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

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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 of *AAIM-1* reduces *P. aeruginosa* colonization. Competitive fitness assays show that *aaim-1* mutants are favoured 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.

Introduction

Microsporidia are a large group of obligate intracellular parasites that infect most types of animals.[1] These ubiquitous parasites possess the smallest known eukaryotic genoms, and are extremely reliant on their host as a result of the loss of many genes involved in metabolism and energy production.[2,3] Microsporidia can have a large impact on the evolution of their hosts, as infection with microsporidia often leads to a reduction in host offspring and the effect of this selective pressure has resulted in resistant animals within a population.[4,5] Microsporidia are currently a major threat to many commercially important species such as honeybees and shrimp.[6,7] Many species also infect humans and infections in immunocompromised individuals can result in lethality.[8] Despite their ubiquitous nature, effective treatment strategies are currently lacking for these poorly understood parasites.[9]

46 Microsporidia infection begins with invasion of host cells. They possess fascinating invasion
47 machinery, a unique structure known as the polar tube.[10] This apparatus, resembling a long thread,
48 is often coiled within a dormant spore. However, once inside of a host, and in proximity to the
49 tissue of interest, the polar tube rapidly emerges or "fires" , releasing the infectious material (the
50 sporoplasm) which is deposited intracellularly either through direct injection, or through the
51 internalization of the sporoplasm.[10,11]
52
53 A number of microsporidia proteins have been demonstrated to play important roles during
54 invasion by insect- and human-infecting species of microsporidia.[10] For example, spore wall
55 proteins can interact with host cells through the recognition of sulfated glycosaminoglycans,
56 heparin binding motifs, integrins, and proteins on the cell surface. [12–17] In
57 *Encephalitozoon* species, polar tube proteins (PTP) can mediate interactions with the host. For
58 instance, O-linked mannosylation on PTP1 has been demonstrated to bind mannose binding
59 receptors, whereas PTP4 interacts with the transferrin receptor (Trf1).[11,18–20] Additionally, the
60 sporoplasm surface protein, EhSSP1, binds to an unknown receptor on the cell surface.[21] These
61 proteins on the spore, polar tube, and sporoplasm have all been shown to promote microsporidia
62 adhesion or invasion of host cells in culture systems, but the role of these proteins during animal
63 infection is unclear.
64
65 The nematode *Caenorhabditis elegans* is infected in its natural habitat by several species of
66 microsporidia, and frequently by *Nematocida parisii.*[22–24] This species infects the intestinal cells
67 of *C. elegans,* which possess similarity to those of mammalian cells, making this animal both a
68 relevant tissue and model to study these infections in vivo.[24,25] Infection of *C. elegans* by *N. parisii*

69 begins when spores are consumed by the worm, where they then pass through the pharynx into the
70 intestinal lumen and fire, depositing sporoplasms inside of intestinal cells. Within 72 hours the
71 sporoplasm will divide into meronts, which differentiate into spores, that then exit the animal,
72 completing the parasite's life cycle.[26,27] Infection with *N. parisii* leads to reduced fecundity and
73 premature mortality in *C. elegans*.[24,26] Several mutants have been shown to affect proliferation and
74 spore exit.[28,29] Immunity that can either prevent infection or clear the pathogen once infected has
75 also been described.[4,27,30–32] In contrast, very little is known about how *N. parisii* invades *C.*
76 *elegans* intestinal cells. Almost all of the microsporidia proteins known to facilitate invasion of
77 host cells are not conserved in *N. parisii* and although host invasion factors described in other
78 species are present in *C. elegans*, there is no evidence that they are being used by microsporidia
79 during invasion of *C. elegans.*[11]
80
81 To understand how microsporidia invade animal cells, we performed a forward genetic screen to
82 identify host factors that promote infection. We identified a novel, nematode-specific protein,
83 AAIM-1, whose loss of function confers resistance to microsporidia infection. This protein is
84 expressed in intestinal cells, secreted into the intestinal lumen, and is necessary to ensure proper
85 spore orientation during intestinal cell invasion. In addition, we show that AAIM-1 limits bacterial
86 colonization of pathogenic *Pseudomonas aeruginosa*. Strikingly, AAIM-1 plays opposing roles on
87 host fitness in the face of pathogenesis. The utilization of a host factor critical for bacterial defense
88 reflects a clever strategy to ensuring microsporidia's reproductive success.
89
90 **Results**
91 **A forward genetic screen identifies *aaim-1* as being necessary for *N. parisii* infection.**

92 To identify host factors needed for infection by microsporidia, we carried out a forward genetic
93 screen using a *C. elegans* model of *N. parisii* infection. We took advantage of the previously
94 described phenotypes of *C. elegans* displaying reduced fitness when infected with *N. parisii,*
95 including reduced progeny production and stunted development.[26,27,33,34] We mutagenized animals
96 and subjected their F2 progeny to *N. parisii* infection. After infecting populations for five
97 subsequent generations, we selected individual worms containing embryos, indicating increased
98 fitness in the presence of infection (see Methods). We identified four independent isolates that
99 when exposed to *N. parisii* reproducibly had higher fractions of animals containing embryos
100 compared to wild type (N2). We named these isolates Fitness Advantage With *Nematocida* (*fawn*
101 1-4) (Figure S1a).
102
103 As *C. elegans* that are less infected with *N. parisii* produce more progeny, we hypothesised that
104 these *fawn* mutants would be resistant to *N. parisii* infection[27]. To determine this, we grew the
105 three isolates with the strongest phenotype, *fawn* 1-3, in the presence and absence of *N. parisii*,
106 and stained each population of worms with the chitin binding dye, Direct-yellow 96 (DY96), at 72
107 hours post infection (hpi). DY96 allows for the visualization of chitinous microsporidia spores as
108 well as worm embryos (Figure 1a). In the absence of infection, there is no difference in the fraction
109 of *fawn-2* and *fawn-3* animals developing into adults containing embryos (gravid adults), although
110 *fawn-1* has a modest defect. In comparison, all three *fawn* isolates generate significantly more
111 gravid adults than N2 animals in the presence of infection (Figure 1b). We next examined the
112 fraction of animals in each strain containing intracellular microsporidia spores and observed that
113 all three *fawn* isolates display significantly fewer numbers of spore-containing worms (Figure 1c).

114 These results suggest that *fawn* mutants are missing an important factor for efficient microsporidia
115 infection.
116
117 To identify the causal mutations underlying the Fawn phenotype, we used a combination of whole-
118 genome sequencing and genetic mapping. We generated F2 recombinants and performed two
119 rounds of infection with microsporidia, selecting for gravid animals. After each round we used
120 molecular inversion probes to determine the region of the genome linked to the causal mutation.[35]
121 This revealed strong signatures of selection on the left arm of chromosome X in all three *fawn*
122 isolates and absent in N2 (Figure S1b). Analysis of whole genome sequencing showed that all four
123 *fawn* isolates contained different alleles of *T14E8.4*, which we named *aaim-1* (Antibacterial and
124 Aids Invasion by Microsporidia-1) for reasons described below (Figure 1d). We validated the role
125 of *aaim-1* in resistance to infection using several additional alleles: an independent allele *aaim-1*
126 (*ok295*), carrying a large gene deletion in both *aaim-1* and *dop-3,* and a CRISPR-Cas9 derived
127 allele, *aaim-1 (kea22),* that contains a large gene deletion. Both of these alleles displayed a fitness
128 advantage when infected with *N. parisii* (Figure 1d,e, S1c,d). These data demonstrate that *aaim-1*
129 is the causative gene underlying the *fawn* 1-4 infection phenotypes. In subsequent experiments we
130 utilized both *aaim-1 (kea22)*, and *fawn-3 (kea28),* carrying a 2.2 kb deletion in *aaim-1,* which was
131 outcrossed to N2 six times (hereafter referred to as *aaim-1 (kea28)*).
132
133 ***aaim-1* is expressed in the pharynx and intestine, and secretion is important for function.**
134 AAIM-1 is a poorly characterized protein that does not possess any known or conserved domains.
135 Homologs of the protein exist in both free-living and parasitic nematodes (Figure S2). To further
136 characterize the role of AAIM-1 during *N. parisii* infection, we generated transgenic

137 extrachromosomal lines of *C. elegans* carrying a reporter transgene of GFP under control of the
138 *aaim-1* promoter. GFP fluorescence was observed in the terminal bulb of the pharynx as well as
139 the posterior of the intestine throughout development (Figure 2a). Embryos and L1 animals display
140 additional expression in the arcade cells of the pharynx (Figure 2a, S3a).
141
142 The first 17 amino acids of AAIM-1 are predicted to encode a signal peptide.[36] This suggests that
143 AAIM-1 may be secreted into the pharyngeal and intestinal lumen, the extracellular space through
144 which *N. parisii* spores pass before invading intestinal cells. To test which tissues AAIM-1
145 functions in and if secretion is important for function, we generated a series of transgenic worms
146 expressing extrachromosomal arrays (Key resources table). First, we generated transgenic *aaim-1*
147 *(kea22)* animals expressing AAIM-1 tagged on the C-terminus with a 3x Flag epitope. Transgenic
148 animals expressing AAIM-1 under its native promoter complement the ability of *aaim-1 (kea22)*
149 animals to develop into adults in the presence of a high amount of *N. parisii* spores (Figure 2b). A
150 construct expressing GFP or GFP::3xFlag does not influence this phenotype nor does the presence
151 of the epitope tag impair the ability of AAIM-1 to rescue the mutant phenotype (Figure S3b). We
152 next generated a signal peptide mutant allele of AAIM-1 missing the first 17 amino acids
153 *(SPΔaaim-1),* which is unable to complement the *aaim-1 N. parisii* infection phenotype. In
154 contrast, AAIM-1 expressed from an intestinal-specific promoter (*spp-5)*[37] can rescue the infection
155 phenotype of *aaim-1 (kea22)* (Figure 2b).
156
157 To determine where AAIM-1 localizes, we dissected the intestines from transgenic worms and
158 performed immunofluorescence using anti-Flag antibodies. We were unable to detect expression
159 of AAIM-1::3xFlag when expressed from its endogenous promoter. However, we observed protein

160 expression in the intestinal cells of animals expressing AAIM-1::3xFlag from a strong, intestinal
161 specific-promoter or when the signal peptide was removed (Figure 2c). We did not observe AAIM-
162 1::3xFlag localized in the extracellular space of the intestinal lumen, possibly due to rapid turnover
163 of intestinal contents or due to loss from dissection of the intestines.[38] The increased expression in
164 the signal peptide mutant suggests an accumulation of protein that is unable to be secreted. Taken
165 together, these data demonstrate that AAIM-1 is secreted and acts within the intestinal lumen to
166 promote *N. parisii* infection.
167
168 **AAIM-1 is only necessary for microsporidia infection at the earliest larval stage.**
169 *N. parisii* infection of *C. elegans* can occur throughout development, but several forms of
170 immunity towards microsporidia have been shown to be developmentally regulated.[4,27] To
171 determine if *aaim-1* mutant animals display developmentally restricted resistance to infection, we
172 infected *fawn* 1-3 at the L1 and L3 stage. For these experiments we took advantage of another
173 intestinal-infecting species of microsporidia, *Nematocida ausubeli*, which has a more severe effect
174 on *C. elegans* fecundity, allowing us to determine fitness defects after the L1 stage.[4,23,26] *fawn*
175 isolates are resistant to *N. ausubeli* as seen by an increase in the fraction of gravid adults in the
176 population after exposure to a medium dose of *N. ausubeli* (Figure 3a). When we initiated
177 infections at the L3 stage of growth, *fawn* isolates do not have increased resistance, and instead
178 exhibit wild-type levels of susceptibility (Figure 3b). To rule out the possibility that this L1
179 restricted phenotype was the result of exposure to sodium hypochlorite treatment, which we used
180 to synchronize worms, we exposed embryos that were naturally laid by adults within a two-hour
181 window to *N. parisii* infection. Animals synchronized in this manner still display a robust

182 resistance to *N. parisii* (Figure S4c). Thus, resistance to infection in *aaim-1* mutants is
183 developmentally restricted and AAIM-1 is utilized by several species of microsporidia.
184
185 **AAIM-1 is needed for efficient invasion of intestinal cells**
186 Resistance to infection could be the result of a block in invasion, proliferation, or through the
187 destruction of the parasite. To test the mechanism of resistance in *aaim-1* mutants, we performed
188 pulse-chase infection assays at the L1 and L3 stage of development.[4,27] Here, we treated animals
189 with a medium-1 dose (as defined in Table S1) of *N. parisii* for 3 hours, washed away any un-
190 ingested spores, and then replated the animals in the absence of spores for an additional 21 hours.
191 We then used an 18S RNA Fluorescent In Situ Hybridization (FISH) probe to detect *N. parisii*
192 sporoplasms, which is the earliest stage of microsporidia invasion. In our *fawn* 1-3 isolates we
193 detect less invasion at 3hpi compared to N2 (Figure S4a). However, there was no reduction in the
194 number of infected animals between 3hpi and 21 hpi, indicating that pathogen clearance was not
195 occurring. This defect in invasion was not present at the L3 stage, providing further support that
196 resistance is restricted to the L1 stage in *aaim-1* mutants (Figure S4b). A reduction in invasion
197 could be due to a feeding defect, leading to a reduction in spore consumption. To test rates of
198 consumption, we measured the intestinal accumulation of fluorescent beads. We find that *aaim-1*
199 alleles displayed wild-type levels of bead accumulation, unlike the feeding defective strain *eat-2*
200 *(ad465)* (Figure S4d).
201
202 For *N. parisii* to invade host cells, spores must first enter the intestinal lumen and fire their polar
203 tube.[27] To test if *aaim-1* mutants have defects in spore entry or spore firing, we infected animals
204 for either 45 minutes or 3 hours, at the L1 and L3 stages. We then fixed and stained animals with

205 both an *N. parisii* 18S RNA FISH probe and DY96 and quantified the number of spores present in
206 the intestinal lumen of animals. Here, *aaim-1* animals infected for 45 minutes or 3 hours at L1 or
207 L3 contained similar amounts of spores as N2 animals (Figure 3c,f, S5a,d). The percentage of fired
208 spores present within these animals is also not significantly different at either developmental stage
209 (Figure 3d,g, S5b,e). We then counted the number of sporoplasms per animal and observed
210 significantly fewer invasion events in *aaim-1* mutant animals infected at L1 (Figure 3e, S5c). In
211 contrast, the number of sporoplasms in L3 stage *aaim-1* alleles are similar to that observed in the
212 N2 strain (Figure 3h, S5f). These results demonstrate that the *N. parisii* invasion defect in *aaim-1*
213 mutants is not caused by differences in spore firing or accumulation. Instead, these results suggest
214 that spores are misfiring, leading to unsuccessful parasite invasion.
215
216 **AAIM-1 plays a role in promoting proper spore orientation**
217 To determine how AAIM-1 promotes *N. parisii* invasion, we further examined the invasion
218 process. We pre-stained spores with Calcofluor white (CFW) and assessed their orientation relative
219 to the intestinal apical membrane using the apical membrane marker PGP-1::GFP in L1 worms
220 infected for 45 minutes (Figure 4a). In N2 animals, 32.4% of spores are angled relative to the
221 apical membrane. In contrast, spores in an *aaim-1* mutant were angled 14.3% of the time (Figure
222 4b). Several host factors that promote microsporidia invasion cause adherence to host cells.[11] To
223 determine if AAIM-1 influences the location of spores relative to intestinal cells in *aaim-1* mutants,
224 we measured the perpendicular distance from the center of a parallel spore to the apical membrane
225 of the intestine. Surprisingly, parallel spores in *aaim-1* alleles were significantly closer to the apical
226 membrane (0.29 μm) than those in N2 (0.34 μm) (Figure 4c). In agreement with resistance being
227 developmentally restricted, *aaim-1* mutants display wild-type spore orientations and distances

228 from the membrane when infections were initiated at the L3 stage (Figure 4d,e). The width of the
229 intestinal lumen at the L1 stage does not differ significantly between N2 and *aaim-1* mutants,
230 however, L3 animals generally possess wider intestinal lumens (Figure S5g,h). Thus, taken
231 together these results suggest that AAIM-1 plays a distinct role in the intestinal lumen at L1 to
232 promote proper spore orientation, through maintaining an appropriate distance and angle to the
233 apical membrane, resulting in successful invasion.
234
235 **AAIM-1 inhibits intestinal colonization by *Pseudomonas aeruginosa***
236 Interestingly, *aaim-1* has been shown to be upregulated by a variety of different fungal and
237 bacterial pathogens, including *P. aeruginosa*. [39,40] Using our transcriptional reporter strain, we
238 sought to confirm this and determine if microsporidia infection could also induce *aaim-1*
239 transcription. N2 animals carrying a transcriptional reporter (p*aaim-1*::GFP::3xFlag) were exposed
240 to *N. parisii, P. aeruginosa* PA14, or *E. coli* OP50-1, and the levels of GFP quantified when grown
241 on these pathogens for 72 hours from the L1 stage, or for 24 hours from the L4 stage. Infection by
242 either *N. parisii* or *P. aeruginosa* PA14 resulted in the upregulation of *aaim-1* as detected by an
243 increase in the GFP signal (Figure 5a, S6f).
244
245 Previously, an *aaim-1* deletion strain, RB563 *(ok295),* was shown to display reduced survival on
246 lawns of *P. aeruginosa* PA14.[41] The enhanced susceptibility previously reported was attributed to
247 *dop-3,* which is also partially deleted in RB563 *(ok295)*. [41] To determine if *aaim-1* mutants are
248 susceptible to pathogenic bacterial infection, we assayed the survival of L4 stage worms in *P.*
249 *aeruginosa* PA14 slow killing assays. A mutant in the p38 MAPK pathway (*pmk-1*) was used as
250 control for susceptibility to PA14[42]. We observed reduced survival in *aaim-1* alleles, although not

251 to the same extent as the *pmk-1* mutant (Figure 5b, S6a,b,c). In contrast to significant susceptibility
252 to the Gram-negative *P. aeruginosa, aaim-1* mutants do not display enhanced susceptibility to the
253 Gram-positive bacterium *Staphylococcus aureus* NCTC8325, suggesting specificity of AAIM-1
254 to PA14 infection (Figure S7a).
255
256 Lethality in slow killing assays is a result of *P. aeruginosa* accumulation within the intestinal
257 lumen.[43,44] To investigate if *aaim-1* alleles displayed higher levels of bacterial burden, animals
258 were grown on lawns of PA14::DsRed at the L1 or L4 stage for 48 hours. *aaim-1* mutant alleles
259 exposed as L4s, but not L1s, displayed higher bacterial burden relative to N2 (Figure 5c, S6d,e).
260 To test if intestinal expression of *aaim-1* was sufficient to limit bacterial colonization, transgenic
261 *aaim-1 (kea22)* overexpressing AAIM-1::3xFlag from the endogenous or an intestinal-specific
262 promoter were exposed to lawns of PA14::DsRed. When grown for 48 hours at the L1 or L4 stage,
263 bacterial burden was significantly reduced, relative to N2 (Figure 5d, e). These results indicate that
264 AAIM-1 plays a role in limiting bacterial colonization, and its loss results in reduced survival due
265 to hyper-colonization of the intestinal lumen.
266
267 **Fitness of *aaim-1* animals is dependent upon microbial environment**
268 To investigate how *aaim-1* alleles can influence population structure, we set up competitive fitness
269 assays. A *C. elegans* strain with a fluorescent marker (RFP::ZNFX-1) was co-plated with N2 or
270 *aaim-1* mutants on *E. coli* OP50-1, *N. parisii* or *P. aeruginosa* PA14. Animals were grown for 8
271 days, such that the population was composed of adult F1s and developing F2s. On *E. coli* OP50-
272 1, there is equal representation of N2 and *aaim-1* mutants in the population (Figure 6a). This is
273 consistent with *aaim-1* mutants not having a developmental delay (Figure 1b) or a decrease in

274 longevity (Figure S7b). In contrast, growth on *N. parisii* resulted in *aaim-1* alleles outcompeting
275 the N2 strain. Conversely, *aaim-1* mutants on *P. aeruginosa* PA14 did significantly worse, being
276 underrepresented in the population compared to N2 (Figure 6a). Interestingly, wild isolates of *C.*
277 *elegans* do not carry any obvious loss of function alleles of *aaim-1* suggesting that natural
278 conditions have selected for its retention (Figure S8). [45]
279
280 Given the opposing fates of *aaim-1* mutants on *N. parisii* and *P. aeruginosa,* we investigated the
281 effects of co-infection. Animals were infected with a maximal dose of *N. parisii* for 3 hours, prior
282 to placement on lawns of PA14. For infections with a single pathogen, we observed similar results
283 as before whereby *aaim-1* mutants have increased fitness in the presence of *N. parisii* and display
284 lower levels of parasite burden but have increased bacterial accumulation when grown on PA14.
285 In the presence of both pathogens, populations of *aaim-1* mutants display fewer gravid adults and
286 increased amounts of *N. parisii* spores. (Figure 6b,c). These results suggests that coinfection with
287 *N. parisii* and *P. aeruginosa* has synergistically negative effects on the fitness of *C. elegans*.
288
289 **Discussion:**
290 To identify host factors needed for microsporidia infection, we isolated mutants from a forward
291 genetic screen that have a fitness advantage when challenged with *N. parisii* infection. This screen
292 identified mutants in the poorly understood protein AAIM-1 (previously T14E8.4). Here, we
293 demonstrate that this protein both promotes microsporidia invasion and limits colonization by
294 pathogenic bacteria. Although we were unable to visualize the localization of secreted AAIM-1,
295 our genetic and infection experiments strongly suggest that this protein acts in the intestinal lumen
296 where both microsporidia invasion and bacterial colonization take place. The key role that AAIM-

297 1 plays in immunity is further exemplified by its transcriptional regulation in response to infection
298 (Figure 7).
299
300 The processes by which microsporidia invade host cells are poorly understood. We show that *N.*
301 *parisii* spores are often angled in wild-type *C. elegans*, suggesting that successful invasion requires
302 a particular spore orientation. In the absence of AAIM-1, spores are more often parallel to the
303 intestinal lumen, where spores may fire without the successful deposition of the sporoplasm inside
304 an intestinal cell. In contrast to previously described host and microsporidia proteins involved in
305 invasion, AAIM-1 does not appear to be involved in promoting adhesion to the surface of host
306 cells.[10,11] Instead, AAIM-1 ensures an adequate distance of spores from the intestinal membrane,
307 possibly allowing spores to be able to properly orient themselves to ensure successful host cell
308 invasion. *N. parisii* spores are ~2.2 μm long by ~0.8 μm wide and the average width of the
309 intestinal lumen at the L1 stage is ~0.6 μm.[23] Therefore, at the L1 stage spores may not be able to
310 move freely, but at the L3 stage, where AAIM-1 is not needed for invasion, there is less of a
311 constraint on spore movement as the luminal width increases to ~1.3 μm. Alternatively, the
312 developmentally restricted role of AAIM-1 could be due stage-specific expression of other factors
313 that work along with AAIM-1 to promote microsporidia invasion. Together, our results highlight
314 the power of studying microsporidia invasion in the context of a whole animal model.
315
316 Several lines of evidence suggest that AAIM-1 plays a role in protecting animals against *P.*
317 *aeruginosa*. First, *aaim-1* is upregulated in the intestine in response to PA14 exposure. Second,
318 overexpression of AAIM-1 significantly decreases PA14 burden in the intestine. Third, loss of
319 *aaim-1* leads to enhanced susceptibility and increased PA14 colonization. Fourth, competition

320 assays show reduced reproductive fitness of *aaim-1* mutants on PA14. The survival phenotype of
321 *aaim-1* mutants (~78% survival compared to wild type) is modest compared to loss of the p38
322 MAPK pathway (~51% survival compared to wild type). However, in competitive fitness assays,
323 *aaim-1* mutants are ~60% less represented than wild type in the F2 generation. Taken together,
324 our data suggests that in addition to promoting microsporidia invasion, AAIM-1, at least in part,
325 limits bacterial colonization and decreases susceptibility to *P. aeruginosa.*
326
327 *C. elegans* employs a variety of proteins to protect against bacterial infection. Many of these
328 proteins belong to several classes of antimicrobial effectors used to eliminate and prevent
329 colonization by pathogenic bacteria[46], are upregulated upon infection, and predicted to be
330 secreted.[47,48] One class of secreted proteins that is known to have immune functions and prevent
331 bacterial adherence are the mucins. These large, glycosylated secreted proteins are upregulated
332 during *C. elegans* infection and their knockdown alters susceptibility to *P. aeruginosa* infection.
333 [49,50] AAIM-1 has many predicted mucin-like O-glycosylation sites on serine and threonine
334 residues.[51–53] Thus, one possibility is that AAIM-1 may be functionally analogous to mucins,
335 preventing the adhesion of microbes to the surface of intestinal cells. As AAIM-1 does not contain
336 any known or conserved domains, further work will be necessary to determine its exact
337 biochemical function.
338
339 *C. elegans* lives in a microbially dense environment containing a wide variety pathogens that *C.*
340 *elegans* has evolved immunity towards.[23,54–57] Although loss of *aaim-1* provides a fitness
341 advantage to *C. elegans* when grown in the presence of microsporidia, obvious loss of function
342 alleles are not present in wild isolates sequenced thus far. Additionally, *aaim-1* mutants do not

343 have observable defects when grown on non-pathogenic *E. coli*. This is in contrast to mutations in
344 *pals-22* or *lin-35*, which negatively regulate the transcriptional response to infection and provide
345 resistance to microsporidia infection when mutated, but at the cost of reduced reproductive
346 fitness[27,58]. Loss of *aaim-1* disadvantages *C. elegans* when grown on *P. aeruginosa*, but not *S.*
347 *aureus,* suggesting AAIM-1 does not broadly promote resistance to all bacterial pathogens. These
348 findings demonstrate that there is a trade-off in host defense between microsporidia and some
349 pathogenic bacteria. The opposing functions of *aaim-1* with different pathogens adds to the limited
350 set of known examples of trade-offs that constrain the evolution of host defense to multiple biotic
351 threats[59,60].
352
353 **Methods**

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
strain, strain background (*Caenorhabditis elegans*)	N2	Caenorhabditis genetic center (CGC)	N2	Wild-type, Bristol strain.

strain, strain background (*Caenorhabditis elegans*)	*fawn-1* (AWR 05)	This paper	*aaim-1 (kea89) X*	C127T , Q43Stop
strain, strain background (*Caenorhabditis elegans*)	*fawn-2* (AWR 11)	This paper	*aaim-1 (kea28) X*	2.2 kb deletion
strain, strain background (*Caenorhabditis elegans*)	*fawn-3* (AWR 17)	This paper	*aaim-1 (kea91) X*	G221A splice site mutation
strain, strain background (*Caenorhabditis elegans*)	*fawn-4* (AWR 03)	This paper	*aaim-1 (kea103) X*	C1286T, A429V
strain, strain background (*Caenorhabditis elegans*)	DM7748	Mok et al. (2020)[61] DOI: 10.1534/g3.120.401656.	VC20019 Ex[*Pmyo-3::YFP*])	Mapping strain

strain, strain background (*Caenorhabditis elegans*)	RB563	Caenorhabditis genetic center (CGC)	*aaim-1 (ok295) X*	Large gene deletion in *aaim-1* and neighbouring gene *dop-3*
strain, strain background (*Caenorhabditis elegans*)	AWR 73	This paper	*aaim-1 (kea22) X*	3x outcrossed CRISPR-Cas9 generated deletion allele of *aaim-1.*
strain, strain background (*Caenorhabditis elegans*)	AWR 83	This paper	*aaim-1 (kea28)* X	6x outcrossed *fawn-2 (kea28)*
strain, strain background (*Caenorhabditis elegans*)	DA465	Caenorhabditis genetic center (CGC)	*eat-2 (ad465) II*	Feeding defective mutant.
strain, strain background (*Caenorhabditis elegans*)	AWR 131	This paper	N2 Ex[p*myo2::mCherry::Unc54,* p*aaim-1::GFP::3xFlag::Unc54]*	*aaim-1* transcriptional reporter in N2 background with a pharyngeal mCherry co-injection marker.

strain, strain background (*Caenorhabditis elegans*)	AWR 125	This paper	*aaim-1(kea22* Ex*[*p*myo2::mCherry::Unc54,* p*aaim-1::GFP::3xFlag::Unc54])*	*aaim-1* transcriptional reporter in *aaim-1 (kea22)* mutant background with a pharyngeal mCherry co-injection marker.
strain, strain background (*Caenorhabditis elegans*)	AWR 122	This paper	*aaim-1(kea22* Ex*[*p*myo3::mCherry::Unc54,* p*aaim-1::GFP::Unc54])*	*aaim-1* transcriptional reporter in *aaim-1 (kea22)* mutant background with a body wall muscle mCherry co-injection marker.
strain, strain background (*Caenorhabditis elegans*)	AWR 115	This paper	*aaim-1 (kea22* Ex*[*p*myo2::mCherry::Unc54,* p*aaim-1::aaim-1::Unc54])*	*aaim-1* over expression in an *aaim-1 (kea22)* mutant background with a pharyngeal mCherry co-injection marker.
strain, strain background (*Caenorhabditis elegans*)	AWR119	This paper	*aaim-1 (kea22* Ex*[*p*myo2::mCherry::Unc54,* p*aaim-1::aaim-1*::3xFlag::*Unc54])*	*aaim-1::3xFlag* over expression in an *aaim-1 (kea22)* mutant background with a pharyngeal mCherry co-injection marker.
strain, strain background (*Caenorhabditis elegans*)	AWR 127	This paper	*aaim-1 (kea22* Ex*[*p*myo2::mCherry::Unc54,* p*aaim-1::SPΔ aaim-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.

strain, strain background (*Caenorhabditis elegans*)	AWR129	This paper	*aaim-1 (kea22* Ex*[pmyo2::mCherry::Unc54, pspp-5:: aaim-1::3xFlag::Unc54])*	Intestinal *aaim-1::3xFlag* over expression in an *aaim-1 (kea22)* mutant background with a pharyngeal mCherry co-injection marker.
strain, strain background (*Caenorhabditis elegans*)	YY1446	Caenorhabditis genetic center (CGC)	*znfx-1(gg634[*HA::tagRFP::*znfx-1*]) *II*.	RFP germ granules
strain, strain background (*Caenorhabditis elegans*)	GK288	Sato et al. (2007)[62] DOI: 10.1038/nature05929	*unc-119(ed3)*; dkIs166[*pop t-2::PGP-1::GFP*, *unc-119*(+)]	Apical intestinal membrane marker.
strain, strain background (*Caenorhabditis elegans*)	KU25	Caenorhabditis genetic center (CGC)	*pmk-1 (km25) IV*	p38 Map kinase loss of function mutant.
strain, strain background (*Caenorhabditis elegans*)	AWR182	This paper	*aaim-1 (kea22) X ;* dkIs166[*pop t-2::PGP-1::GFP*, *unc-119*(+)] *IV*	*aaim-1 (kea22)* mutant allele crossed into GK288.

strain, strain background (*Escherichia coli*))	OP50-1	Caenorhabditis genetic center (CGC)	OP50-1	Uracil auxotroph. B strain.
strain, strain background (*Escherichia coli*))	5-alpha competent *E. coli*	New England Biolabs (NEB)	Cat#: C2987H	E. coli background in which transformations for molecular cloning were performed.
strain, strain background (*Nematocida parisii*)	*N. parisii* (ERTm1)	Troemel et al. (2008)[63] doi: 10.1371/journal.pbio.0060309.	*N. parisii* (ERTm1)	Nematode intestinal infecting species of microsporidia.
strain, strain background (*Nematocida ausubeli*)	*N. ausubeli* (ERTm2)	Troemel et al. (2008)[63] doi: 10.1371/journal.pbio.0060309	*N. ausubeli* (ERTm2)	Nematode intestinal infecting species of microsporidia.
strain, strain background (*Pseudomonas aeruginosa*)	PA14::DsRed	Dunn et al. (2006)[64] DOI: 10.1128/AEM.72.1.802-810.2006	PA14::DsRed	DsRed labelled strain of PA14.
strain, strain background (*Staphylococcus*	NCTC 8325	Sifri et al. (2003) [65] DOI: 10.1128/IAI.71.4.2208-2217.2003	NCTC 8325	*S. aureus* isolate used for C. elegans killing assays.

aureus)				
antibody	M2 anti Flag (Mouse monoclonal)	Sigma	Cat#: F1804	IF: 1:250
antibody	Anti mouse Alexafluor 594 (Goat polyclonal)	Thermo Fisher	Cat#: A32742	IF 1:300
sequence-based reagent	Reverse primer	Integrated DNA technologies (IDT)	Reverse primer to amplify *aaim-1*	5’-ttaattttttgctggtgagg-3’
sequence-based reagent	Forward primer	Integrated DNA technologies (IDT)	Forward primer to generate *SP⊿aaim-1*	5'-atgctaaaggatttcttgccgtg-3'
sequence-based reagent	Forward primer	Integrated DNA technologies (IDT)	Forward primer to amplify p*aaim-1*	5'-ttagtttggaaatgcacaaaaaaactgatctct-3'
sequence-based reagent	Reverse primer	Integrated DNA technologies (IDT)	Reverse primer to amplify p*aaim-1*	5-cagtggacttctgcttattaaaatgacttc-3'
sequence-based reagent	Forward primer	Integrated DNA technologies (IDT)	Forward primer to amplify p*myo2*	5'-cattttatatctgagtagtatcctttgctttaaatgtcc-3'

sequence-based reagent	Reverse primer	Integrated DNA technologies (IDT)	Reverse primer to amplify p*myo2*	5'- gcatttctgtgtctgacgat-3'
sequence-based reagent	Forward primer	Integrated DNA technologies (IDT)	Forward primer to amplify p*spp5*	5'-aaagcaaaatatcattatttgggaaaatc-3'
sequence-based reagent	Reverse primer	Integrated DNA technologies (IDT)	Reverse primer to amplify p*spp5*	5'-tctgtaataaaataaattgaaatgaaacac-3'
sequence-based reagent	Forward primer	Integrated DNA technologies (IDT)	Forward primer to amplify GFP from pDD282	5'-atgagtaaaggagaagaattgttcact-3'
sequence-based reagent	Reverse primer	Integrated DNA technologies (IDT)	Reverse primer to amplify GFP from pDD282	5'-ttacttgtagagctcgtccattccg-3'
sequence-based reagent	Forward Ultramer	Integrated DNA technologies (IDT)	Forward ultramer to add a Gly Ala Gly Ser **linker** and 3x Flag with *stop codon* to C-Terminal end of constructs in **pDDONR221**	5'-**ggagccggatct**gattataaagacgatgacgataagcgtgactacaaggacgacgacgaca agcgtgattacaaggatgacgatgacaagaga*taa***acccagctttcttgtacaaagttg**-3'

			via round the horn PCR.[66]	
sequence-based reagent	MicroB FISH probe conjugated to Cal Fluor 610	LGC Biosearch Technologies	18s RNA FISH probe	5’-ctctcggcactccttcctg-3’
sequence-based reagent	Alt-R CRISPR-Cas9 tracrRNA 5nmol	Integrated DNA technologies (IDT)	Cat#: 1072532	
sequence-based reagent	5’ sgRNA	Integrated DNA technologies (IDT)	Guide RNA	5'-aataaatggcataagttaag-3'
sequence-based reagent	3’ sgRNA	Integrated DNA technologies (IDT)	Guide RNA	5'-tttacaggcgtgtttcattg-3'
recombinant protein	Alt-R S.p. Cas9 Nuclease V3, 100ug	Integrated DNA technologies (IDT)	Cat#: 1081058	
recombinant protein	Phusion High-Fidelity DNA Polymerase	New England Biolabs (NEB)	Cat#: M0530L	DNA polymerase used for all molecular cloning steps.
Recombinant DNA reagent	pBSK	Ponchon et al. (2009) [67]DOI: 10.1038/nprot.2009.67.	pBSK	Addgene ID: 67504

(plasmid)				
Recombinant DNA reagent (plasmid)	Gateway ™ pDONR ™221	Invitrogen	Cat#: 12536017	
Recombinant DNA reagent (plasmid)	pCFJ90	Frøkjær-Jensen et al. (2008)[68] DOI: 10.1038/ng.248.	pCFJ90	Addgene ID: 19327
Recombinant DNA reagent (plasmid)	pDD282	Dickinson et al. (2015)[69] DOI: 10.1534/genetics.115.178335.	pDD282	Addgene ID: 66823
commercial assay or kit	NEBuilder ® HiFi DNA assembly	New England biolabs (NEB)	Cat#: 3E2621	Kit used for Gibson assembly.
commercial assay or kit	Monarch PCR and DNA Cleanup Kit	New England biolabs (NEB)	Cat#: T1030S	PCR purification kit for amplicons used in downstream molecular cloning steps.
commercial assay or kit	QIAprep spin miniprep kit	Qiagen	Cat#: 27106	Kit used for extraction of DNA from bacterial clones.

chemical compound, drug	Direct yellow 96	Sigma-Aldrich	Cat#: S472409-1G	Chitin binding dye.
chemical compound, drug	Calcofluor white	Sigma-Aldrich	Cat#: 18909	Chitin binding dye.
chemical compound, drug	Everbrite™Mounting Medium	Biotium	Cat#: 23002	Mounting medium with DAPI
software, algorithm	FIJI	Schindelin et al. (2012)[70] DOI: 10.1038/nmeth.2019	FIJI	Image analysis software
software, algorithm	GraphPad Pism 9.0	GraphPad Pism 9.0	https://www.graphpad.com	Statistical analysis software
other	0.2 μm green fluorescent polystyrene beads	Degradex Phosphorex	Cat#: 2108B	Fluorescent beads for bead feeding assays.

354
355
356

357 **Strain maintenance**

358 *C. elegans* strains were grown at 21°C on nematode growth media (NGM) plates seeded with 10x
359 saturated *Escherichia coli* OP50-1.[27] Strains used in this study are listed in the key resources table.
360 For all infection assays, 15-20 L4 staged animals were picked onto 10cm seeded NGM plates 4
361 days prior to sodium hypchlorite/1M NaOH treatment. After 4 days, heavily populated non-starved

362 plates were washed off with 1 ml M9, treated twice with 1 ml of sodium hypochlorite/1M NaOH
363 solution, and washed three times in 1 ml M9. Embryos were then resuspended in 5 ml of M9 and
364 left to rock overnight at 21°C. L1s were used in subsequent experiments no later than 20 hours
365 after bleach treatment. All centrifugation steps with live animals/embryos were performed in
366 microcentrifuge tubes at 845xg for 30s.
367
368 Throughout the paper, L1 refers to the stage immediately post hatching or bleach synchronization,
369 L3 refers to 24 hours and L4 refers to 48 hours post plating of bleach synchronized L1s at 21°C.
370 L3 and L4 stage animals were washed off plates in M9 + 0.1% Tween-20, followed by an
371 additional wash to remove residual bacteria before infection with microsporidia, or plating on
372 PA14.
373
374 **Forward Genetic Screen**
375 6,000 L4 N2 hermaphrodites were mutagenized with a combination of 50 mM EMS and 85.4 mM
376 ENU for 4 hours to achieve a large diversity of mutations within the genome.[71] P0 animals were
377 then split and placed onto 48 10cm NGM plates, F1s bleached and resulting F2s pooled onto 5
378 separate plates. 180,000 L1 F2 animals were plated onto a 10 cm plate with 10 million *N. parisii*
379 spores and 1 ml 10x saturated OP50-1. Animals were grown for 72 hours, to select for animals
380 that display a fitness advantage phenotype with respect to N2. Each population was bleached and
381 grown in the absence of infection for one generation, in order to prevent the effects of
382 intergenerational immunity[27]. Two more cycles of infection followed by growing worms in the
383 absence of infection was performed. Populations of bleached L1s were then infected with either
384 20 or 40 million spores and grown for 76 hours. Worms were then washed into 1.5 ml

385 microcentrifuge tubes and 1 ml of stain solution (1x PBS/0.1% Tween-20/2.5 mg/ml DY96/1%
386 SDS) was added. Samples were incubated with rotation for 3.5 hours and then washed 3 times
387 with M9 + 0.1% Tween-20. Individual worms that had embryos, but not spores, were picked to
388 individual plates. Each of the four *fawn* strains was isolated from a different mutant pool.
389
390 **Whole genome sequencing**
391 N2 and *fawn* isolates were each grown on a 10 cm plate until all *E. coli* was consumed. Each strain
392 was washed off with M9 and frozen at -80°C. DNA was extracted using Gentra puregene Tissue
393 Kit (QIAGEN). Samples were sequenced on an Illumina HiSeq 4000, using 100 base paired end
394 reads.
395
396 **MIP-Map**
397 Molecular inversion probes were used to map the underlying causal mutations in *fawn* isolates as
398 previously described.[35] Briefly, *fawn* hermaphrodites were crossed to males of the mapping strain
399 DM7448 (VC20019 Ex[*pmyo3::*YFP*])* hereafter referred to as VC20019. Next, 20 F1
400 hermaphrodite cross progeny, identified as those carrying *pmyo3*::YFP, were isolated and allowed
401 to self. F2s were then bleached, and 2,500 L1s were exposed to a medium-2 dose of *N. parisii*
402 spores representing the first round of selection. Two plates of 2,500 F3 L1s were set up. The
403 experimental plate was grown in the absence of infection for one generation, to negate
404 intergenerational immunity.[27] A second plate of 2,500 L1s was allowed to grow for 72 hours and
405 then frozen in H_2O at -80°C, until used for genomic preparation. The selection and rest steps were
406 repeated once more, and a second frozen sample of worms was taken at the end of the mapping
407 experiment. This process was also performed for a cross between N2 hermaphrodites and males

408 of the mapping strain VC20019, as a negative control to identify non-causal loci that may be
409 selected for reasons other than resistance to infection. Two genomic preparations, corresponding
410 to the two rounds of selection, were used as template for MIP capture, to generate multiplexed
411 libraries for sequencing. An Illumina Mini-seq was used to generate sequencing data that was
412 subjected to demultiplexing via R, and selection intervals were defined as those immediately
413 adjacent to the region on the chromosome carrying the fewest proportion of reads corresponding
414 to the mapping strain, VC20019. This interval was then used to scan for putative causal alleles,
415 resulting in the identification of the four *aaim-1* alleles in the four *fawn* isolates.
416

417 **Identification of causal gene**

418 Variants were identified using a BWA-GATK pipeline. Briefly, sequencing reads were checked
419 for sequence quality using FastQC (http://www.bioinformatics.babraham.ac.uk/projects/fastqc/)
420 and bases lower than a quality threshold of 30 were trimmed off with Trimmomatic using a sliding
421 window of 4 bases and minimum length of 36 bases.[72] Reads were aligned to the *C. elegans* N2
422 reference genome (release W220) using BWA-mem.[73] Alignments were sorted by coordinate order
423 and duplicate reads removed using Picard (https://github.com/broadinstitute/picard). Prior to
424 variant calling, reads were processed in Genome Analysis Tool Kit (GATK) v3.8.1,[74] to perform
425 indel realignment and base quality score recalibration using known *C. elegans* variants from
426 dbSNP, build 138 (http://www.ncbi.nlm.nih.gov/SNP/). GATK HaplotypeCaller was used to call
427 variants, and results were filtered for a phred-scaled Qscore > 30 and to remove common variants
428 found previously in multiple independent studies. Finally, Annovar [75] was used to obtain a list of
429 annotated exonic variants for each sequenced strain.
430

431 **Microsporidia infection assays**

432 *N. parisii* (ERTm1) and *N. aususbeli* (ERTm2) spores were prepared as described previously.[27]
433 All infections were carried out on 6-cm NGM plates, unless otherwise specified by spore dose (see
434 Supplemental table 1), or experimental method. 1,000 bleach-synchronized L1s were added into a
435 microcentrifuge tube containing 400 µl of 10X *E. coli* OP50-1, and spores. After pipetting up and
436 down, this mixture was top plated onto an unseeded 6-cm NGM plate, and left to dry in a clean
437 cabinet, prior to incubation at 21°C for 72 hours. Infections set up on 3.5-cm plates used 160 µl of
438 10x *E. coli* OP50-1 and 400 L1s.

439

440 **Infection of embryos hatched on plates**

441 Twenty-five 72-hour old synchronized animals of each strain were picked onto 3.5-cm unseeded
442 NGM plates seeded with 16 µl of 10x *E. coli* OP50-1. Plates were incubated at 21°C for two hours.
443 Adults were then picked off, and a mixture of 144 µl of 10x *E. coli* OP50-1 and a low dose of *N.*
444 *parisii* spores were added to each plate. Animals were fixed and stained after 72 hours.

445

446 **Pulse-chase infection assay**

447 6,000 bleach synchronized animals were exposed to a medium-1 (Figure S4) or medium-3 (Figure
448 3) dose of spores, 10 µl of 10x *E. coli* OP50-1 in a total volume of 400 µl made up with M9. To
449 assay pathogen clearance 3 hpi, animals were washed off in 1 ml M9 + 0.1%Tween-20, and split
450 into two populations. The first half was fixed with acetone to represent initial infectious load, while
451 the other half was washed twice in M9 + 0.1% Tween-20 to remove residual spores in the
452 supernatant and prevent additional infection from occurring. These washed worms were then

453 plated on 6-cm unseeded NGM plates with 40 µl 10x OP50-1, and 360 µl M9 and left to incubate
454 at 21°C for 21 additional hours before fixation.
455
456 **Spore localization and firing assays**
457 Strains were infected as described for the pulse infection assays for either 45 minutes or 3 hours.
458 Animals were then washed off plates, fixed, and stained with DY96 and an *N. parisii* 18S RNA
459 FISH probe. $FISH^+$ $DY96^+$ events represent unfired spores, $FISH^-$ $DY96^+$ events represent fired
460 spores, and $FISH^+$ $DY96^-$ events represent sporoplasms. Percentage of fired spores is defined as
461 the number of $FISH^-$ $DY96^+$ events over the total number of spores.
462
463 To assess spore orientation, the localization of Calcofluor White spores relative to the apical
464 membrane of the apical intestine was measured in live anaesthetized animals using differential
465 interference contrast microscopy. To determine if a spore was angled, straight lines were extended
466 from both ends of the spore independently. If either of these two lines crossed the apical membrane,
467 a spore was considered angled. If not, the spore was considered parallel. Distance of spores from
468 the apical membrane was assessed by measuring perpendicular distance from the central edge of
469 a parallel spore to the apical membrane. All measurements were performed with FIJI[70] using the
470 angle tool or the straight line tool respectively, followed by the Analyze → measure option. Images
471 in Figure 4a were taken in N2 and *aaim-1 (kea22)* animals carrying PGP-1::GFP to label the apical
472 intestinal membrane, thus outlining the lumen.
473
474 **Intestinal lumen measurements**

475 Measurements were performed on live anaesthetized worms used for spore localization assays (see
476 above). The width of the lumen was determined by extending a straight line from the apical
477 membrane on one end of the worm to that directly across on the other end, at the midpoint of the
478 intestine, and the distance measured in FIJI, via the straight line tool followed by the Analyze →
479 measure option.
480
481 **Fixation**
482 Worms were washed off infection plates with 700 µl M9 +0.1% Tween-20 and washed once in 1
483 ml M9+0.1%Tween-20. All microsporidia infected samples were fixed in 700 µl of acetone for 2
484 minutes at room temperature prior to staining. All *P. aeruginosa* PA14::DsRed infected samples,
485 as well as competitive fitness assays involving RFP::ZNFX-1 were fixed in 500 µl of 4%
486 paraformaldehyde (PFA) for 30 minutes at room temperature prior to mounting on slides.
487
488 **Live imaging**
489 Animals were mounted on 2% Agarose pads in 10 µl of 10-25mM Sodium Azide. This technique
490 was used for spore localization assays, transcriptional reporter imaging, and assessing
491 PA14::DsRed colonization in transgenic animals.
492
493 **Chitin Staining**
494 The chitin binding dye Direct yellow 96 (DY96) was used to assess host fitness (gravidity) as well
495 as parasite burden. 500 µl of DY96 solution (1 x PBST, 0.1% SDS, 20 µg/ml DY96) was added to
496 washed worm pellets and left to rock for 20-30 minutes at room temperature. Worms were then

497 resuspended in 20 µl of EverBrite™ Mounting Medium (Biotium), and 10 µl mounted on glass
498 slides for imaging.
499
500 To prestain spores prior to infection, 0.5 µl of Calcofluor white solution (CFW) (Sigma- Aldrich
501 18909) was added per 50 µl of spores, pipetted up and down gently and left for 2 minutes at room
502 temperature prior to infection.
503
504 **FISH staining**
505 To quantify the number of sporoplasms in *N. parisii* infected animals, the MicroB FISH probe
506 (ctctcggcactccttcctg) labelling *N. parisii* 18S RNA was used. Animals were fixed in acetone,
507 washed twice in 1 ml PBST, and once in 1 ml of hybridization buffer (0.01% SDS, 900 mM NaCl,
508 20 mM TRIS pH 8.0). Samples were then incubated overnight in the dark at 46 °C with 100 µl of
509 hybridization buffer containing 5 ng/µl of the MicroB FISH probe conjugated to Cal Fluor 610
510 (LGC Biosearch Technologies). Samples were then washed in 1ml of wash buffer (Hybridization
511 buffer + 5 mM EDTA), followed by incubation with 500 µl wash buffer at 46 °C in the dark. To
512 visualize sporoplasms and spores simultaneously, the final incubation was replaced with 500 µl
513 DY96 solution and incubated in the dark at room temperature prior to resuspension in 20 µl of
514 EverBrite™ Mounting Medium (Biotium).
515
516 **Microscopy and image quantification**
517 All imaging was performed using an Axio Imager.M2 (Zeiss), except for images of the
518 transcriptional reporter in Figure S6, which were generated using an Axio Zoom V.16 (Zeiss) at a
519 magnification of 45.5x. Images were captured via Zen software and quantified under identical

520 exposure times per experiment. Gravidity is defined as the presence of at least one embryo per
521 worm, and animals were considered infected by 72 hours if clumps of spores were visible in the
522 body of animals as seen by DY96. FISH-stained animals were considered infected if at least one
523 sporoplasm was visible in intestinal cells.
524
525 To quantify fluorescence within animals (Pathogen burden, bead accumulation, and GFP), regions
526 of interest were used to outline every individual worm from anterior to posterior, unless otherwise
527 specified in the methods. Individual worm fluorescence from variable assays (GFP or DsRed) were
528 subjected to the "threshold" followed by "measure" tools in FIJI.[70] To assess PA14::DsRed burden
529 in transgenic animals, regions of interest were generated from the beginning of the intestines (int1)
530 to the posterior end of the worm to prevent the p*myo2*::mCherry co-injection marker signal from
531 interfering with quantifications. When assessing pathogen burden in gravid animals stained with
532 DY96, thresholding was used to quantify spore signal without including signal from embryos.
533
534 ***Pseudomonas aeruginosa* infection experiments**
535 For all *Pseudomonas* assays, a single colony was picked into 3 ml of LB and grown overnight at
536 37°C, 220 rpm for 16-18 hours. 10 μl (for 3.5-cm plate) or 50 μl (for 6-cm plate) of culture was
537 spread onto slow killing (SK) plates to form a full lawn, except in the case of competitive fitness
538 assays (see below). Seeded plates were placed at 37°C for 24 hours, followed by 25°C for 24 hours
539 prior to use. Plates were seeded fresh prior to each experiment. To assess colonization, 1,000
540 synchronized animals were grown on PA14::DsRed for either 24 or 48 hours at 25°C. Animals
541 were washed off with 1 ml M9+ 0.1% Tween-20, and washed twice thereafter, prior to fixation.
542

543 To quantify survival of individual strains on PA14, 3.5-cm SK plates were seeded with 10 ul of
544 PA14::DsRed, to form full lawns. 60 L4s were picked onto each of three, 3.5-cm plates per strain,
545 and 24 hours later, 30 animals from each were picked onto a new 3.5-cm plate (T24hrs). Survival
546 was monitored from 24 hours post L4, three times per day. Survival was assessed based on
547 response to touch. Carcasses were removed, and surviving animals were placed onto fresh 3.5-cm
548 plates every 24 hours. Animals were grown at 25°C for the duration of the experiment. Technical
549 triplicate data was pooled to represent a single biological replicate. The experiment was carried
550 out until no more worms had survived. Survival curves were generated via GraphPad Prism 9.0,
551 and the Log rank (mantel-cox) test was used to generate P-values. TD_{50} values were calculated as
552 previously described,[41] utilizing GraphPad Prism 9.0 and applying a non-linear regression analysis
553 on survival curves.
554
555 ***Staphylococcus aureus* infection experiments**
556 3.5 cm Tryptic soy agar (TSA) plates supplemented with 10ug/ml Nalidixic acid (Nal) and seeded
557 with *S. aureus* NCTC8325 were utilized and survival quantified as described previously.[76] Briefly,
558 a 1:10 dilution of an overnight *S. aureus* culture was utilized to seed 3.5 cm TSA + Nal plates,
559 incubated at 37°C for 3 hours and stored at 4°C overnight. 30 L4s were picked onto three TSA+Nal
560 plates per strain, and survival quantified three times a day until all animals were dead. Animals
561 were transferred to new seeded TSA + Nal plates every 24 hours. Survival was assessed based on
562 response to touch. Technical triplicate data was pooled to represent a single biological replicate.
563 Survival curves were generated via GraphPad Prism 9.0, and the Log rank (mantel-cox) test was
564 used to generate P-values.
565

566 **Transgenic strain construction**

567 N2 or *aaim-1 (kea22)* animals were injected with a 100 ng/µl injection mix composed of
568 50 ng/µl of template, 5 ng/µl of p*myo2*::mCherry, and 45 ng/µl of pBSK. Three independent lines
569 were generated for each injected construct.

570

571 Gateway BP cloning[77,78] was performed to insert AAIM-1 and GFP into pDONR221. Around the
572 horn PCR,[66] was used to insert a 3x Flag sequence at the C-terminus of this construct. Gibson
573 assembly was used to generate different tissue specific clones driving *aaim-1* expression. P*aaim-*
574 *1, aaim-1* and p*spp-5* were cloned from N2 genomic DNA, *pmyo2* was cloned from pCFJ90. GFP
575 and 3x Flag sequences were cloned from pDD282. *SPΔaaim-1*was amplified from *aaim-1*::3xFlag
576 in pDONR221 by omitting the first 17 amino acids, the putative secretion signal as predicted via
577 SignalP 5.0.[36] All clones possessed an *unc-54* 3' UTR. See key resources table for primer
578 sequences.

579

580 **CRISPR-Cas9 mutagenesis**

581 To generate a deletion allele of *aaim-1* via CRISPR-Cas9 mutagenesis, steps were taken as
582 described here.[79] Briefly, 2 crRNA's were designed using CRISPOR,[80] near the start and stop sites
583 of *aaim-1* and generated via IDT. A repair template was designed to contain 35 base pairs of
584 homology upstream and downstream of the cut sites. *Streptococcus pyogenes* Cas9 3NLS
585 (10ug/ul) IDT and tracrRNA (IDT #1072532) were utilized. Reaction mixes were prepared as
586 described previously.[79] pRF4[81] was co-injected with the Cas9 ribonucleoprotein, and F1 rollers
587 picked. Deletions were identified via PCR primers situated outside the cut sites.

588

589 **Bead-feeding assays**

590 1,000 synchronized L1 animals were mixed with 0.2 μm green fluorescent polystyrene beads
591 (Degradex Phosphorex) at a ratio of 25:1 in a final volume of 400 μl containing 10 μl of 10x *E.*
592 *coli* OP50-1, 16 μl of beads and up to 400 μl with M9. Animals were incubated with beads for 3
593 hours, washed off with M9 + 0.1% Tween-20 and fixed with 4% PFA for 30 min at room
594 temperature. Bead accumulation was measured as a percentage of the total animal exhibiting
595 fluorescent signal, using FIJI.

596

597 **Lifespan Assays**

598 Lifespan assays were performed as described previously.[82] In brief, 120 synchronized L4 animals
599 were utilized per strain, with every 15 animals placed on a single 3.5-cm NGM plate (A total of 8
600 plates, with 15 animals each per strain). Animals were transferred to a new seeded 3.5-cm NGM
601 plate every 2 days, for a total of 8 days (4 transfers), ensuring no progeny were transferred
602 alongside adults. After day 8, survival was quantified daily, on the same plate, via response to
603 touch. Any animals that exhibited internal hatching, protruding intestines, or were found
604 desiccated on the edges of the plate were censored. Survival curves were generated via GraphPad
605 Prism 9, and the Log rank (mantel-cox) test was used to generate P values.

606

607 **Immunofluorescence (IF)**

608 IF was performed as described previously,[83] however all steps post-dissection were performed in
609 microcentrifuge tubes, and intestines were pelleted on a mini tabletop microcentrifuge for a few
610 seconds. Briefly, animals were dissected to extrude intestinal tissue. Two 25-mm gauge needles
611 on syringes were used to create an incision near the head and/or tail of the animals. Dissections

612 were performed in 5 µl of 10 mM levamisole on glass slides to encourage intestinal protrusion.
613 Fixation, permeabilization and blocking was performed as described previously.[83] Primary M2
614 anti-Flag antibody (Sigma F1804) was used at 1:250 overnight at 4°C, and secondary goat anti-
615 mouse Alexa fluor 594 (Thermo Fisher A32742) at 1:300 for 1 hour at room temperature. Animals
616 were mounted in 20 µl of EverBrite™ Mounting Medium (Biotium) and placed on glass slides for
617 imaging.
618
619 **Competitive fitness assays**
620 N2 or *aaim-1* mutants were grown together with RFP::Znfx1 YY1446 *(gg634)*, which labels the
621 germ granules and can be observed in all developmental stages[84]. For *N. parisii* infections, 10-cm
622 NGM plates were seeded with 1 ml of 10x OP50-1 and a medium-2 dose of spores (no spores were
623 used for uninfected plates). 10 L1s from each strain were picked onto lawns of spores and *E. coli*
624 OP50-1 immediately after drying, and grown for 8 days at 21°C, washed off with M9 + 0.1%
625 Tween-20, and fixed. For *P. aeruginosa* infections, 3.5-cm SK plates were seeded with a single
626 spot of 20 µl of PA14 in the center of the plate. 10 L1s of each strain were placed on plates and
627 grown at 21°C for 8 days and then washed off with M9 + 0.1% Tween-20. The percentage of
628 animals that did not display RFP germ granules (i.e. N2 or *aaim-1* mutants) was determined by
629 quantifying all animals on the plate, including F1 adults and L1/L2 stage F2 animals.
630
631 **Co- infections with *N. parisii* and *P. aeruginosa***
632 Co-infection assays were performed by first pulse infecting co-infection and *N. parisii* single
633 infection groups with a maximal dose of spores for three hours on unseeded 6-cm NGM plates as
634 described above. PA14::DsRed single infections were pulsed with a volume of M9 to match that

635 of the spores. Animals were then washed off in 1ml of M9 + 0.1%Tween-20, followed by 2 more
636 washes, prior to placement on full lawns of PA14::DsRed on a 6-cm SK plates prepared as
637 described above. *N. parisii* single infections were placed on a 6-cm NGM plate pre-seeded with
638 200 µl of 10x OP50-1. Plates were incubated at 21°C.
639
640 **Phylogenetic analysis**
641 Homology between AAIM-1 and other proteins was determined with protein BLAST
642 (https://blast.ncbi.nlm.nih.gov/Blast.cgi) using default parameters. Sequences with less than E-5
643 were aligned using MUSCLE (https://www.ebi.ac.uk/Tools/msa/muscle/) using default
644 parameters. Phylogenetic tree of homologs was generated using RAxML BlackBox https://raxml-
645 ng.vital-it.ch/#/ using default parameters and 100 boot straps. Tree was visualized using FigTree
646 v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree/).
647
648 **Statistical analysis**
649 All data analysis was performed using GraphPad Prism 9.0. One-way Anova with post hoc (Tukey
650 test) was used for all experiments unless otherwise specified in figure legends. Statistical
651 significance was defined as $p < 0.05$.
652
653 **Acknowledgements**
654 We thank Ashley M. Campbell, Alexandra R. Willis, and Kristina Sztanko for providing helpful
655 comments on the manuscript. This work was supported by the Canadian Institutes of Health
656 Research grant no. 400784 and an Alfred P. Sloan Research Fellowship FG2019-12040 (to
657 A.W.R.). This work was supported by National Institutes of Health (www.nih.gov) under R01

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Author contributions:

H.T.E.J. and A.W.R. designed experiments, analyzed results, and co-wrote the paper.

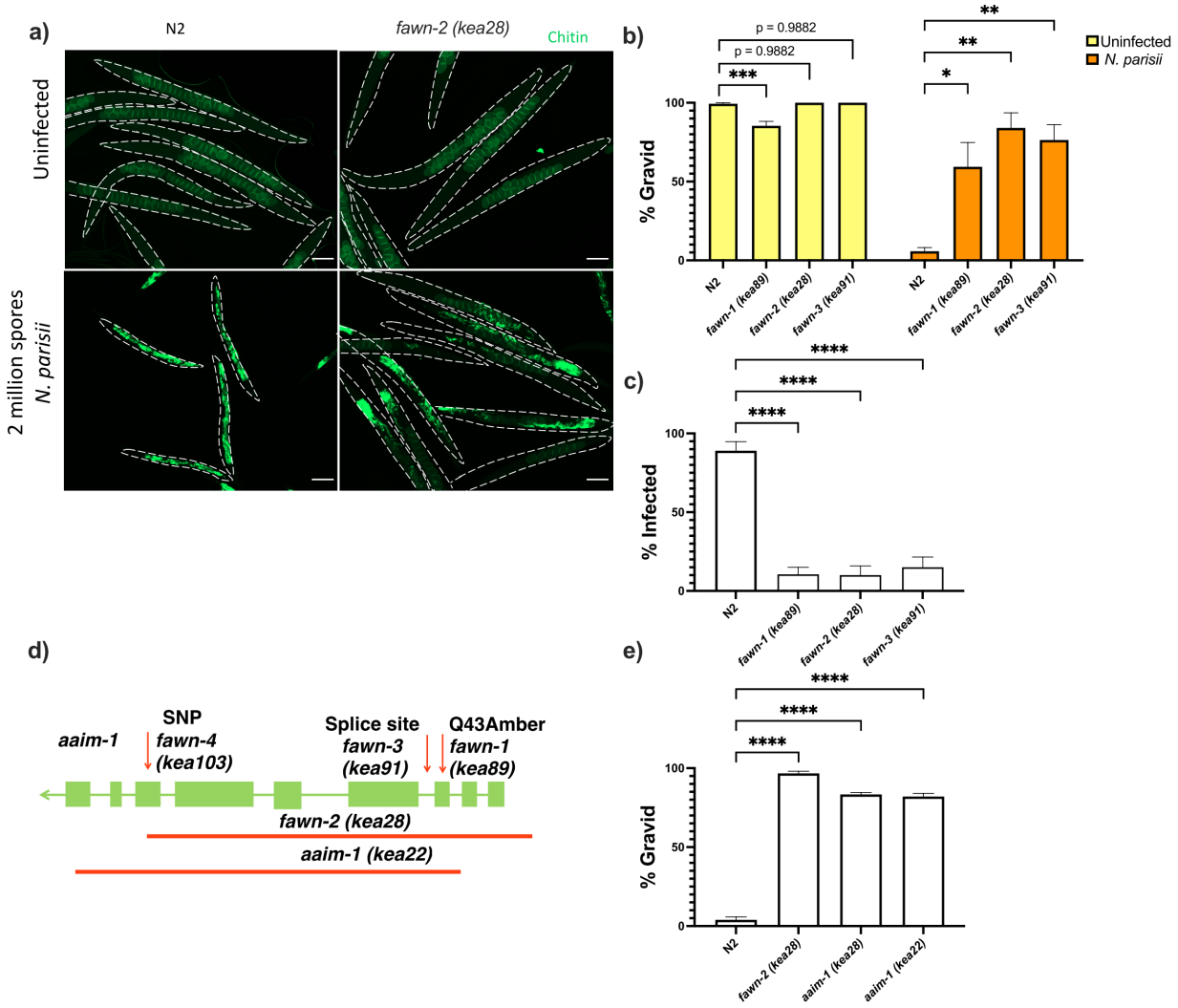
H.T.E.J. conducted all experiments, except the initial forward genetic screen performed by **A.W.R.**

C.M. designed and performed bioinformatic analysis for the MIP-map experiment.

M.R.S. analyzed whole genome sequencing to identify causal mutations in *fawn* animals.

E.R.T., A.G.F., and A.W.R. provided mentorship and acquisition of funding.

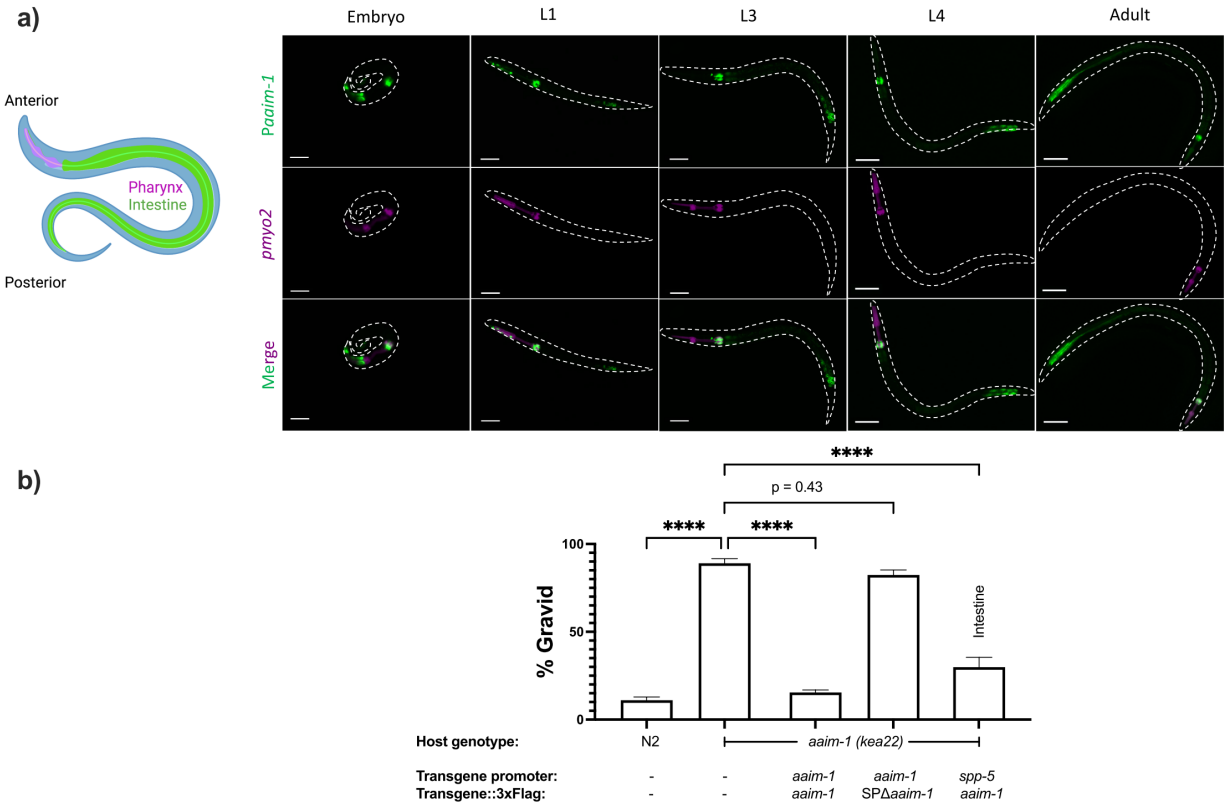
Competing interests: The authors declare they have no competing interests.

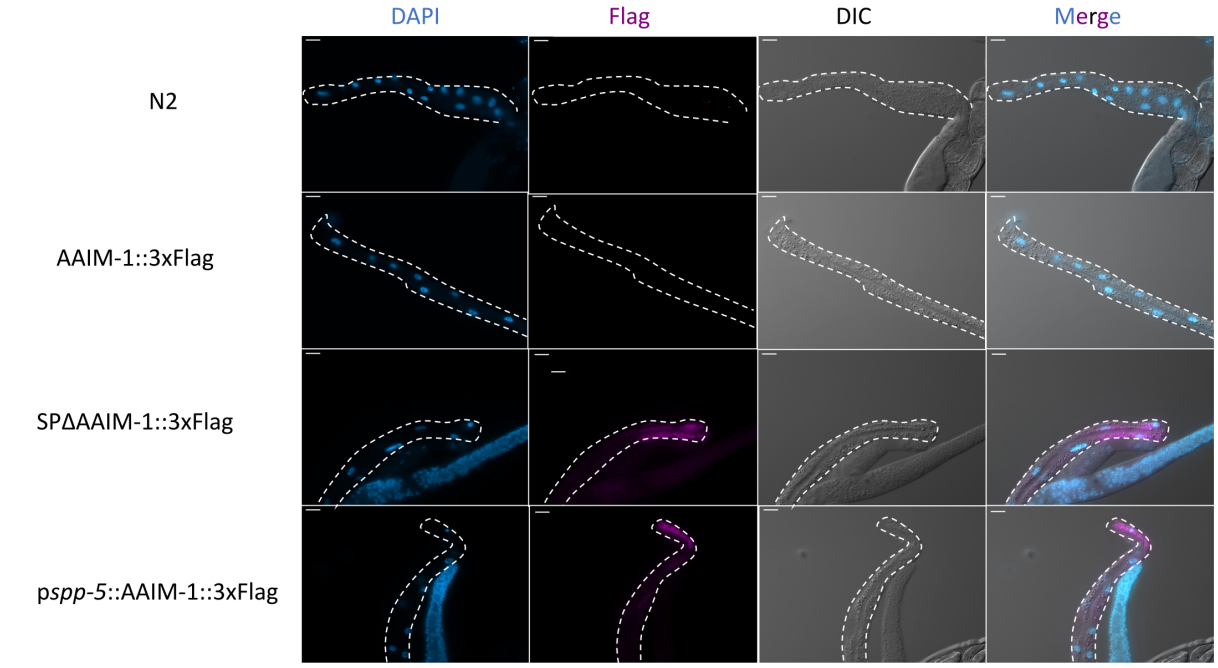


671 **Figure 1: Mutations in *aaim-1* result in resistance to *N. parisii* infection.**

672 (a-c, and e) L1 stage wild-type (N2) and *aaim-1* mutant animals were infected with either a high
673 dose (a, b, and e) or a very lose dose (c) of *N. parisii*, fixed at 72 hours, and stained with direct-
674 yellow 96 (DY96). (a) Representative images stained with DY96, which stains *C. elegans* embryos
675 and microsporidia spores. Scale bars, 100 µm. (b and e) Graph displays percentage of gravid
676 worms. (c) Percentage of worms that contain newly formed *N. parisii* spores. (d) Schematic
677 depicting the nature and location of the different *aaim-1* alleles. Boxes represent exons, and
678 connecting lines represent introns. Arrows depict point mutations, and the solid red lines depict

679 deletions. *fawn-2 (kea28)* has a 2.2 kb deletion and *aaim-1 (kea22)* has a 2.3 kb deletion. *fawn-1*
680 *(kea89)* carries a C127T, Q43Stop mutation, *fawn-3 (kea91)* carries a G221A splice site mutation
681 and *fawn-4 (kea103)* carries a C1286T, A429V mutation in *aaim-1*. (b,c, and e) Data is from three
682 independent replicates of at least 90 worms each. Mean ± SEM represented by horizontal bars. P-
683 values determined via one-way ANOVA with post hoc. Significance defined as: * $p < 0.05$, ** p
684 < 0.01, *** $p < 0.001$, **** $p < 0.0001$.


a)
Embryo
L1
L3
L4
Adult
Anterior
Pharynx
Intestine
Posterior
Paaim-1
pmyo2
Merge
b)
****
p = 0.43
****
****
100
50
0
% Gravid
Intestine
Host genotype:
N2
aaim-1 (kea22)
Transgene promoter:
-
-
aaim-1
aaim-1
spp-5
Transgene::3xFlag:
-
-
aaim-1
SPΔaaim-1
aaim-1


c)
DAPI
Flag
DIC
Merge
N2
AAIM-1::3xFlag
SPΔAAIM-1::3xFlag
pspp-5::AAIM-1::3xFlag

687

688

689 **Figure 2: AAIM-1 is secreted from intestinal cells.**

690 (a) Wild-type worms containing an extrachromosomal array expressing GFP from the *aaim-1*
691 promoter and mCherry (labelled in magenta) in the pharyngeal muscles were imaged at the
692 embryo, L1, L3, L4, and adult stage. Embryo, L1, and L3 animals were imaged at 40x, scale bar
693 20 μm and L4 and adult animals were imaged at 20x, scale bar 50 μm. L1 to L4 animals are
694 oriented anterior to posterior and the adult animal is oriented posterior to anterior from left to right.
695 Schematic made with Biorender.com (b) N2, *aaim-1, and aaim-1* expressing extrachromosomal
696 arrays were infected with a medium-2 dose of *N. parisii*. Graph displays percentage of gravid
697 worms. Data is from three independent replicates of at least 90 worms each. Mean ± SEM
698 represented by horizontal bars. P-values determined via one-way ANOVA with post hoc.
699 Significance defined as **** $p < 0.0001$ (c) Intestines (denoted by dashed lines) of 72-hour post-
700 L1 adults were dissected and stained using anti-Flag (magenta) and DAPI (blue). Images taken at
701 40x, scale bar 20 μm.

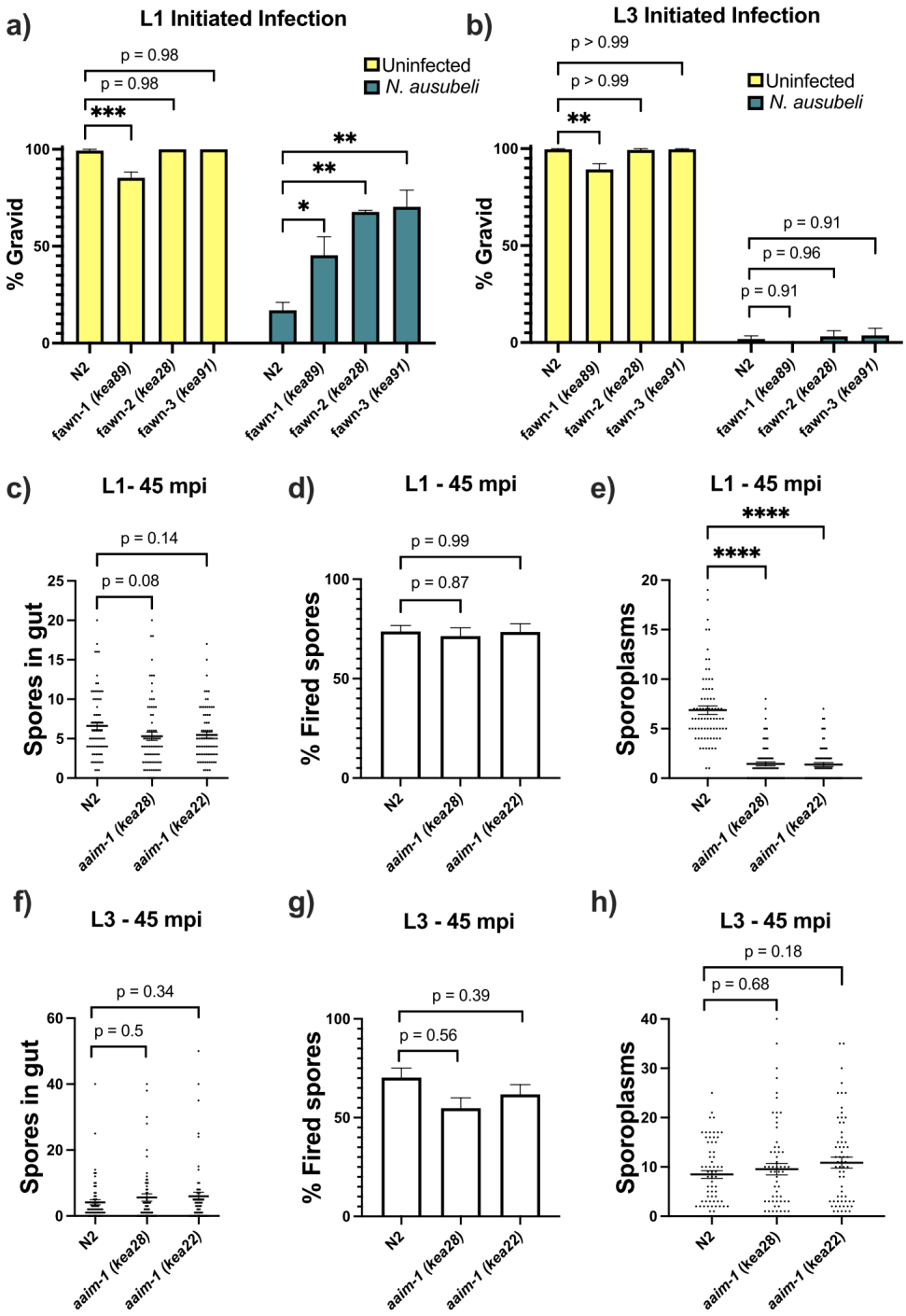
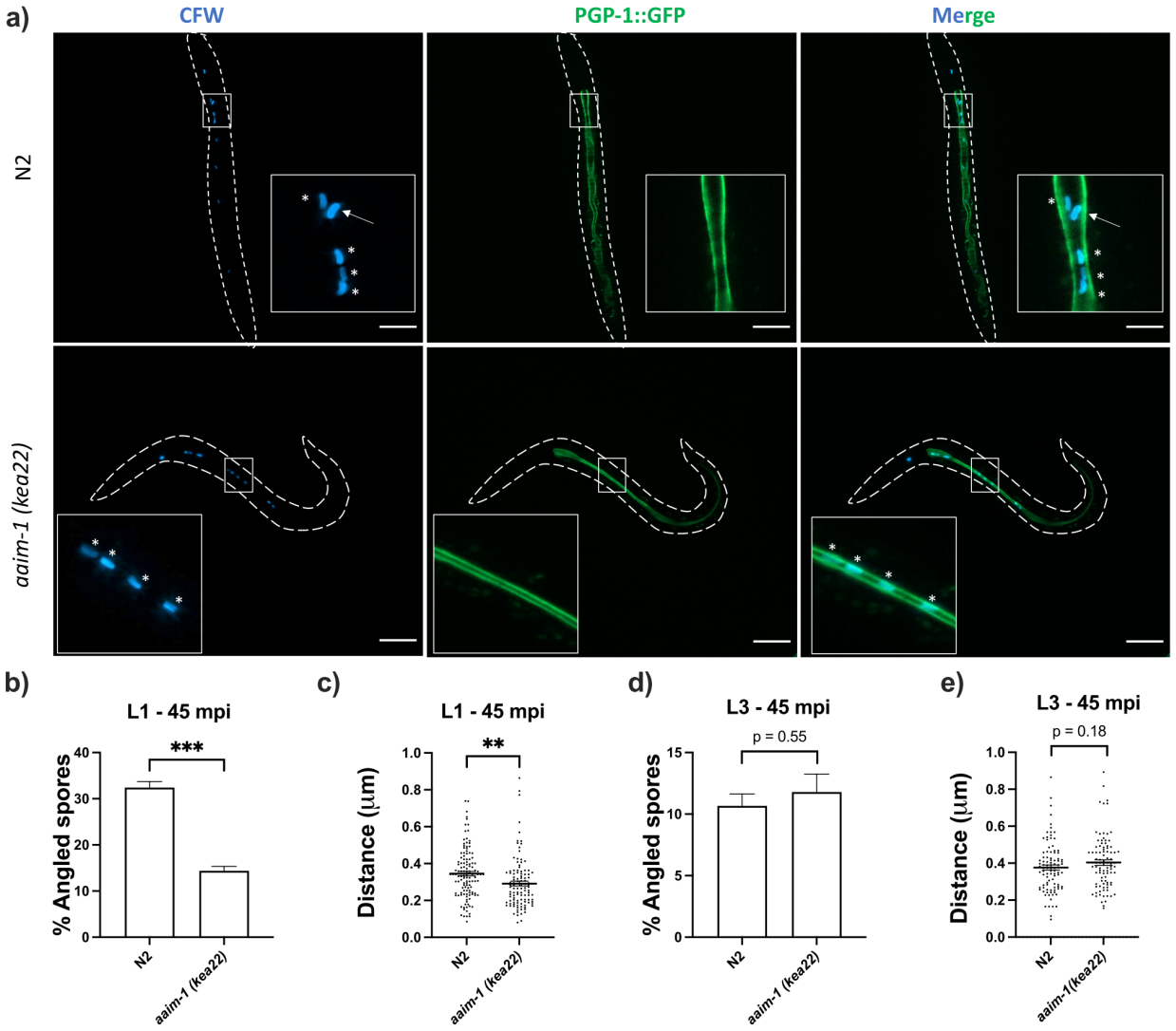


Figure 3: *aaim-1* mutants are resistant to microsporidia at the earliest larval stage due to spore misfiring. (a-b) N2 and *aaim-1* mutants were infected with a medium dose of *N. ausubeli* at either the L1 stage for 72 hours (a) or a high dose of *N. ausubeli* at the L3 stage for 48 hours (b)

706 Graph displays percentage of gravid worms. (c-f) N2 and *aaim-1* animals were infected with a
707 medium-3 dose of *N. parisii* for 45 minutes at L1 (c-e) or L3 (f-h), fixed, and then stained with
708 DY96 and an *N. parisii* 18S RNA fish probe. The number of spores per animal (c,f), the percentage
709 of spores fired (d,g), and the number of sporoplasm per worm (e,h) are displayed. Data is from
710 three independent replicates of at least 100 worms each (a-b) or 20-30 worms each (c-h). (a-h)
711 Mean ± SEM represented by horizontal bars. P-values determined via one-way ANOVA with post
712 hoc. Significance defined as: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.
713



715 **Figure 4: Spores in *aaim-1* mutants display improper orientation and distance to the apical**
716 **intestinal membrane.**
717 (a-e) PGP-1::GFP and *aaim-1(kea22);* PGP-1::GFP animals were infected with a very high dose
718 of Calcofluor white (CFW) pre-stained *N. parisii* spores for 45 minutes at either the L1 stage (a-
719 c) or the L3 stage (d-e). (a) Representative images of live animals containing stained spores (blue)
720 relative to the apical intestinal membrane (GFP). Arrow indicates an example of an angled spore
721 and asterisks indicate parallel spores. Images taken at 63x, scale bar 20 μm. (b, d) Percentage of
722 angled spores. Data is from three independent replicates of at least 90 spores each. (c, e) Distance
723 from the center of each spore to the intestinal apical membrane. Data is from three independent
724 replicates of at least 25 spores each. Mean ± SEM represented by horizontal bars. P-values
725 determined via unpaired Student's t-test. Significance defined as ** $p < 0.01$, *** $p < 0.001$.
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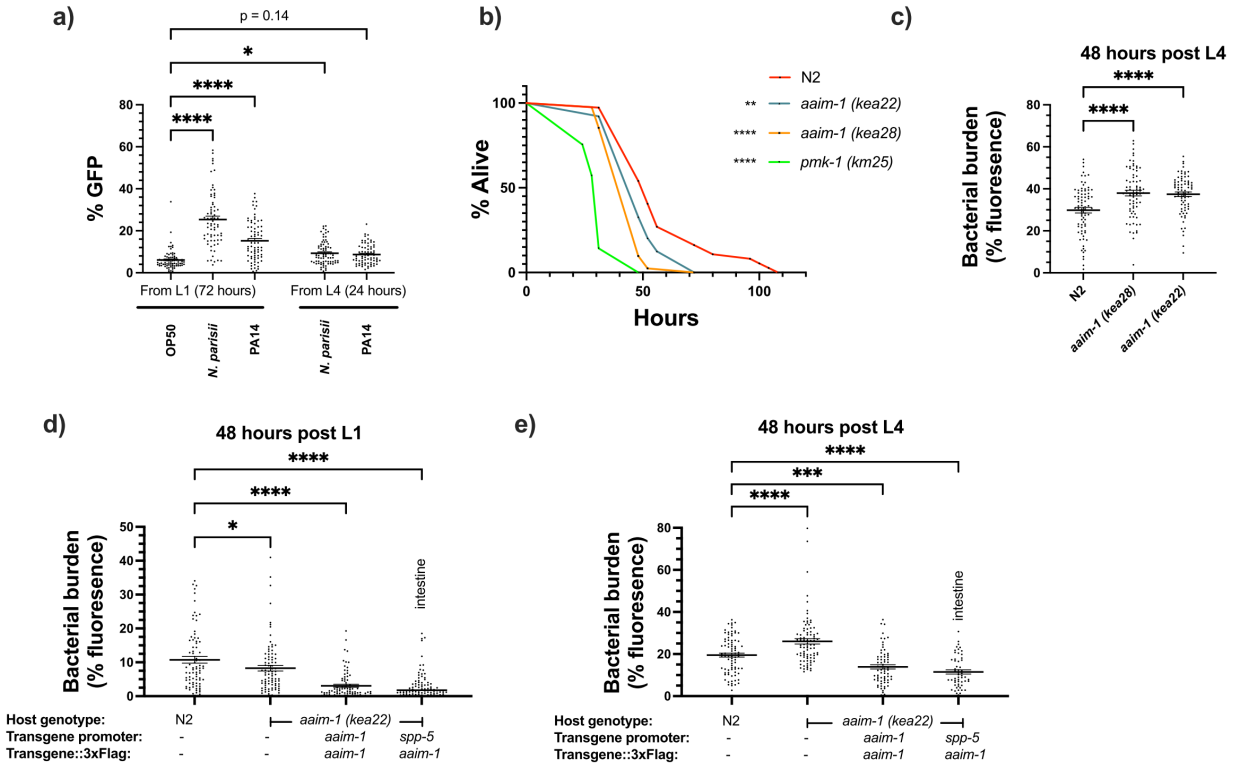

Figure 5: *aaim-1* is upregulated by *N. parisii and P. auerginosa* and *aaim-1* animals are susceptible to infection by *P. aeruginosa*.

(a) Expression of p*aaim*-1::GFP::3xFlag in response to infection with either PA14 or *N. parisii* for either 72 hours from L1 or 24 hours 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 hours. TD_{50} : N2 48 hours, aaim-1 *(kea28)* 44 hours, *aaim-1 (kea22)* 33 hours, and *pmk-1 (km25)* 28 hours. Three independent replicates were carried out, and a representative replicate is displayed. At least 37 worms were quantified per strain. P-values

740 determined via Log-rank (Mantel-Cox) test. Significance defined as * $p < 0.05$, ** $p < 0.01$. (c-e)
741 N2, *aaim-1,* or *aaim-1* animals with different extrachromosomal arrays were plated on
742 PA14::DsRed at either the L1 stage (d) or L4 stage (c,e) for 48 hours. Bacterial burden was
743 measured as the percentage of the animal containing PA14::DsRed. Data is from three independent
744 replicates of 20-30 worms each. Every point represents a single worm. Mean ± SEM represented
745 by horizontal bars. P- values determined via two-way (a) or one-way ANOVA(c-e) with post hoc.
746 Significance defined as * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.
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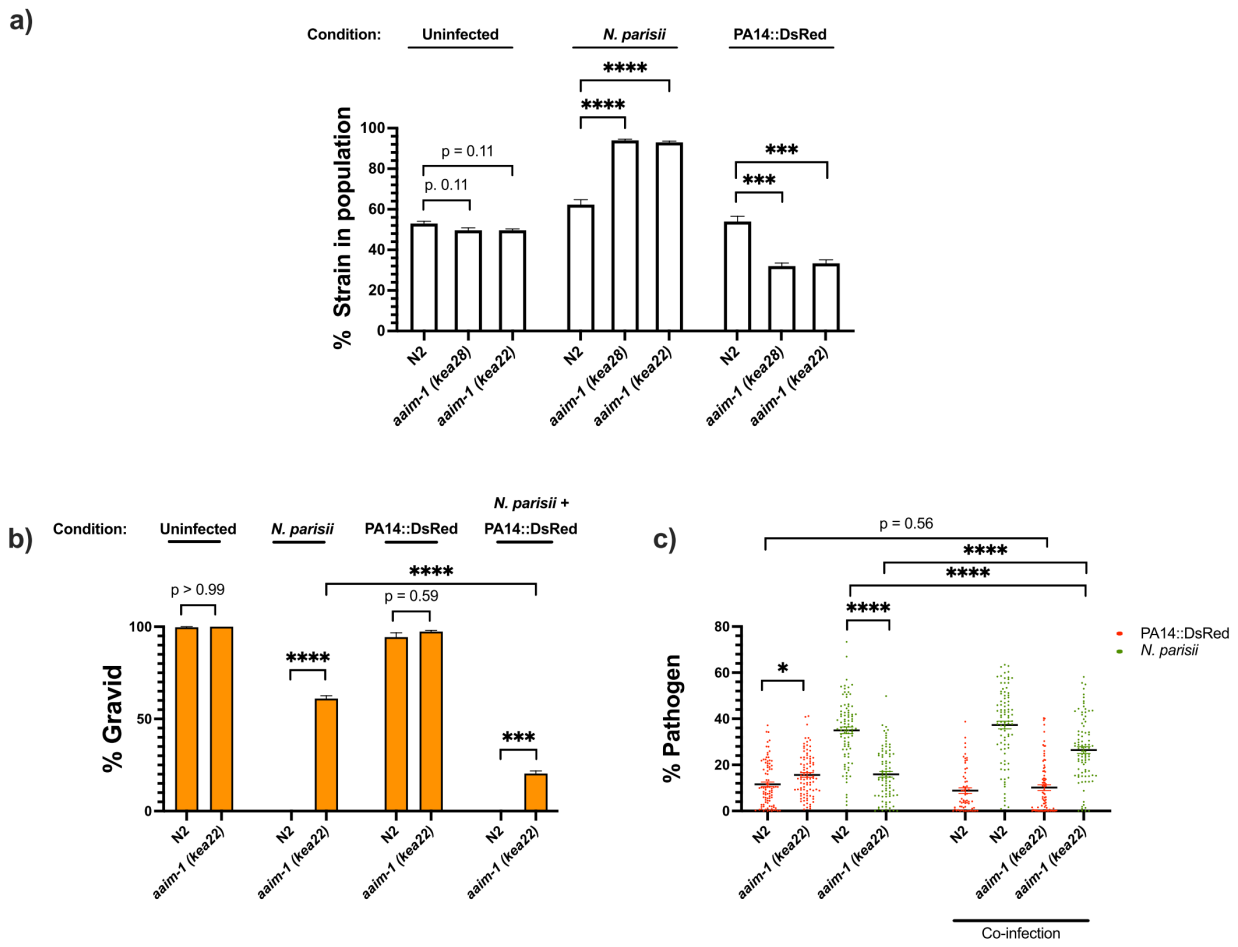
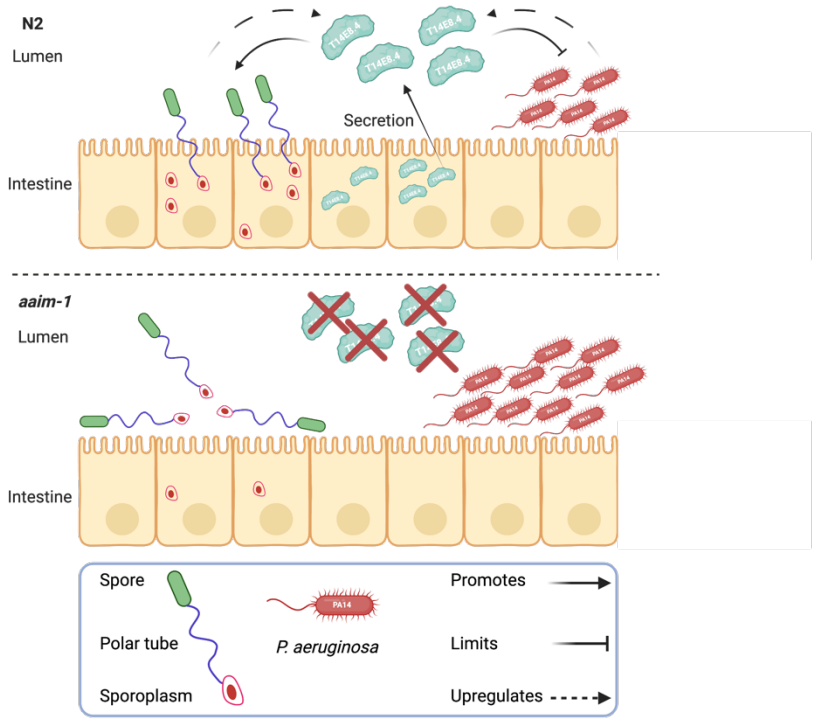


755 **Figure 6: *aaim-1* alleles display enhanced fitness on *N. parisii*, but reduced fitness on *P.***
756 ***aeruginosa*.**

757 (a) Competitive fitness assays performed with a fluorescently marked strain (RFP::ZNFX1)
758 mixed with either N2 or *aaim-1* mutants. These mixed populations of animals were plated at the
759 L1 stage on either *E. coli*, a medium-2 dose of *N. parisii*, or on *P. aeruginosa*. After 8 days, the
760 fraction of animals that did not display fluorescent germ granules was counted. Data is from
761 three independent replicates of 20-270 worms each. (b,c) L1 stage N2 and *aaim-1* animals were
762 either uninfected or infected with a maximal dose of *N. parisii*. These infected and uninfected
763 population of animals were then washed and placed on either *E. coli* or PA14::DsRed. After 69
764 hours, animals were fixed and stained with DY96. Data is from three independent replicates of

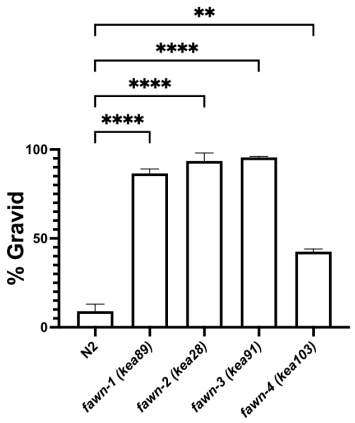


770 **Figure 7: Secreted AAIM-1 functions in the intestinal lumen to limit bacterial colonization**
771 **but is exploited by microsporidia to ensure successful invasion of intestinal cells**.
772 AAIM-1 is secreted from intestinal cells, where the protein limits bacterial colonization in the
773 lumen. Additionally, AAIM-1 is parasitized by *N. parisii* spores to ensuring successful orientation
774 and firing during intestinal cell invasion. Infection by either of these two pathogens results in the
775 upregulation of AAIM-1. Figure made with Biorender.com.

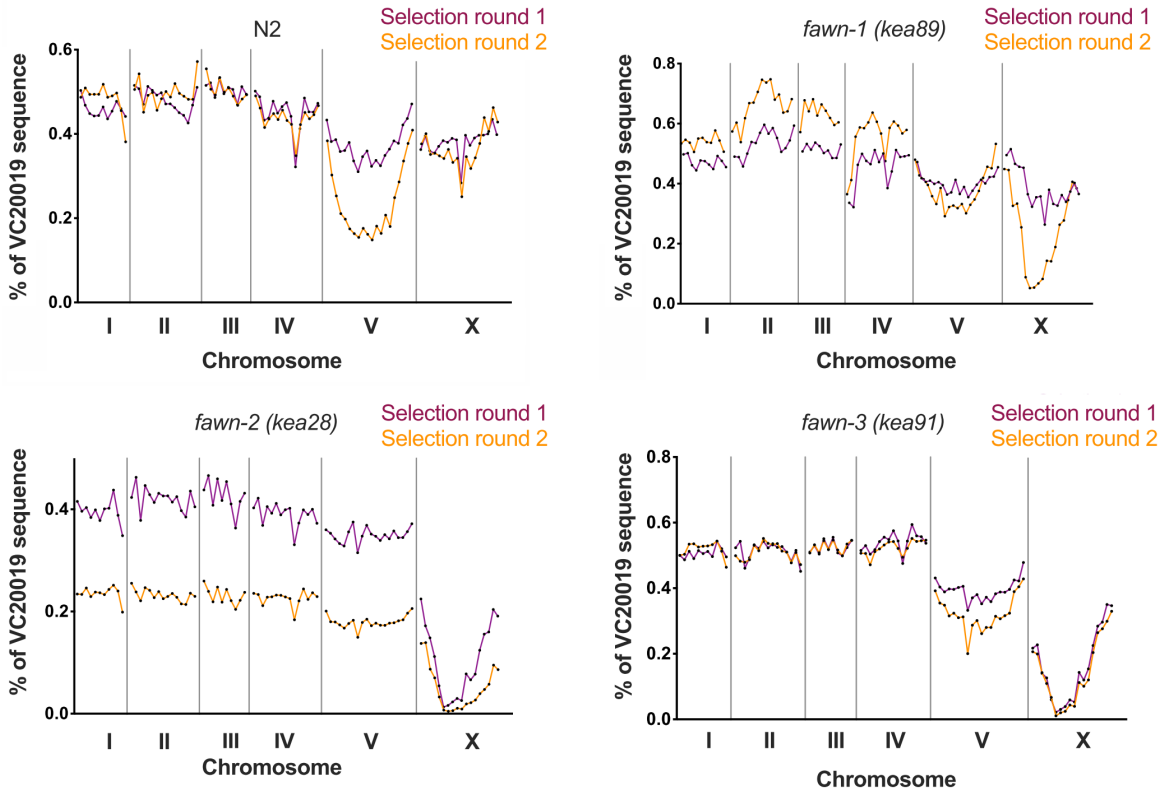
776 **Supplemental material**

777 **Figure S1. Mapping and validation of *aaim-1* as the gene associated with resistance to *N.***
778 ***parisii*.**
779 **Figure S2: AAIM-1 is conserved in both free-living and parasitic nematodes.**
780 **Figure S3: *aaim-1* is expressed in arcade cells and presence of C-terminal 3x Flag tag does**
781 **not disrupt AAIM-1 function.**
782 **Figure S4: *aaim-1* mutants do not clear *N. parisii* and developmentally restricted *N. parisii***
783 **invasion defect is not due to a feeding defect.**
784 **Figure S5: Invasion defects in *aaim-1* only occur at the L1 stage of development and a**
785 **mutation in *aaim-1* does not alter the width of the intestinal lumen.**
786 **Figure S6: Susceptibility to *P. aeruginosa* PA14 appears at L4.**
787 **Figure S7: A mutation in *aaim-1* does not influence *C. elegans* defense against *S. aureus* or**
788 **lifespan.**
789 **Figure S8: List of naturally occurring *aaim-1* variants in wild isolates of *C. elegans*.**
790 **Supplemental table 1: Spore doses utilized in this study.**
791

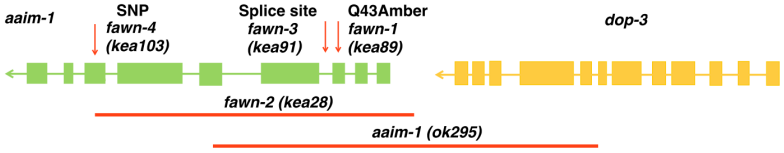
a)


**
****
****
****
% Gravid
100
50
0
N2
fawn-1 (kea89)
fawn-2 (kea28)
fawn-3 (kea91)
fawn-4 (kea103)

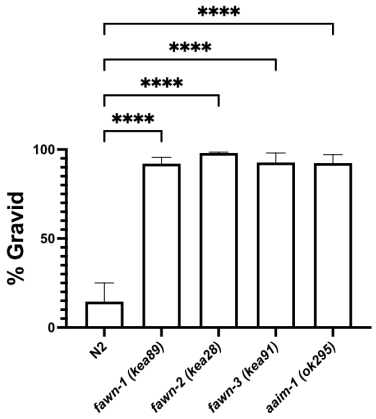
b)


N2
fawn-1 (kea89)
fawn-2 (kea28)
fawn-3 (kea91)
Selection round 1
Selection round 2
% of VC20019 sequence
Chromosome
I
II
III
IV
V
X

c)


aaim-1
SNP
fawn-4
(kea103)
Splice site
fawn-3
(kea91)
Q43Amber
fawn-1
(kea89)
dop-3
fawn-2 (kea28)
aaim-1 (ok295)

d)


****
****
****
****
% Gravid
100
50
0
N2
fawn-1 (kea89)
fawn-2 (kea28)
fawn-3 (kea91)
aaim-1 (ok295)

793

794 **Figure S1. Mapping and validation of *aaim-1* as the gene associated with resistance to *N.***
795 ***parisii*.**

796 (a) N2 or *fawn* animals were infected with a medium-3 dose of *N. parisii* spores on 6-cm plates,
797 fixed at 72 hours, and stained with direct-yellow 96 (DY96). Graph displays percentage of gravid
798 worms. Data is from three independent replicates of 66-300 worms each. (b) F2 recombinants
799 between the mapping strain VC20019 and either N2, *fawn-1*, *fawn-2*, or *fawn-3* were infected with
800 a medium-2 dose of *N. parisii*. Two rounds of selection were performed (see methods). The
801 percentage of sequencing reads mapping to the reference strain VC20019 are depicted on the Y-
802 axis, and the linkage groups are depicted on the X-axis. Sequencing of MIPs resulted in capturing
803 the identity of the genome at 89 distinct regions which are represented as points by their location
804 along the X-axis coordinates. A significantly diminished percentage of VC20019 indicates an
805 enrichment of non-mapping genomic sequence in that region. (c) Schematic representing the
806 location and nature of the different *aaim-1* alleles. Boxes represent exons, and connecting lines
807 represent introns. Arrows represent point mutations and solid red lines represent large deletions.
808 *fawn-2 (kea28)* has a 2.2 kb deletion and *aaim-1 (kea22)* has a 2.3 kb deletion. *aaim-1 (ok295)*
809 possesses a large deletion overlapping two different genes, *aaim-1* and *dop-3*, the boundaries of
810 which are unclear.[41,85] (d) L1 stage N2 and *aaim-1* mutant animals were infected with a high dose
811 of *N. parisii*, fixed at 72 hours, and stained with direct-yellow 96 (DY96). Graph displays
812 percentage of gravid worms. Data is from three independent replicates of at least 100 worms each.
813 Mean ± SEM represented by horizontal bars. P-values determined via One-way Anova with post
814 hoc. Significance defined as ** $p < 0.01$, **** $p < 0.0001$.

815

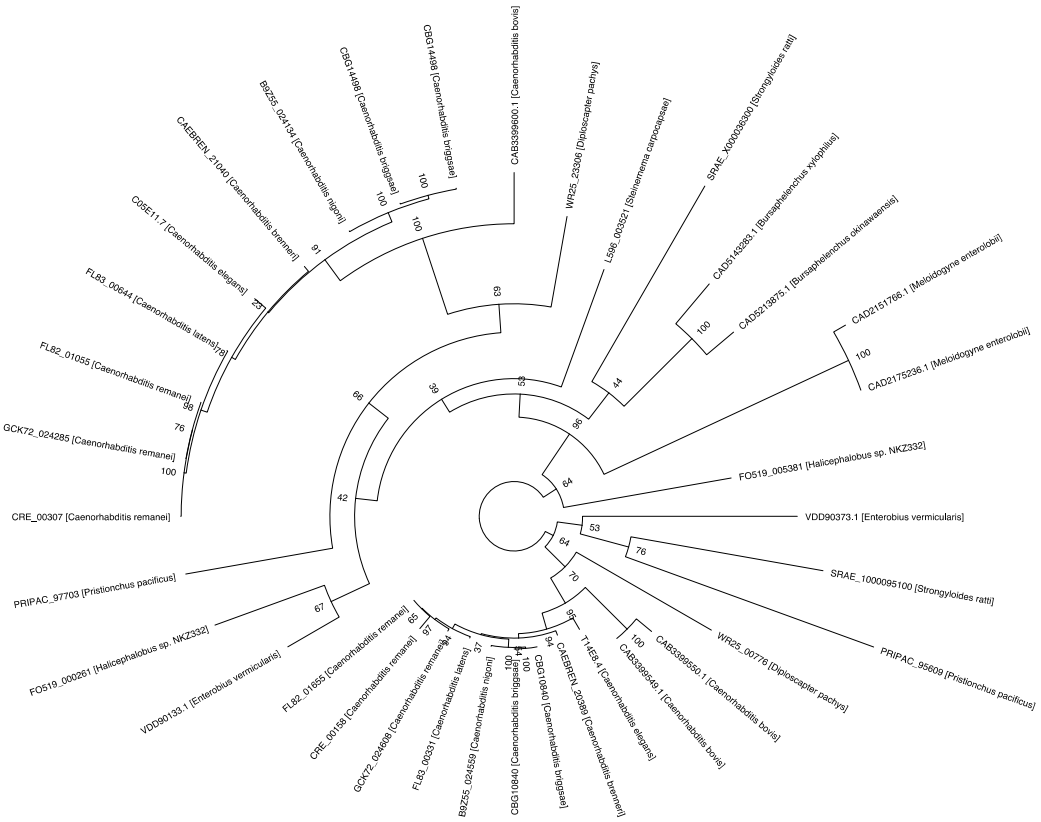


Figure S2: AAIM-1 is conserved in both free-living and parasitic nematodes. Phylogenetic tree of AAIM-1 homologs. Bootstrap values are shown at the nodes.

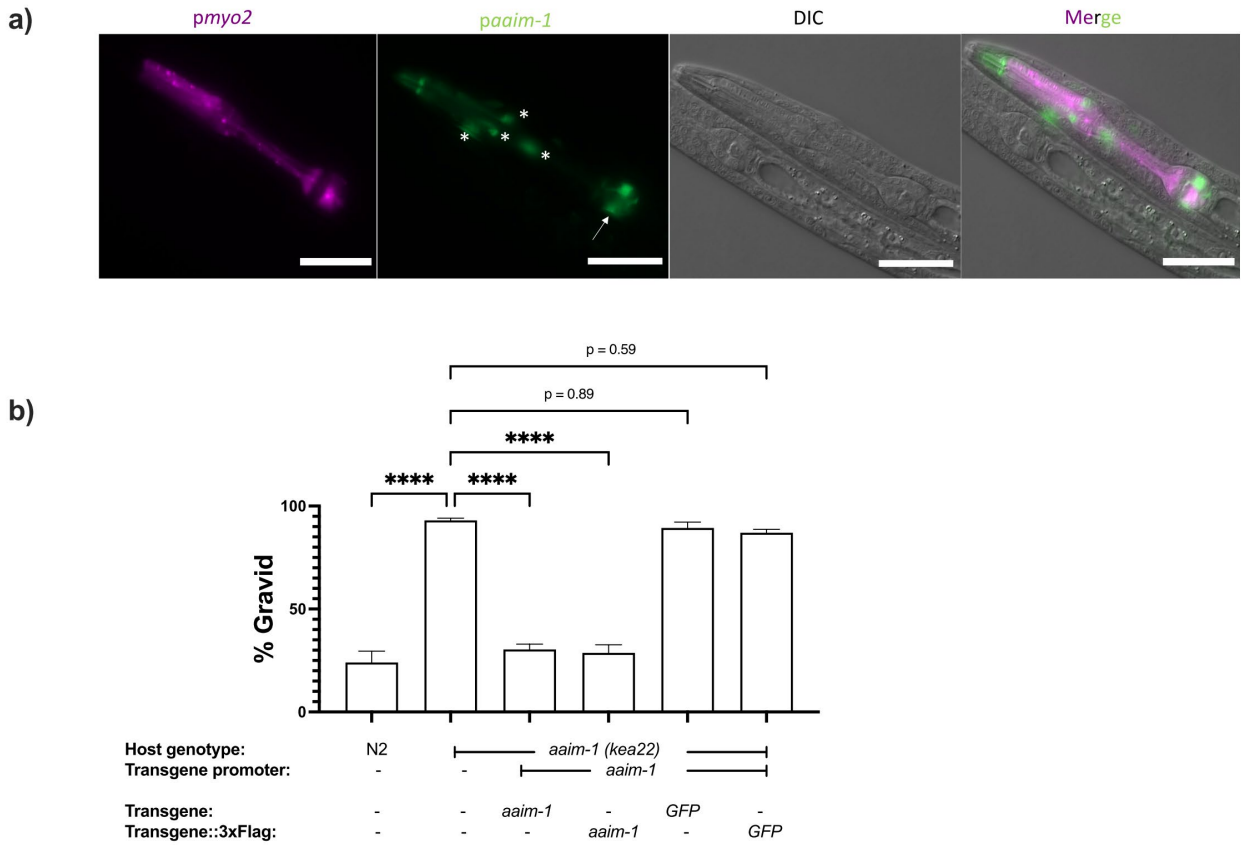


Figure S3: *aaim-1* is expressed in arcade cells and presence of C-terminal 3x Flag tag does not disrupt AAIM-1 function.

(a) N2 containing an extrachromosomal array expressing GFP from the *aaim-1* promoter and mCherry (labelled in magenta) in the pharyngeal muscles were imaged at the L1 stage at 40x. Scale bar 20 μm. Arrow indicates terminal bulb, and asterisks represent arcade cells. (b) N2, *aaim-1,* and *aaim-1* expressing extrachromosomal arrays of wild-type or 3x Flag tagged constructs were infected with a medium-2 dose of *N. parisii*, fixed at 72 hours, and stained with direct-yellow 96 (DY96). Graph displays percentage of gravid worms. Data is from three independent replicates of at least 100 worms each. Mean ± SEM represented by horizontal bars. P-values determined via one-way ANOVA with post hoc. Significance defined as **** $p < 0.0001$.

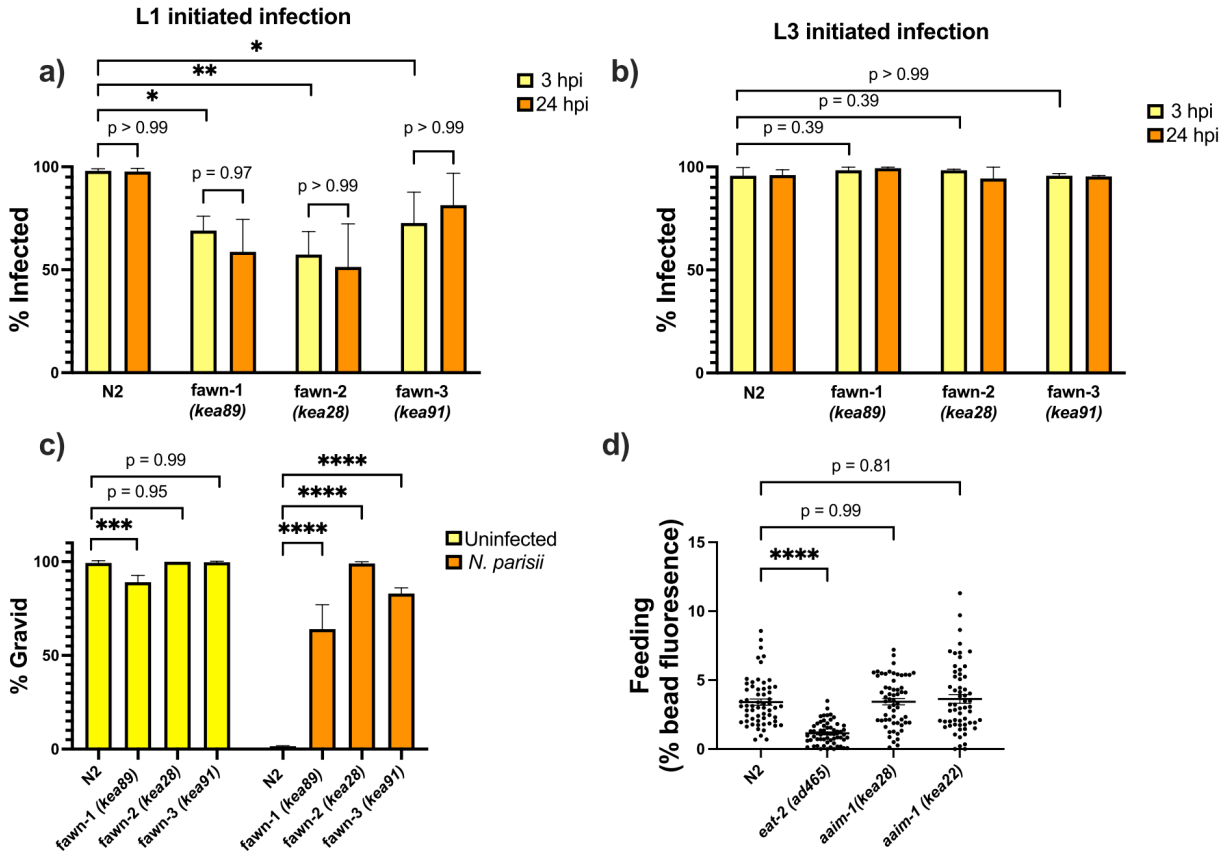
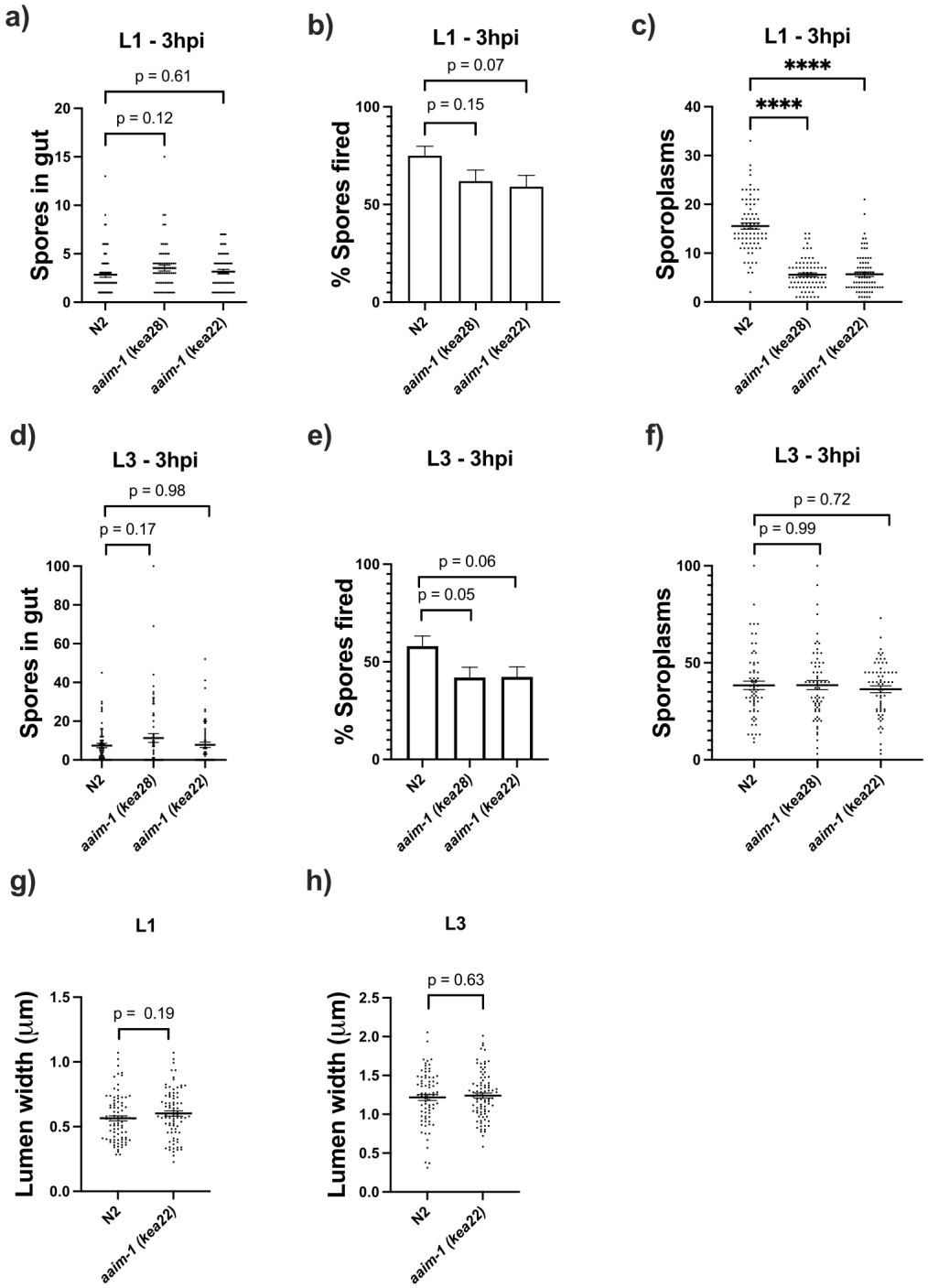


Figure S4: *aaim-1* mutants do not clear *N. parisii* and developmentally restricted *N. parisii* invasion defect is not due to a feeding defect. (a-b) N2 and *aaim-1* mutants were infected at either the L1 stage (a) or the L3 stage (b) with a medium-1 dose of *N. parisii* spores for 3 hours. Animals were then washed to remove spores and re-plated for an additional 21 hours. Worms were fixed at both the 3 hour and 24 hour timepoints and stained with an *N. parisii* 18S RNA fish probe. Worms containing either sporoplasm or meronts were counted as infected. (c) N2 and *aaim-1* adults were allowed to lay embryos on plates. Adults were removed and a low dose of *N. parisii* was added to the plate. Animals were fixed at 72 hours and stained with direct-yellow 96 (DY96). Graph displays percentage of gravid worms. (d) N2 and *aaim-1* mutants were fed fluorescent beads for 3 hours. Quantification of percentage of worm with bead fluorescence. Data is from three

848 independent replicates of at least 100 worms each (a-c) or 20-30 worms each (d). Mean ± SEM
849 represented by horizontal bars. P-values determined via one-way ANOVA with post hoc.
850 Significance defined as * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$.



852 **Figure S5: Invasion defects in *aaim-1* only occur at the L1 stage of development and a**
853 **mutation in *aaim-1* does not alter the width of the intestinal lumen.**
854 (a-f) N2 and *aaim-1* animals were infected for 3 hours at L1 (a-c) or L3 (d-f), fixed, and then
855 stained with DY96 and an *N. parisii* 18S RNA fish probe. The number of spores per animal (a,d)
856 the percentage of spores fired (b,e) and the number of sporoplasm per worm (c,f) are displayed.
857 (g,h) The width of the intestinal lumen was measured in L1 (g) or L3 (h) wild-type or *aaim-1*
858 animals. (a-h) Data is from three independent replicates of 16-30 worms each. Mean ± SEM
859 represented by horizontal bars. P-values determined via one-way ANOVA with post hoc (a-f) or
860 Unpaired Student's t-test (g,h). Significance defined as **** $p < 0.0001$.
861

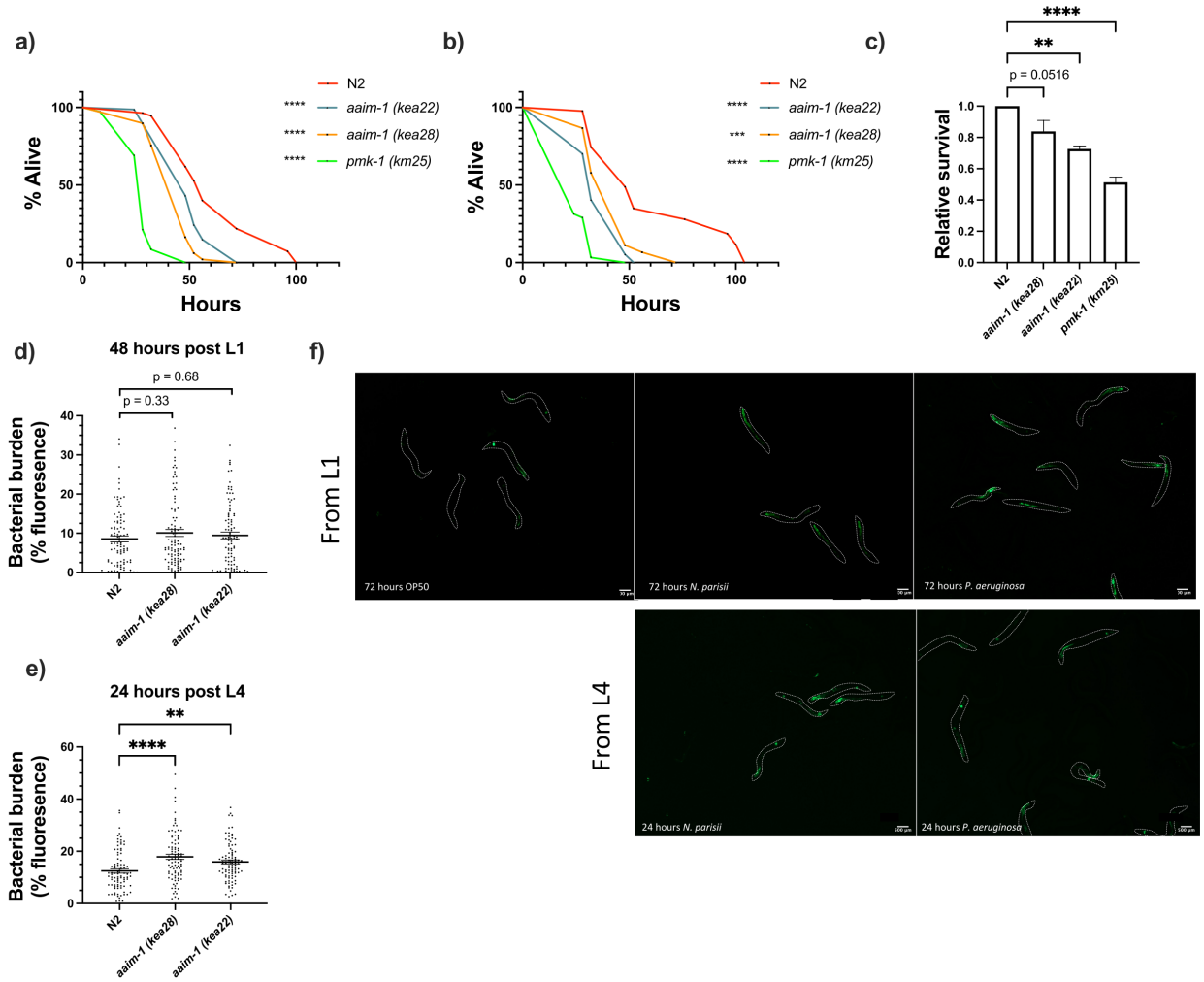
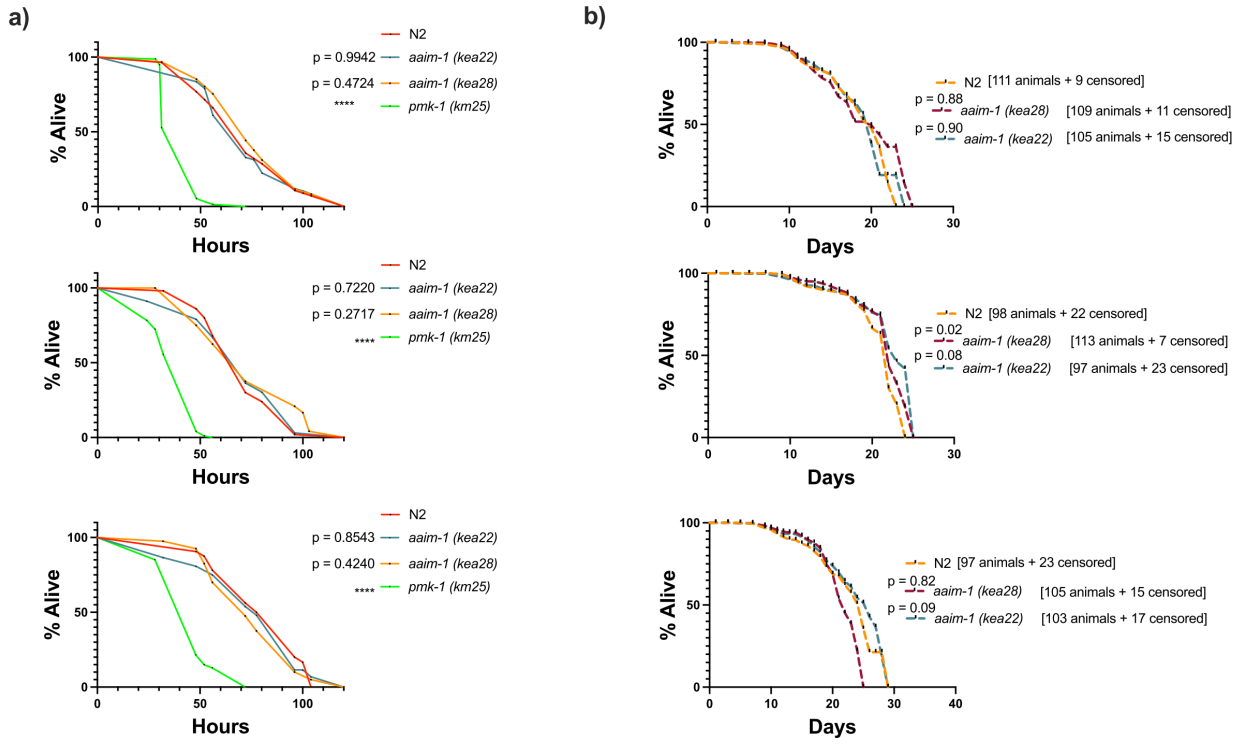


Figure S6: Susceptibility to *P. aeruginosa* PA14 appears at L4.

(a,b) Additional replicates of survival assays of animals grown on full lawns of PA14::DsRed as in Figure 5a. (a) TD_{50} : N2 51 hours, aaim-1 *(kea28)* 46 hours, *aaim-1 (kea22)* 38 hours, and *pmk-1 (km25)* 25 hours. (b) TD_{50} : N2 43 hours, aaim-1 *(kea28)* 30 hours, *aaim-1 (kea22)* 32 hours, and *pmk-1 (km25)* 20 hours. (c) Relative survival of mutants to N2 as calculated by mean strain TD_{50}/mean N2 TD_{50}. (d-e) N2 and *aaim-1* mutants were grown on PA14::DsRed 48 hours post L1 (d) or 24 hours post L4 (e). Data is from three independent replicates of 20-30 worms each. Every

872 point represents a single worm. Bacterial burden was measured as the percentage of the animal
873 containing PA14::DsRed via FIJI. Mean ± SEM represented by horizontal bars. (f) p*aaim-*
874 *1*::GFP::3xFlag were exposed to either PA14 or *N. parisii* 72 hours post L1 or 24 hours post L4.
875 Animals were imaged at 45.5x, scale bar 500 µm. P-values determined via one-way ANOVA with
876 post hoc. Significance defined as ** $p < 0.01$, **** $p < 0.0001$.



878 **Figure S7: A mutation in *aaim-1* does not influence *C. elegans* defense against *S. aureus* or**
879 **lifespan.**

880 (a) L4 stage N2 and *aaim-1* were plated on full lawns of *S. aureus* NCTC8325 and the percentage
881 of animals alive was counted over the course of 120 hours. Three independent replicates are
882 displayed. At least 40 worms were quantified per strain. (b) N2 and *aaim-1* mutants were grown
883 on *E. coli* OP50-1 for one month, and survival measured as number of animals responsive to touch.
884 The number of animals quantified, as well as those censored are denoted on the graph. Three

885 independent survival assays are displayed. P-values determined via Log-rank (Mantel-Cox) test.

886 Significance defined as **** $p < 0.001$.

T14E8.4 (X-6559570-6562366)

CHROM	POS	REF	ALT	AF	allele	effect	impact	gene_name	gene_id	feature_id	transcript_biotype	nt_change	aa_change
X	6559573	A	G	0	G	synonymous_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.1545T>C	p.Asn515Asn
X	6560363	A	G	0	G	synonymous_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.1284T>C	p.Ser428Ser
X	6560426	A	G	0	G	synonymous_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.1221T>C	p.Tyr407Tyr
X	6560445	T	TA	0	TA	splice_region_variant&intron_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.1204-3_1204-2insT	NA
X	6560485	A	G	0.77	G	splice_region_variant&intron_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.1203+7T>C	NA
X	6560524	C	G	0	G	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.1171G>C	p.Val391Leu
X	6560647	C	A	0.02	A	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.1048G>T	p.Ala350Ser
X	6560670	A	G	0	G	missense_variant&splice_region_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.1025T>C	p.Val342Ala
X	6560810	T	A	0.01	A	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.940A>T	p.Ile314Phe
X	6560841	G	A	0.01	A	synonymous_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.909C>T	p.Thr303Thr
X	6560869	A	T	0.02	T	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.881T>A	p.Val294Glu
X	6560873	C	T	0.01	T	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.877G>A	p.Val293Ile
X	6560876	T	C	0	C	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.874A>G	p.Lys292Glu
X	6560955	C	T	0	T	synonymous_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.795G>A	p.Ser265Ser
X	6561004	C	T	0.09	T	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.746G>A	p.Arg249Lys
X	6561012	G	T	0.07	T	synonymous_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.738C>A	p.Ile246Ile
X	6561013	A	T	0.01	T	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.737T>A	p.Ile246Asn
X	6561030	C	T	0.54	T	synonymous_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.720G>A	p.Thr240Thr
X	6561062	C	T	0	T	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.688G>A	p.Ala230Thr
X	6561122	T	A	0	A	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.628A>T	p.Ile210Phe
X	6561199	G	T	0.03	T	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.551C>A	p.Thr184Asn
X	6561201	T	A	0.02	A	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.549A>T	p.Leu183Phe
X	6561212	A	G	0	G	splice_region_variant&intron_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.544-6T>C	NA
X	6561830	G	A	0	A	synonymous_variant	LOW	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.403C>T	p.Leu135Leu
X	6562016	G	C	0.01	C	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.217C>G	p.Gln73Glu
X	6562145	A	T	0	T	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.138T>A	p.Asn46Lys
X	6562349	A	T	0	T	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.18T>A	p.Phe6Leu
X	6562355	T	A	0.05	A	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.12A>T	p.Leu4Phe
X	6562361	C	G	0.01	G	missense_variant	MODERATE	T14E8.4	WBGene00043981	T14E8.4.1	protein_coding	c.6G>C	p.Arg2Ser

887

888 **Figure S8: List of naturally occurring *aaim-1(T14E8.4)* variants in wild isolates of *C. elegans*.**

889 This table represents a list of *aaim-1* coding variants found to naturally occur in wild isolates of

890 *C. elegans* generated by the CeNDR variant browser.[45] The reference allele (REF) as well as the

891 alternate variant (ALT) and the allele frequency (AF) are displayed for various sites (POS) across

892 *aaim-1*. The nature (effect) and impact of these variants are depicted as well as the nucleotide

893 changes (nt_change) and the corresponding amino acid change (aa_change). *aaim-1* does not

894 possess any variants predicted to have a high impact, implying that there are no obvious loss of

895 function alleles and that its retention in the wild is advantageous.

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904 **Supplemental table 1: Spore doses utilized in this study.**

Species	**Dose**	**Plate concentration (spores/cm^2)**	**Total spores on assay plate (Millions) Plate size: *3.5 cm, **6 cm, ***10 cm**
N. parisii	Very low	25,984	0.25*
	low	207,875	2.0*
	Medium-1	1,247,232	3.0*
	Medium-2	115,050	3.25
	Medium-2	41,380	3.25**
	Medium-3	141,600	4.0
	High	194,700	5.50
	Very high	318,600	9.0
	Maximal	637,200	18.0
N. ausubeli	Medium	103,936	1.0*
	High	519,680	5.0*

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