall, virulence protein from the shrimp microsporidian Enteroctozytozoon hepatopeini (EHP). Parasites & Vectors 11:177. DOI: https://doi.org/10.1186/s13071-018-2758-z, PMID: 29530076

Jensen PH, Kolarich D, Packer NH. 2010. Mucin-type O-glycosylation—putting the pieces together. The FEBS Journal 277:81–94. DOI: https://doi.org/10.1111/j.1742-4658.2009.07429.x, PMID: 19919547

Kim DH, Feinbaum R, Alloing G, Emerson FE, Garsin DA, Inoue H, Tanaka-Hino M, Hisamoto N, Matsumoto K, Kim DH, Mak R, Troemel ER. 2017. In vivo mapping of tissue- and subcellular-specific proteomes. Science 359:623–626. DOI: https://doi.org/10.1126/science.1073759, PMID: 12142542

Kirienko NV, Cezairilyan BO, Ausubel FM, Powell JR. 2014. Pseudomonas aeruginosa PA14 pathogenesis in Caenorhabditis elegans. Methods in Molecular Biology 1149:653–669. DOI: https://doi.org/10.1007/978-1-4939-0473-0_50, PMID: 24818940

Li H, Durbin R. 2009. Fast and accurate short read alignment with burrows-wheeler transform. Bioinformatics 25:1754–1760. DOI: https://doi.org/10.1093/bioinformatics/btp324, PMID: 19451168

Li Y, Wu Z, Pan G, He W, Zhang R, Hu J, Zhou Z. 2009. Identification of a novel spore wall protein (SWP26) from microsporidia Nosema bombycis. International Journal for Parasitology 39:391–398. DOI: https://doi.org/10.1016/j.ijpara.2008.08.011, PMID: 18854188

Luallen RJ, Bakowski MA, Troemel ER. 2015. Characterization of microsporidia-induced developmental arrest and a transmembrane leucine-rich protein in Caenorhabditis elegans. PLOS ONE 10:e0124065. DOI: https://doi.org/10.1371/journal.pone.0124065, PMID: 25874557

Luallen RJ, Reinke AW, Tong L, Botts MR, Félix MA, Troemel ER. 2016. Discovery of a Natural Microsporidian Pathogen with a Broad Tissue Tropism in Caenorhabditis elegans. PLOS Pathogens 12:e1005724. DOI: https://doi.org/10.1371/journal.ppat.1005724, PMID: 27362540

Martín-Hernández R, Bartolomé C, Chejanovsky N, Le Conte Y, Dalmon A, Dussaibat C, García-Palencia P, Meana A, Pinto MA, Soroker V, Higes M. 2018. Nosema ceranae in Apis mellifera: a 12 years postdetection perspective. Environmental Microbiology 20:1302–1329. DOI: https://doi.org/10.1111/1462-2920.14103, PMID: 29575513

McGhee J, Ghafouri S. 2007. Bacterial residence time in the intestine of C. elegans. Nematology 9:87–91. DOI: https://doi.org/10.1111/j.1568-5410.2006.00797.x, PMID: 17468471

Mello CC, Kramer JM, Stinchcomb D, Ambros V. 1991. Efficient gene transfer in C. elegans: extrachromosomal maintenance and integration of transforming sequences. The EMBO Journal 10:3959–3970 PMID: 19359141

Mok C, Belmarez G, Edgley ML, Moerman DG, Waterston RH. 2020. MIP-MAP: High-Throughput Mapping of Caenorhabditis elegans Temperature-Sensitive Mutants via Molecular Inversion Probes. Genetics 207:447–463. DOI: https://doi.org/10.1534/genetics.117.300179, PMID: 28827289

Moore SD, Prevelige PE. 2002. A P22 scaffold protein mutation increases the robustness of head assembly in the presence of excess portal protein. Journal of Virology 76:10245–10255. DOI: https://doi.org/10.1128/jvi.76.20.10245-10255.2002, PMID: 12239300

Murareanu BM, Knox J, Roy PJ, Reinke AW. 2021a. High-throughput Small Molecule Screen Identifies Inhibitors of Microsporidia Invasion and Proliferation in C. elegans. [bioRxiv]. DOI: https://doi.org/10.1101/2021.09.06.459184

Murareanu BM, Sukhdeo R, Qu R, Jiang J, Reineke AW. 2021b. Generation of a microsporidia species attribute database and analysis of the extensive ecological and phenotypic diversity of microsporidia. MBio 12:e0149021. DOI: https://doi.org/10.1128/mBio.01490-21, PMID: 34182782

Poncione L, Beauvais G, Nonin-Lecomte S, Dardel F. 2009. A generic protocol for the expression and purification of recombinant RNA in Escherichia coli using a tRNA scaffold. Nature Protocols 4:947–959. DOI: https://doi.org/10.1038/nprot.2009.67, PMID: 19478810

Powell JR, Ausubel FM. 2008. Models of Caenorhabditis elegans infection by bacterial and fungal pathogens. Methods in Molecular Biology 415:403–427. DOI: https://doi.org/10.1007/978-1-59745-570-1_24, PMID: 18370168

Reddy KC, Dorr T, Sowa JN, Panek J, Chen K, Lim ES, Wang D, Troemel ER. 2017. An intracellular pathogen response pathway promotes proteostasis in C. elegans. Current Biology 27:3544–3553. DOI: https://doi.org/10.1016/j.cub.2017.10.009, PMID: 29103937

Reddy KC, Dorr T, Underwood RS, Osman GA, Elder CR, Desjardins CA, Cuomo CA, Barkoulas M, Troemel ER. 2019. Antagonistic paralogs control a switch between growth and pathogen resistance in C. elegans. PLOS Pathogens 15:e1007528. DOI: https://doi.org/10.1371/journal.ppat.1007528, PMID: 30640956

Reinke AW, Mak R, Troemel ER, Bennett EJ. 2017. In vivo mapping of tissue- and subcellular-specific proteomes in Caenorhabditis elegans. Science Advances 3:e160242. DOI: https://doi.org/10.1126/sciadv.1602426
Wadi L, Reinke AW. 2020. Evolution of microsporidia: An extremely successful group of eukaryotic intracellular parasites. *PLOS Pathogens* 16:e1008276. DOI: https://doi.org/10.1371/journal.ppat.1008276, PMID: 32053705

Walhout AJ, Temple GF, Brasch MA, Hartley JL, Lorson MA, van den Heuvel S, Vidal M. 2000. GATEWAY recombinational cloning: application to the cloning of large numbers of open reading frames or ORFeomes. *Methods in Enzymology* 328:575–592. DOI: https://doi.org/10.1016/s0076-6879(00)28419-x, PMID: 11075367

Wan G, Fields BD, Spracklin G, Shukla A, Phillips CM, Kennedy S. 2018. Spatiotemporal regulation of liquid-like condensates in epigenetic inheritance. *Nature* 557:679–683. DOI: https://doi.org/10.1038/s41586-018-0132-0, PMID: 29769721

Wang K, Li M, Hakonarson H. 2010. ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. *Nucleic Acids Research* 38:e164. DOI: https://doi.org/10.1093/nar/gkq603, PMID: 20601685

Willis AR, Zhao W, Sukhdeo R, Wadi L, El Jarkass HT, Claycomb JM, Reinke AW. 2021. A parental transcriptional response to microsporidia infection induces inherited immunity in offspring. *Science Advances* 7:eabf3114. DOI: https://doi.org/10.1126/sciadv.abf3114, PMID: 33952520

Wu Z, Li Y, Pan G, Tan X, Hu J, Zhou Z, Xiang Z. 2008. Proteomic analysis of spore wall proteins and identification of two spore wall proteins from *Nosema bombycis* (Microsporidia). *Proteomics* 8:2447–2461. DOI: https://doi.org/10.1002/pmic.200700584, PMID: 18563739

Xu Y, Takvorian P, Cali A, Weiss LM. 2003. Lectin binding of the major polar tube protein (PTP1) and its role in invasion. The *Journal of Eukaryotic Microbiology* 50 Suppl:600–601. DOI: https://doi.org/10.1111/j.1550-7408.2003.tb00644.x, PMID: 14736177

Xu Y, Takvorian PM, Cali A, Orr G, Weiss LM. 2004. Glycosylation of the major polar tube protein of *Encephalitozoon hellem*, a microsporidian parasite that infects humans. *Infection and Immunity* 72:6341–6350. DOI: https://doi.org/10.1128/IAI.72.11.6341-6350.2004, PMID: 15501762

Zhang G, Sachse M, Prevost MC, Lualien RJ, Troemel ER, Felix MA. 2016. A large collection of novel nematode-infecting microsporidia and their diverse interactions with *Caenorhabditis elegans* and other related nematodes. *PLOS Pathogens* 12:e1006093. DOI: https://doi.org/10.1371/journal.ppat.1006093, PMID: 27942022
## Appendix 1

### Appendix 1—key resources table

| Reagent type (species) or resource | Designation | Source or reference | Identifiers | Additional information |
|-----------------------------------|-------------|---------------------|-------------|------------------------|
| Gene (Caenorhabditis elegans) | aaim-1 | This paper | T14E8.4 | Wormbase ID: WBGene00043981 |
| Genetic reagent (Caenorhabditis elegans) | N2 | Caenorhabditis genetic center (CGC) | N2 RRID:SCR_007341 | Wild-type, Bristol strain |
| Genetic reagent (Caenorhabditis elegans) | fawn-1 (AWR 05) | This paper | aaim-1 (kea89) X | C127T, Q43Stop |
| Genetic reagent (Caenorhabditis elegans) | fawn-2 (AWR 11) | This paper | aaim-1 (kea28) X | 2.2 kb deletion |
| Genetic reagent (Caenorhabditis elegans) | fawn-3 (AWR 17) | This paper | aaim-1 (kea91) X | G221A splice site mutation |
| Genetic reagent (Caenorhabditis elegans) | fawn-4 (AWR 03) | This paper | aaim-1 (kea103) X | C1286T, A429V |
| Genetic reagent (Caenorhabditis elegans) | DM748 | Mok et al., 2020 DOI: 10.1534/g3.120.401656. VC20019 (Ex[myo-3::YFP]) | | Mapping strain |
| Genetic reagent (Caenorhabditis elegans) | R8563 | Caenorhabditis genetic center (CGC) | aaim-1 (ok295) X | Large gene deletion in aaim-1 and neighbouring gene dop-3 |
| Genetic reagent (Caenorhabditis elegans) | AWR 73 | This paper | aaim-1 (kea22) X | 3 × outcrossed CRISPR-Cas9 generated deletion allele of aaim-1 |
| Genetic reagent (Caenorhabditis elegans) | AWR 83 | This paper | aaim-1 (kea28) X | 6 × outcrossed fawn-2 (kea28) |
| Genetic reagent (Caenorhabditis elegans) | DA465 | Caenorhabditis genetic center (CGC) | eat-2 (ad465) | Feeding defective mutant |
| Genetic reagent (Caenorhabditis elegans) | AWR 131 | This paper | | |
| Genetic reagent (Caenorhabditis elegans) | AWR 125 | This paper | aaim-1(kea22 Ex[myo2::mCherry::Unc54, paaaim-1::GFP::3xFlag::Unc54]) | aaim-1 transcriptional reporter in N2 background with a pharyngeal mCherry co-injection marker. |
| Genetic reagent (Caenorhabditis elegans) | AWR 122 | This paper | aaim-1(kea22 Ex[myo3::mCherry::Unc54, paaaim-1::GFP::Unc54]) | aaim-1 transcriptional reporter in aaim-1 (kea22) mutant background with a pharyngeal mCherry co-injection marker. |
| Genetic reagent (Caenorhabditis elegans) | AWR 115 | This paper | aaim-1(kea22 Ex[myo2::mCherry::Unc54, paaaim-1::aaaim-1::Unc54]) | aaim-1 over expression in an aaim-1 (kea22) mutant background with a pharyngeal mCherry co-injection marker. |

Appendix 1 Continued on next page
## Appendix 1 Continued

| Reagent type (species) or resource | Designation | Source or reference | Identifiers | Additional information |
|-----------------------------------|-------------|---------------------|-------------|------------------------|
| Genetic reagent (Caenorhabditis elegans) | AWR119 | This paper | aaim-1 (kea22 Ex[pmyo2::mCherry::Unc54, paaim-1::aim-1::3xFlag::Unc54]) | aaim-1::3xFlag over expression in an aaim-1 (kea22) mutant background with a pharyngeal mCherry co-injection marker. |
| Genetic reagent (Caenorhabditis elegans) | AWR 127 | This paper | aaim-1 (kea22 Ex[pmyo2::mCherry::Unc54, paaim-1::3xFlag::Unc54]) | Signal peptide mutant aaim-1::3xFlag over expression in an aaim-1 (kea22) mutant background with a pharyngeal mCherry co-injection marker. |
| Genetic reagent (Caenorhabditis elegans) | AWR129 | This paper | aaim-1 (kea22 Ex[pmyo2::mCherry::Unc54, paaim-1::3xFlag::Unc54]) | Intestinal aaim-1::3xFlag overexpression in an aaim-1 (kea22) mutant background with a pharyngeal mCherry co-injection marker. |
| Genetic reagent (Caenorhabditis elegans) | YY1446 | Caenorhabditis genetic center (CGC) | znfx-1[ggek3k48A::tagRFP::znfx-1.1] | RFP germ granules |
| Genetic reagent (Caenorhabditis elegans) | GK288 | Sato et al., 2007 DOI: 10.1038/nature05999 | unc-119(ed3); dklis116[popt-2::PGP-1::GFP, unc-119(+)] | Apical intestinal membrane marker. |
| Genetic reagent (Caenorhabditis elegans) | KU25 | Caenorhabditis genetic center (CGC) | pmk-1 (lmo25) IV | p38 Map kinase loss of function mutant. |
| Genetic reagent (Caenorhabditis elegans) | AWR182 | This paper | aaim-1 (kea22 X; dklis116[popt-2::PGP-1::GFP, unc-119(+)]) IV | aaim-1 (kea22) mutant allele crossed into GK288. |
| Genetic reagent (Escherichia coli) | OP50-1 | Caenorhabditis genetic center (CGC) | | Uracil auxotroph. B strain. Streptomycin resistant. |
| Genetic reagent (Escherichia coli) | S-alpha competent E. coli | New England Biolabs (NEB) | Catt#: C2997H | E. coli background in which transformations for molecular cloning were performed. |
| Genetic reagent (Nematocida parisii) | N. parisii (ERTm1) | This paper | | Nematode intestinal infecting species of microsporidia. |
| Genetic reagent (Nematocida ausubeli) | N. ausubeli (ERTm2) | This paper | | Nematode intestinal infecting species of microsporidia. |
| Genetic reagent (Pseudomonas aeruginosa) | PA14:DsRed | Dunn et al., 2006 DOI: 10.1128/AEM.72.1.802–810.2006 | PA14:DsRed | DsRed labelled strain of PA14. |
| Genetic reagent (Staphylococcus aureus) | NCTC 8325 | Sifri et al., 2003 DOI: 10.1128/IAI.71.4.2208–2217.2003 | NCTC 8325 | S. aureus isolate used for C. elegans killing assays. |
| Antibody | M2 anti Flag (Mouse monoclonal) | Sigma | Catt#: F1804 RRID:AB_262044 | IF (1:250) |
| Antibody | Anti mouse Alexafluor 594 (Goat polyclonal) | Thermo Fisher | Catt#: A32742 RRID:AB_2762825 | IF (1:300) |
| Sequence-based reagent | Reverse primer | Integrated DNA technologies (IDT) | Reverse primer to amplify aaim-1 | S'-taaattttttctggtgacctggc-3' |
| Sequence-based reagent | Forward primer | Integrated DNA technologies (IDT) | Forward primer to generate SPAAaim-1 | S'-agctgctagcttctctcctcctgctgcc-3' |
| Sequence-based reagent | Forward primer | Integrated DNA technologies (IDT) | Forward primer to amplify paaim-1 | S'-tagttgtgaagcagcagaaaaagcagctcttc-3' |

Appendix 1 Continued on next page
| Reagent type (species) or resource | Designation | Source or reference | Identifiers | Additional information |
|----------------------------------|-------------|---------------------|-------------|------------------------|
| Sequence-based reagent           | Reverse primer | Integrated DNA technologies (IDT) | Reverse primer to amplify paa1-1 | S'-caggtggacttcttcctattatggactcttt
|                                  |             |                     |             |                        |
| Sequence-based reagent           | Forward primer | Integrated DNA technologies (IDT) | Forward primer to amplify pmyo2 | S'-cattatataatctctcgtagctttcagttct
|                                  |             |                     |             |                        |
| Sequence-based reagent           | Reverse primer | Integrated DNA technologies (IDT) | Reverse primer to amplify pmyo2 | S'-gatctttggtgctgtagct
|                                  |             |                     |             |                        |
| Sequence-based reagent           | Forward primer | Integrated DNA technologies (IDT) | Forward primer to amplify papp5 | S'-gaagcotaataaatcattatggagaaaaatc
|                                  |             |                     |             |                        |
| Sequence-based reagent           | Reverse primer | Integrated DNA technologies (IDT) | Reverse primer to amplify papp5 | S'-ttgatgtaaatatatttgaaatga
|                                  |             |                     |             |                        |
| Sequence-based reagent           | Forward primer | Integrated DNA technologies (IDT) | Forward primer to amplify GFP from pDD282 | S'-agtgaattggagaggagagttaagttggttact
|                                  |             |                     |             |                        |
| Sequence-based reagent           | Reverse primer | Integrated DNA technologies (IDT) | Reverse primer to amplify GFP from pDD282 | s'-tacggtagcgccttgctatcccg
|                                  |             |                     |             |                        |
| Sequence-based reagent           | Forward Ulramer | Integrated DNA technologies (IDT) | Forward ulramer to add a Gly Ala Gly Ser linker and 3 x Flag with stop codon to C- Terminal end of constructs in pDDONR221 via round the horn PCR | S'-gagccccgagtgtgtggtggtggtgctgacgaggagccagcaacagcctggtgctgactagttggtggtggtg
|                                  |             |                     |             |                        |
| Sequence-based reagent           | MicroR FISH probe conjugated to Cal Fluor 610 | LGC Biosearch Technologies | 18 s RNA FISH probe | S'-ccctgaggactcctctg
|                                  |             |                     |             |                        |
| Sequence-based reagent           | Alt-R CRISPR-Cas9 tracrRNA | Integrated DNA technologies (IDT) | Catt#: 1072532 |                        |
|                                  |             |                     |             |                        |
| Sequence-based reagent           | 5' sgRNA | Integrated DNA technologies (IDT) | Guide RNA | S'-ttaaattacgagctagtaagagaagaggcag
|                                  |             |                     |             |                        |
| Sequence-based reagent           | 3' sgRNA | Integrated DNA technologies (IDT) | Guide RNA | S'-ttttaacgtgaagagatcagtt
|                                  |             |                     |             |                        |
| Recombinant protein              | Alt-R S.p. Cas9 Nuclease V3, 100 ug | Integrated DNA technologies (IDT) | Catt#: 1081058 | DNA polymerase used for all molecular cloning steps |
|                                  |             |                     |             |                        |
| Recombinant protein              | Phusion High-Fidelity DNA Polymerase | New England Biolabs (NEB) | Catt#: M0530L |                        |
|                                  |             |                     |             |                        |
| Recombinant DNA reagent          | pBSK | Poncho et al., 2009 DOI: 10.1038/nprot.2009.67, pBSK RRID:Addgene_67504 | Addgene ID: 67,504 |                        |
|                                  |             |                     |             |                        |
| Recombinant DNA reagent          | Gateway pDONR221 | Invitrogen | Catt#: 12536017 |                        |
|                                  |             |                     |             |                        |
| Recombinant DNA reagent          | pCFJ90 | Frejka-Jensen et al., 2008 DOI: 10.1038/ng.248, pCFJ90 RRID:Addgene_19327 | Addgene ID: 19,327 |                        |
|                                  |             |                     |             |                        |
| Recombinant DNA reagent          | pDD282 | Dickinson et al., 2015 DOI: 10.1534 genetics.115.178335, pDD282 RRID:Addgene_66823 | Addgene ID: 66,823 |                        |
|                                  |             |                     |             |                        |
| Commercial assay or kit          | NEBuilder HiFi DNA assembly | New England biolabs (NEB) | Catt#: 3E2621 | Kit used for Gibson assembly |
|                                  |             |                     |             |                        |
| Commercial assay or kit          | Monarch PCR and DNA Cleanup Kit | New England biolabs (NEB) | Catt#: T10305 | PCR purification kit for amplicons used in downstream molecular cloning steps |
|                                  |             |                     |             |                        |
| Commercial assay or kit          | QIAprep spin miniprep kit Qiagen | Qiagen | Catt#: 27,106 | Kit used for extraction of DNA from bacterial clones |
|                                  |             |                     |             |                        |
| Chemical compound, drug          | Direct yellow 96 | Sigma- Aldrich | Catt#: S47240-1G | Chitin binding dye |
|                                  |             |                     |             |                        |
| Chemical compound, drug          | Calcofluor white | Sigma- Aldrich | Catt#: 18,909 | Chitin binding dye |

Appendix 1 Continued on next page
### Appendix 1 Continued

| Reagent type (species) or resource | Designation | Source or reference | Identifiers | Additional information |
|-----------------------------------|-------------|---------------------|-------------|------------------------|
| Chemical compound, drug          | EverbriteMounting Medium | Biotium | Cat#: 23,002 | Mounting medium with DAPI |
| Software, algorithm               | FIJI        | Schindelin et al., 2012 DOI: 10.1038/nmeth.2019 | RRID:SCR_002285 | Image analysis software |
| Software, algorithm               | GraphPad Psm 9.0 | GraphPad Psm 9.0 | RRID:SCR_002798 | Statistical analysis software |
| Other                             | 0.2 μm green fluorescent polystyrene beads | Degradex Phosphorex | Cat#: 2,108B | Fluorescent beads for bead feeding assays |