

1 **Prevalence, geographic distribution, and transmission pathway of *Camponotus yamaokai* virus**

2 Authors: Erika Okada<sup>1</sup>, Kazuma Chiyoda<sup>2</sup>, Kanata Sakaya Inoue<sup>2</sup>, Kazuhisa Yamasaki<sup>2</sup>, Mamoru  
3 Takata<sup>3</sup>, Toshiyuki Satoh<sup>1,2</sup>, Satoshi Koyama<sup>1,2\*</sup>

4  
5 Author affiliation

6 <sup>1</sup> Faculty of Agriculture, Tokyo University of Agriculture and Technology, Fuchu, Tokyo, Japan

7 <sup>2</sup> Institute of Agriculture, Tokyo University of Agriculture and Technology, 3-5-8 Saiwai, Fuchu,  
8 Tokyo, Japan.

9 <sup>3</sup> Graduate School of Agriculture, Kyoto University, Kitashirakawa Oiwakecho, Kyoto 606-8502,  
10 Japan

11  
12 \*Corresponding author: Satoshi Koyama

13 E-mail: skoyama@cc.tuat.ac.jp

14 Tel: +81-42-367-5623

15 FAX: +81-42-367-5628

16  
17 **Abstract**

18 The relationship between hosts and viruses is influenced by various factors. One potential factor is  
19 sociality. In social organisms such as ants, the interaction between hosts and viruses might differ from  
20 those of solitary organisms due to their unique ecology. We previously isolated a double-stranded RNA  
21 toti-like virus, *Camponotus yamaokai* virus (CYV), from the arboreal ant *Camponotus yamaokai*. The  
22 ant exhibits a polygynous colony structure with multiple queens and within-nest mating behaviors.  
23 Such unique ecological traits may have driven the evolution of a distinctive relationship with the virus.  
24 However, the biological characteristics of CYV have not been sufficiently studied. In this study, we  
25 investigated the biological characteristics of CYV through rearing experiments and field surveys. As  
26 a result, no horizontal transmission was detected between workers and broods. There were no  
27 significant differences in prevalence between castes. CYV was detected at all seven surveyed locations,  
28 with location prevalence ranging from 60% to 95%. The high CYV prevalence across the host's  
29 distribution range indicates that the geographical distribution of CYV aligns with that of its host. These  
30 results suggest that CYV has spread throughout the host population, primarily relying on vertical  
31 transmission.

32  
33 **Keywords:** Totiviridae, ant, social insect, prevalence, vertical transmission

34

35 **Introduction**

36 The spatial distribution and the frequency of interactions between individuals can influence the  
37 prevalence of viruses [1]. Social organisms, which live at high densities and engage in direct contact  
38 or the exchange of materials through social interactions, may be more prone to virus transmission.  
39 They, however, have developed preventive mechanisms at both social and individual levels to control  
40 the spread of infections [2]. This suggests that social organisms, such as ants, may exhibit unique host-  
41 virus relationships that are not observed in solitary organisms. Previous studies on the interaction  
42 between ants and viruses have been conducted, with significant progress made in those focusing on  
43 invasive species such as fire ant (*Solenopsis invicta*) and Argentine ant (*Linepithema humile*) [3, 4].  
44 Given the diverse behaviors and social structures across different ant species [6, 7], the relationship  
45 between viruses and their hosts might be linked to such ecological aspects of ants.

46 A toti-like virus, Camponotus yamaokai virus (CYV), was reported from the arboreal ant  
47 *Camponotus (Myrmamblyus) yamaokai* [8]. *Totiviridae* are double-stranded RNA viruses with two open  
48 reading frames (ORFs) coding for capsid protein (CP) and RNA-dependent RNA polymerase (RdRp),  
49 respectively. They have been known to infect yeasts, fungi, and protozoa [9]. Recently, toti-like viruses  
50 have been isolated from a wide range of hosts, including plants, shrimps, mosquitoes, and fish [10–  
51 13]. Toti-like viruses have also been detected in invasive ants, such as the fire ant (*Solenopsis invicta*)  
52 and the Argentine ant (*Linepithema humile*) [14, 15]. *C. yamaokai*, the host of CYV, is an arboreal ant  
53 species distributed in Honshu, Shikoku, and Kyushu in Japan, nesting in cavities of small branches [16].  
54 The worker ant of this species ranges from 3.5 to 4.5 mm in length and exhibits dimorphism: major  
55 and minor workers. This species shows a high degree of polydomy, and individuals freely move among  
56 the nests in the same colony [16]. They exhibit a polygynous colony structure with multiple queens,  
57 where alate females engage in within-nest mating with males. Virus particles have been observed in  
58 the ovaries and oocytes of CYV-infected queens, suggesting reproductive vertical transmission via  
59 eggs [8]. Such a unique ecology of the host may have driven the evolution of a distinctive relationship  
60 with the virus. However, the biological characteristics of CYV have not been sufficiently studied.

61 In this study, we investigated the biological characteristics of CYV, including its transmission  
62 routes, prevalence, and distribution. First, *C. yamaokai* was collected from seven sites, and two of  
63 these sites were used to investigate whether there was a caste difference in CYV infection. Then, the  
64 intranidal infection rates at all sites were examined. Next, workers of *C. nawai*, which were not  
65 infected with CYV [8], were used to rear *C. yamaokai* eggs to adulthood. This allowed us to test  
66 whether CYV, transmitted through reproductive vertical transmission via parental gametes, could be  
67 maintained to adulthood without further CYV infections. Finally, source colonies of *C. yamaokai* with  
68 different CYV infection statuses were created. Using these source colonies, experimental colonies  
69 with different CYV infection statuses in eggs and rearing workers were established. This experiment  
70 aimed to examine whether food exchange (trophallaxis) between larvae and workers could lead to

71 behavioral horizontal transmission of CYV.

72

### 73 **Materials and methods**

#### 74 1. Ant collection

75 The host ant, *Camponotus yamaokai*, was collected from seven locations in Japan including Miyagi,  
76 Saitama, Tokyo, Kanagawa, Shizuoka, Miyazaki, and Kagoshima (Fig.1). We brought back the ants  
77 along with the branches containing their nests to the laboratory. The collected nests were kept in  
78 complete darkness at  $25 \pm 1^\circ\text{C}$  and fed twice a week with artificial bee food (Bee Hatcher, FEED ONE  
79 Co.), house cricket (*Acheta domesticus*) and 6% honey solution.

80

#### 81 2. Real-Time PCR

82 To detect the virus, the following procedures were performed. RNA was extracted from the entire body  
83 of the insects using ISOGEN (Nippon Gene, Tokyo, Japan) according to the manufacturer's protocol.  
84 cDNA was synthesized using the PrimeScript™ RT reagent Kit with gDNA Eraser (Perfect Real Time)  
85 (Takara Bio, Shiga, Japan) according to the manufacturer's protocol with a modification: the reverse  
86 transcription reaction mixture contained 20% dimethyl sulfoxide for chemical denaturation. The  
87 presence of the virus was determined by real-time PCR using GoTaq® qPCR master mix (Promega,  
88 WI, USA) according to the manufacture's protocol, with the Thermal Cycler Dice® Real Time System  
89 II (Takara Bio). Primer sequences used in real-time PCR were as follows: for ORF1 of CYV (GenBank  
90 accession number LC026053), qPCR\_F215-234 (5'- TCTGACCAGTCAAGCGACAG-3') and  
91 qPCR\_R323-304 (5'-GTCTTGTCGCGAAAATGTTG-3'); for RdRp motif of CYV, Motif3-F (5'-  
92 ATAACAACAACAATGGCATC-3') and Motif4-R (5'-CAAACCGTTCACCGTCAATA-3'); for  $\beta$ -  
93 actin of the ant (GenBank accession number LC492075.1), Yam\_βactinF (5'-  
94 ACTGGGACGACATGGAAAAG-3') and Yam\_βactinR (5'-AGTCATCTTCTCGCGATTGG-3').  $\beta$ -  
95 actin was used to verify nucleic acid integrity. The reaction conditions started with denaturation at  
96  $94^\circ\text{C}$  for 2 minutes, followed by 45 cycles of  $94^\circ\text{C}$  for 30 seconds,  $60^\circ\text{C}$  for 30 seconds, and  $72^\circ\text{C}$   
97 for 30 seconds. Fragment specificity was checked in a melting curve. The samples showing an  
98 amplification with either or both CYV specific primer pairs were determined to be positive for the  
99 virus.

100

#### 101 3. CYV prevalence

102 The CYV infection status was examined individually for all castes (21 queens, 22 major workers, 27  
103 minor workers, 8 alate females and 16 males) from 27 nests collected in Kanagawa, and for 15 queens,  
104 15 major workers, and 101 minor workers from 7 nests collected in Tokyo. For the alate females and  
105 males collected in Tokyo, virus detection was not performed due to an insufficient number of  
106 specimens. Additionally, to examine the CYV infection status within the nests, 15 minor workers were

107 sampled from five nests across all seven locations.

108

#### 109 4. Interspecific fostering experiment

110 To investigate whether CYV undergoes reproductive vertical transmission, we conducted a  
111 interspecific fostering experiment in which *C. yamaokai* eggs were reared by workers of *C. nawai*.  
112 Since *C. nawai* is not infected with CYV [8], this experimental setup minimizes possibility of infection  
113 other than reproductive vertical transmission. Minor workers of *C. nawai* collected in Shizuoka, Japan,  
114 were used to create three experimental colonies. Each experimental colony consisted of three major  
115 workers and 12 minor workers as nurse individuals. All these workers were marked with paint on their  
116 mesonotum. Approximately 100 eggs from five nests of *C. yamaokai* collected in Yokohama were  
117 introduced into each experimental colony. The infection rate in these eggs should be similar to that  
118 observed in the Kanagawa site. These experimental colonies were reared until the introduced eggs  
119 emerged into adult *C. yamaokai*. Rearing conditions of the experimental colonies containing *C. nawai*  
120 workers and *C. yamaokai* eggs were the same as those described above for the maintenance of *C.*  
121 *yamaokai*. Adult *C. yamaokai* that emerged from the introduced eggs were distinguished from *C.*  
122 *nawai* by the absence of markings. The newly emerged *C. yamaokai* were stored at -80°C until  
123 verification of the CYV infection. To determine whether *C. nawai* adults became infected with CYV  
124 through the rearing process, the infection status of the *C. nawai* nurse individuals was also examined.  
125 From each experimental colony where eggs emerged, three *C. nawai* workers were randomly collected  
126 at the end of the experiment and examined for CYV infection.

127

#### 128 5. Intraspecific fostering experiment

##### 129 5.1 Creation of source colony

130 This experiment investigated whether behavioral horizontal transmission occurs between nurse  
131 workers and broods of *C. yamaokai*. For this purpose, it was necessary to establish source colonies  
132 with different CYV infection statuses. Six experimental colonies were established from nests of *C.*  
133 *yamaokai* collected in Kanagawa, each consisting of one queen and five workers. The workers were  
134 marked with paint on their mesonotum. Afterward, the colonies were reared until three offspring  
135 workers of the queen emerged, at which point the initially marked workers were removed. The colonies  
136 were then reared for two years until the number of offspring workers increased to about ten. All  
137 emerging workers were collected and examined for CYV infection.

138

##### 139 5.2 Fostering experiment

140 To investigate whether CYV is horizontally transmitted from infected to uninfected hosts through  
141 trophallaxis among nestmates, four source colonies were created using the methods described in 5.1.  
142 The colonies were reared until the number of workers reached about 15. Three workers from each

143 source colony were sampled to check for the presence of the CYV, confirming that the virus infection  
144 status among workers was consistent within each colony. From each source colony, 10 minor workers  
145 were taken to create experimental colonies. If the experimental colony was CYV-positive (infection  
146 rate ~ 100%), eggs were taken from a CYV-negative source colony (infection rate = 0%), and vice  
147 versa (Fig.2). This ensured that in the experimental colonies, workers cared for broods with a different  
148 virus infection status than themselves. The experimental colonies were then kept for three months,  
149 until the introduced eggs developed into adults. All adult ants that emerged, as well as the nurse  
150 workers, were collected and examined for the presence of the virus.

151

## 152 **Results**

### 153 1. Caste differences in CYV prevalence

154 In the ants collected in Kanagawa, the CYV prevalence of all castes was similar, around 80% (Fisher's  
155 exact test,  $p = 0.897$ ; Fig. 3; Supplemental table S1). Additionally, in the Tokyo population, the CYV  
156 prevalence of queen and worker castes (major and minor workers) were similar, around 80% ( $p =$   
157  $0.927$ ).

158

### 159 2. CYV prevalence

160 The CYV prevalence was investigated at seven locations across Japan. Most of all nests had prevalence  
161 exceeding 60% (Fig.4). In one nest collected from Tokyo, the prevalence was as low as 6.7%. In one  
162 nest from Kagoshima, the CYV was not detected in any of the individuals analyzed. The average CYV  
163 prevalence within locations was over 60%. The average prevalence per colony (mean  $\pm$  SE) for  
164 locations was as follows: Miyagi:  $97.3 \pm 2.4\%$ , Saitama:  $78.8 \pm 2.2\%$ , Tokyo:  $78.7 \pm 16.2\%$ ,  
165 Kanagawa:  $77.3 \pm 6.8\%$ , Shizuoka:  $94.7 \pm 2.2\%$ , Miyazaki:  $92.0 \pm 3.5\%$ , Kagoshima:  $61.3 \pm 14.9\%$ .

166

### 167 3. Interspecific fostering experiment

168 In three experimental colonies with *C. nawai* workers, a total of 267 *C. yamaokai* eggs were introduced  
169 (Table 1). Most of the introduced eggs disappeared from the experimental colonies. No eggs  
170 introduced into colony 1 developed into adults, but a total of 12 minor workers emerged from colonies  
171 2 and 3. When these workers were examined for CYV infection, 9 were positive and 3 were negative,  
172 with prevalence of 75%, which was similar to the prevalence of the ants in Kanagawa from which the  
173 eggs were sourced. CYV was not detected in any of the *C. nawai* workers collected from colonies 2  
174 and 3.

175

### 176 4. Intraspecific fostering experiment

#### 177 4.1 Creation of source colony

178 A total of 61 minor workers were obtained from the six colonies (Table 2). In two of the colonies, the

179 virus was not detected in any of the workers analyzed. In the other four colonies, the virus was detected  
180 in 91% to 100% of the workers.

181

#### 182 4.2 Fostering experiment

183 In two experimental colonies with CYV-uninfected nurse workers, a total of 61 eggs were introduced  
184 from CYV-infected source colonies (Table 3). Fifteen workers emerged from among them, most of  
185 which are CYV positive. CYV-negative workers remained non-infected after caring for infected eggs  
186 through to emerge in adults.

187 A total of 49 eggs were introduced from CYV-uninfected source colonies into two experimental  
188 colonies with CYV-infected nurse workers, and 8 adults emerged. None of these individuals were  
189 infected with the virus (Table 3).

190

### 191 **Discussion**

192 Hosts with unique ecologies and viruses may establish distinctive relationships. This study examined  
193 the characteristics of CYV that infect ants exhibiting polydomy and polygyny. CYV was detected in  
194 all nests except for one of the host ant *Camponotus yamaokai*, and the prevalence of CYV at collection  
195 sites was over 60% for all locations. There was no significant difference in CYV prevalence among  
196 castes. Horizontal transmission of CYV among nestmates was not detected, suggesting that the main  
197 transmission route is vertical. These results indicate that CYV is widely distributed across the habitat  
198 range of *C. yamaokai* through vertical transmission.

199

#### 200 **1. CYV prevalence**

201 *Camponotus yamaokai* has queens, alate females, and males as reproductive castes, and major and  
202 minor workers as labor castes within the nest [16]. Each caste exhibits distinct morphology and  
203 physiological mechanisms. Furthermore, the division of labor among individuals leads to differences  
204 in pathogen exposure [17, 18]. Therefore, the susceptibility to CYV and prevalence might vary among  
205 castes. However, no significant differences in CYV prevalence among castes were detected. In ants,  
206 sex is determined by whether the egg is fertilized; females develop from fertilized eggs, while males  
207 develop from unfertilized eggs through parthenogenesis [19]. Whether female eggs become workers  
208 or queens is generally determined by environmental and social factors during development [20]. In  
209 CYV-infected queens, virus particles were observed within oocytes [8], suggesting that the  
210 transmission of CYV to eggs occurs independent of caste determination, assuming there is no vertical  
211 transmission from males. We did not test the vertical transmission from males. If vertical transmission  
212 from males occurs, a difference in infection rates between the queens and the offspring would be  
213 expected; however, such a difference was not detected. Therefore, without the mechanisms discussed  
214 below, the vertical transmission from males either does not occur or is rare. Since *C. yamaokai* is

215 polygynous [21], the CYV prevalence in the colony is likely largely determined by the infection status  
216 of the queens, independent of the caste. Vertical transmission of CYV is likely to be related to the  
217 infection rate.

218 If vertically transmitted viruses reduce host fitness, non-infected individuals will be selected,  
219 causing the prevalence in the host population to decrease. If the virus does not affect host fitness  
220 (neutral), selection due to infection will not occur, and stochastic fluctuations will cause the prevalence  
221 in the host population to approach either 0% or 100% [22]. However, the wild population-level  
222 prevalence of CYV was over 60% at all collection sites. The following factors could explain the  
223 maintenance of such a prevalence. I) CYV may influence host traits, affecting the reproduction and  
224 survival of the colony. In eusocial insects, genetic diversity within the colony can enhance foraging  
225 efficiency and resistance to pathogens, thus increasing colony fitness [23, 24]. If CYV impacts host  
226 traits, the presence of both infected and uninfected individuals in the colony could produce effects  
227 similar to genetic diversity, potentially increasing colony fitness. Therefore, selective pressure may be  
228 acting to maintain the observed CYV prevalence in the wild. II) The vertical transmission rate of  
229 CYV from infected queens to eggs is not 100%, meaning that even if the queen is infected, some of  
230 the next generation remain uninfected. In intraspecific fostering experiments, some source colonies  
231 showed CYV prevalence of about 90%. This suggests that vertical transmission of CYV was not  
232 observed in some individuals. Because some of the next generation of queens remain uninfected, a  
233 certain proportion of uninfected hosts are maintained. In this case, to sustain the infection, some  
234 mechanisms, such as vertical transmission from males, are needed to compensate for the decrease in  
235 prevalence caused by such incomplete vertical transmission from queens. Otherwise, the prevalence  
236 of CYV would quickly drop to 0%. It should be noted that the vertical transmission rate in the fostering  
237 experiments may be influenced by the experimental treatments.

238

## 239 **2. CYV transmission pathways**

240 CYV was suggested to undergo vertical transmission, but horizontal transmission has not been verified.  
241 In intraspecific rearing experiments, horizontal transmission of CYV through trophallaxis between  
242 adult and larval *C. yamaokai* was not detected. In addition, in these experiments, the number of  
243 emerged workers was low relative to the number of eggs introduced to the experimental colonies.  
244 Many of the broods were likely consumed by adult ants; however, CYV was not detected in the nurse  
245 workers. These results suggest that horizontal transmission of CYV through food intake including  
246 trophallaxis is rare, if any. Although the possibility of horizontal transmission of CYV between adults  
247 has not been tested, trophallaxis in ants of the subfamily Formicinae is frequent and occurs among all  
248 colony members, including between adults and larvae, and among adults[25]. Therefore, if horizontal  
249 transmission were to occur, it is expected that the prevalence among adults would quickly reach 100%.  
250 However, the prevalence in the wild remains around 80%, suggesting that horizontal transmission

251 among adults is also either non-existent or rare, like that between adults and larvae. Furthermore, the  
252 results that CYV was detected in adult *C. yamaokai* reared by non-infected *C. nawai* support the notion  
253 that horizontal transmission is not necessary for maintaining CYV infection.

254 Virus particles were observed within the cytoplasm of oocytes [8], suggesting that these particles  
255 serve as a source of infection for the next generation of host ants. Parasites that rely primarily on  
256 vertical transmission tend to reduce their pathogenicity through coevolution with their hosts [26]. No  
257 clear pathology has been detected in ants infected with CYV, suggesting that CYV may have evolved  
258 to reduce or lose its pathogenicity through vertical transmission. However, for viruses with biparental  
259 vertical transmission from males and females, even with increased pathogenicity, the infection can  
260 still be sustained, unlike viruses that rely solely on vertical transmission from females [27–29].

261

### 262 **3. CYV distribution**

263 To understand the relationship between CYV and its host ants, we examined the geographical  
264 distribution of CYV in Japan. The host ant, *C. yamaokai*, is endemic to Japan and is distributed from  
265 Kyushu to Tohoku [16], and we collected the ants from seven locations from the host distribution  
266 across Japan. We detected CYV in all seven locations in this study. This suggests that the distribution  
267 of the host ant and CYV coincides. Since CYV was not detected in closely related species of  
268 *Camponotus* [8], and vertical transmission is primary route of CYV infection, the initial population of  
269 the host ant might be infected with CYV early in its speciation process. As the infected *C. yamaokai*  
270 expanded its distribution across Japan, CYV's distribution expanded as well.

271

### 272 **4. Conclusion**

273 In this study, we examined the characteristics of the toti-like virus infecting ants with unique ecology.  
274 We found no caste differences in the virus infection rate, and most colonies exhibited a substantially  
275 high infection rate, suggesting that CYV infects the host before the caste is determined. Furthermore,  
276 the geographical distribution and transmission pathways of CYV indicate that it expanded its  
277 distribution along with the host's spread, primarily due to vertical transmission. The mechanisms by  
278 which CYV is maintained within the host population remain to be elucidated in future studies.

279

280 **Acknowledgment**

281 We would like to express our sincere gratitude to Professor Toshiyuki Fukuhara for granting us access  
282 to the analytical equipment, which greatly contributed to this research.

283 We would like to express our gratitude to Tatsuya Ishizuka, Takuto Hashizume, Kohei Nakatsuji,  
284 Tsubasa Nozaki, Atushi Saito, Ryota Seki, Soki Shinkawa, Yu Takatani, and Hiro Yoshimura for their  
285 assistance in the field. We also thank the staff of the Shiiba Research Forest of Kyushu University for  
286 their support in conducting this research.

287

288 **Funding information**

289 This work was supported by JSPS KAKENHI Grant Numbers JP20K22648, JP24K08932.

290

291 **Conflict of Interest**

292 Authors declare no conflict of interest.

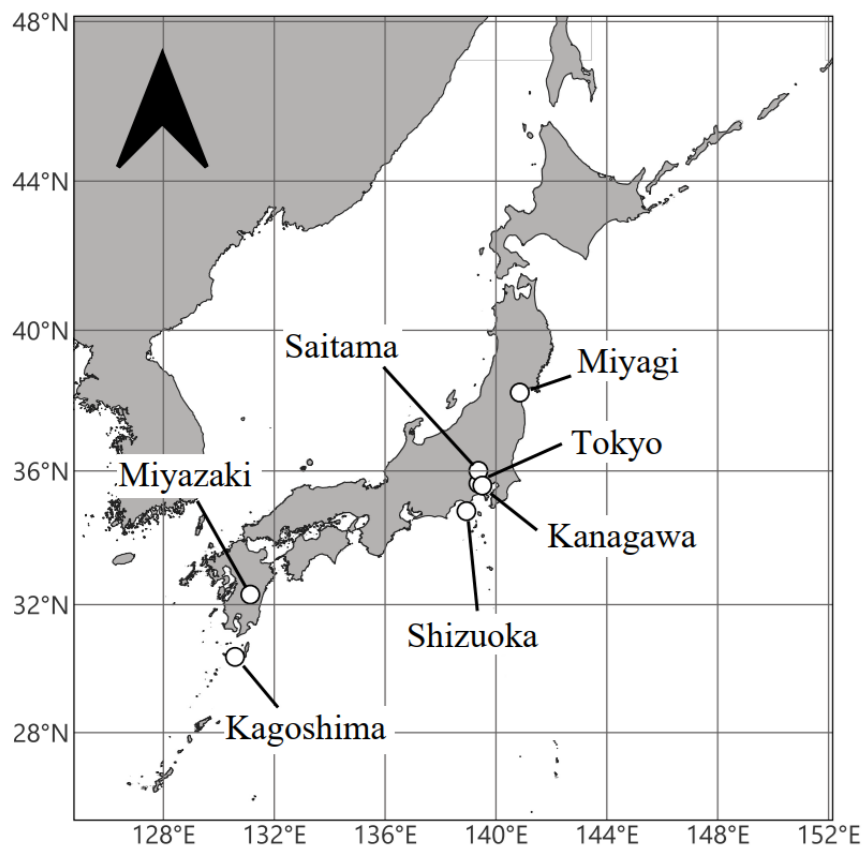
293

294 **References**

- 295 1. Cressler CE, McLeod D V., Rozins C, et al (2016) The adaptive evolution of virulence:  
296 A review of theoretical predictions and empirical tests. *Parasitology* 143:915–930.  
297 <https://doi.org/10.1017/S003118201500092X>
- 298 2. Meunier J (2015) Social immunity and the evolution of group living in insects. *Philos*  
299 *Trans R Soc B* 370: 20140102. <https://doi.org/10.1098/rstb.2014.0102>
- 300 3. Valles SM (2012) Positive-strand RNA viruses infecting the red imported fire ant,  
301 *Solenopsis invicta*. *Psyche* 2012:14. <https://doi.org/10.1155/2012/821591>
- 302 4. Sébastien A, Lester PJ, Hall RJ, et al (2015) Invasive ants carry novel viruses in their  
303 new range and form reservoirs for a honeybee pathogen. *Biol Lett* 11:20150610.  
304 <https://doi.org/10.1098/rsbl.2015.0610>
- 305 5. Baty JW, Bulgarella M, Dobelmann J, et al (2020) Viruses and their effects in ants  
306 (Hymenoptera: Formicidae). *Myrmecol News* 30:213–228.  
307 [https://doi.org/10.25849/myrmecol.news\\_030:213](https://doi.org/10.25849/myrmecol.news_030:213)
- 308 6. Hölldobler B, Edward O. Wilson (1990) *The ants*. Harvard University Press,  
309 Berlin, Germany
- 310 7. Parker J, Kronauer DJC (2021) How ants shape biodiversity. *Curr Biol* 31:R1208–  
311 R1214. <https://doi.org/10.1016/j.cub.2021.08.015>
- 312 8. Koyama S, Urayama SI, Ohmatsu T, et al (2015) Identification, characterization and  
313 full-length sequence analysis of a novel dsRNA virus isolated from the arboreal ant  
314 *Camponotus yamaokai*. *J Gen Virol* 96:1930–1937.  
315 <https://doi.org/10.1099/vir.0.000126>

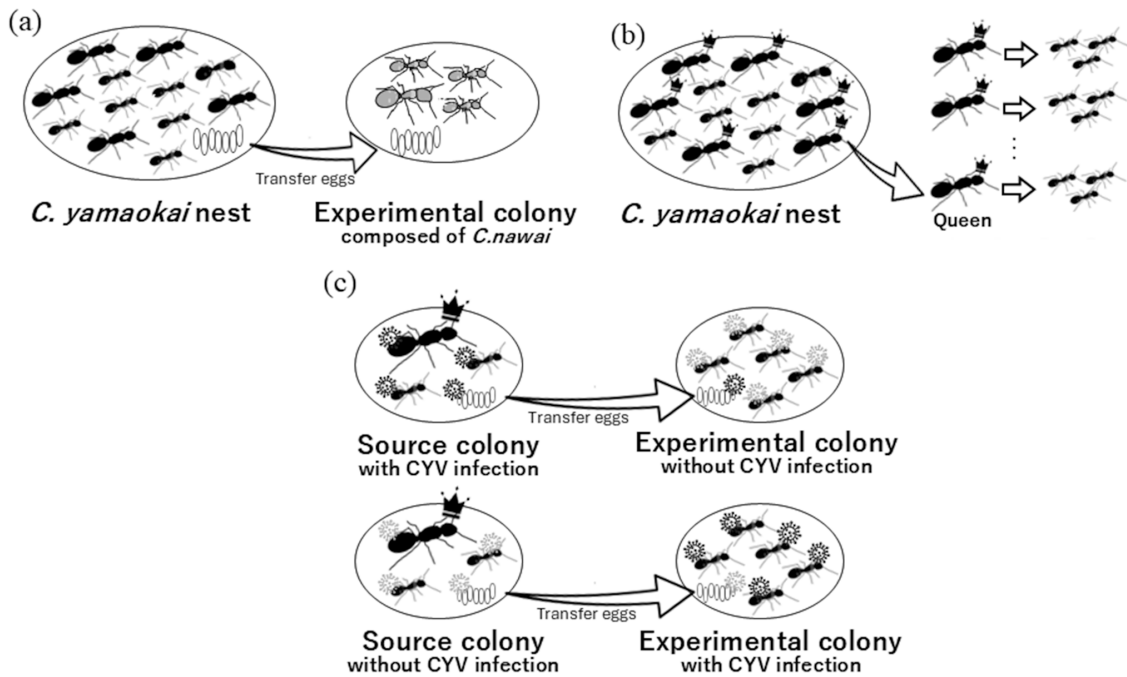
- 316 9. Ghabrial SA, Nibert ML (2009) *Victorivirus*, a new genus of fungal viruses in the  
317 family *Totiviridae*. Arch Virol 154:373–379. [https://doi.org/10.1007/s00705-008-](https://doi.org/10.1007/s00705-008-0272-x)  
318 0272-x
- 319 10. Chen S, Cao L, Huang Q, et al (2016) The complete genome sequence of a novel  
320 maize-associated totivirus. Arch Virol 161:487–490. [https://doi.org/10.1007/s00705-](https://doi.org/10.1007/s00705-015-2657-y)  
321 015-2657-y
- 322 11. Nibert ML (2007) “2A-like” and “shifty heptamer” motifs in penaeid shrimp infectious  
323 myonecrosis virus, a monosegmented double-stranded RNA virus. J Gen Virol  
324 88:1315–1318. <https://doi.org/10.1099/vir.0.82681-0>
- 325 12. Zhai Y, Attoui H, Jaafar FM, et al (2010) Isolation and full-length sequence analysis of  
326 *Armigeres subalbatus* totivirus, the first totivirus isolate from mosquitoes representing  
327 a proposed novel genus (*Artivirus*) of the family *Totiviridae*. J Gen Virol 91:2836–2845.  
328 <https://doi.org/10.1099/vir.0.024794-0>
- 329 13. Haugland Ø, Mikalsen AB, Nilsen P, et al (2011) Cardiomyopathy Syndrome of  
330 Atlantic Salmon (*Salmo salar* L.) Is Caused by a Double-Stranded RNA Virus of the  
331 *Totiviridae* Family. J Virol 85:5275–5286. <https://doi.org/10.1128/jvi.02154-10>
- 332 14. Valles SM, Rivers AR (2019) Nine new RNA viruses associated with the fire ant  
333 *Solenopsis invicta* from its native range. Virus Genes 55:368–380.  
334 <https://doi.org/10.1007/s11262-019-01652-4>
- 335 15. Viljakainen L, Holmberg I, Abril S, Jurvansuu J (2018) Viruses of invasive Argentine  
336 ants from the European Main supercolony: characterization, interactions and evolution.  
337 J Gen Virol 99:1129–1140. <https://doi.org/10.1099/jgv.0.001104>
- 338 16. Mamoru Terayama, Toshiyuki Satoh (1990) A New Species of the Genus *Camponotus*  
339 from Japan, with Notes on Two Known Forms of the Subgenus *Myrmamblyx*  
340 (Hymenoptera, Formicidae). Jpn J Entomol 58:405-414.
- 341 17. Abril S, Jurvansuu J (2020) Season- And caste-specific variation in RNA viruses in the  
342 invasive Argentine ant European supercolony. J Gen Virol 101:322–333.  
343 <https://doi.org/10.1099/JGV.0.001384>
- 344 18. Paul Schmid-Hempel (1998) Parasites in social insects. Princeton University Press,  
345 New Jersey, USA
- 346 19. Cook JM (1993) Sex determination in the Hymenoptera: a review of models and  
347 evidence. Heredity 71:421–435. <https://doi.org/10.1038/hdy.1993.157>
- 348 20. Smith CR, Anderson KE, Tillberg C V., et al (2008) Caste determination in a  
349 polymorphic social insect: Nutritional, social, and genetic factors. Am Nat 172:497–  
350 507. <https://doi.org/10.1086/590961>
- 351 21. Satoh T, Masuko K, Matsumoto T (1997) Colony genetic structure in the mono - and

- 352 polygynous sibling species of the ants *Camponotus nawai* and *Camponotus yamaokai*:  
353 DNA fingerprint analysis. *Ecol Res* 12:71–76. <https://doi.org/10.1007/BF02523612>
- 354 22. Ebert D (2013) The epidemiology and evolution of symbionts with mixed-mode  
355 transmission. *Annu Rev Ecol Evol Syst* 44:623–643. <https://doi.org/10.1146/annurev-ecolsys-032513-100555>  
356
- 357 23. Hughes WOH, Boomsma JJ (2004) Genetic diversity and disease resistance in leaf-  
358 cutting ant societies. *Evolution* 58:1251–1260. <https://doi.org/10.1111/j.0014-3820.2004.tb01704.x>  
359
- 360 24. Ugelvig L V., Kronauer DJC, Schrempf A, et al (2010) Rapid anti-pathogen response  
361 in ant societies relies on high genetic diversity. *Proc R Soc B* 277.1695:2821-2828.  
362 <https://doi.org/10.1098/rspb.2010.0644>
- 363 25. Meurville MP, LeBoeuf AC (2021) Trophallaxis: the functions and evolution of social  
364 fluid exchange in ant colonies (Hymenoptera: Formicidae). *Myrmecol News* 31:1–30.  
365 [https://doi.org/10.25849/myrmecol.news\\_031:001](https://doi.org/10.25849/myrmecol.news_031:001)
- 366 26. Lipsitch M, Siller S, Nowak MA (1996) The evolution of virulence in pathogens with  
367 vertical and horizontal transmission. *Evolution* 50:1729–1741.  
368 <https://doi.org/10.1111/j.1558-5646.1996.tb03560.x>
- 369 27. Fine PEM (1975) Vectors and vertical transmission: an perspective. *Ann N Y Acad Sci*  
370 266:173–194. <https://doi.org/10.1111/j.1749-6632.1975.tb35099.x>
- 371 28. Wayne ML, Blohm GM, Brooks ME, et al (2011) The prevalence and persistence of  
372 sigma virus, a biparentally transmitted parasite of *Drosophila melanogaster*. *Evol Ecol*  
373 *Res* 13:323–345
- 374 29. Longdon B, Jiggins FM (2012) Vertically transmitted viral endosymbionts of insects:  
375 Do sigma viruses walk alone? *Proc R Soc B* 279:3889–3898.  
376 <https://doi.org/10.1098/rspb.2012.1208>  
377  
378



379  
380  
381

**Figure 1** Collection locations of *Camponotus yamaokai*.



382

383

384

385

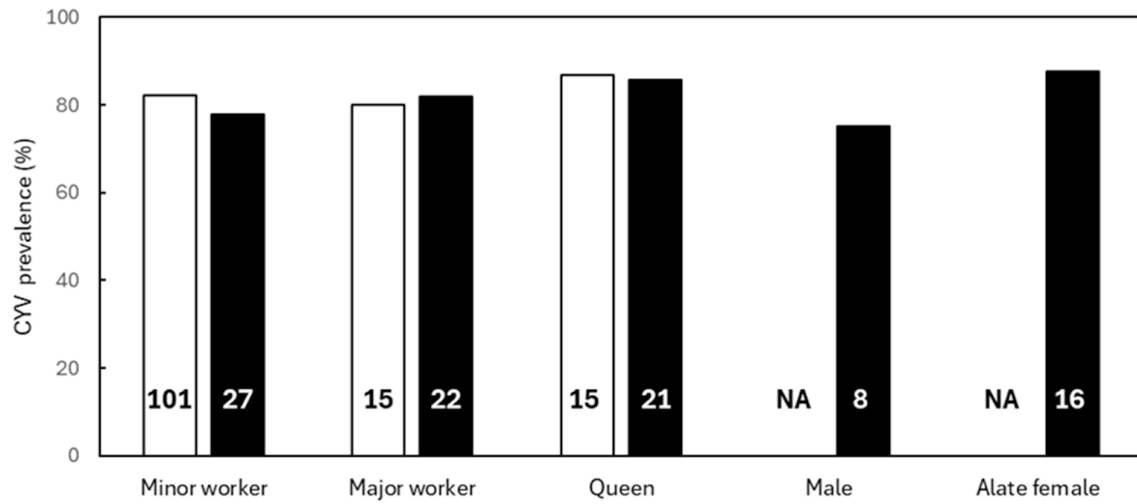
386

387

388

389

**Figure 2** Diagrams of interspecific and intraspecific fostering experiments. (a) Interspecific fostering experiment. This experiment examined whether CYV is transmitted vertically through reproduction. (b) Creation of source colony. Each source colony consists of the offspring of a single queen. This experiment was conducted to confirm that CYV infection remained consistent within the source colony. (c) Intraspecific fostering experiment. This experiment examined whether CYV is transmitted horizontally through trophallaxis.



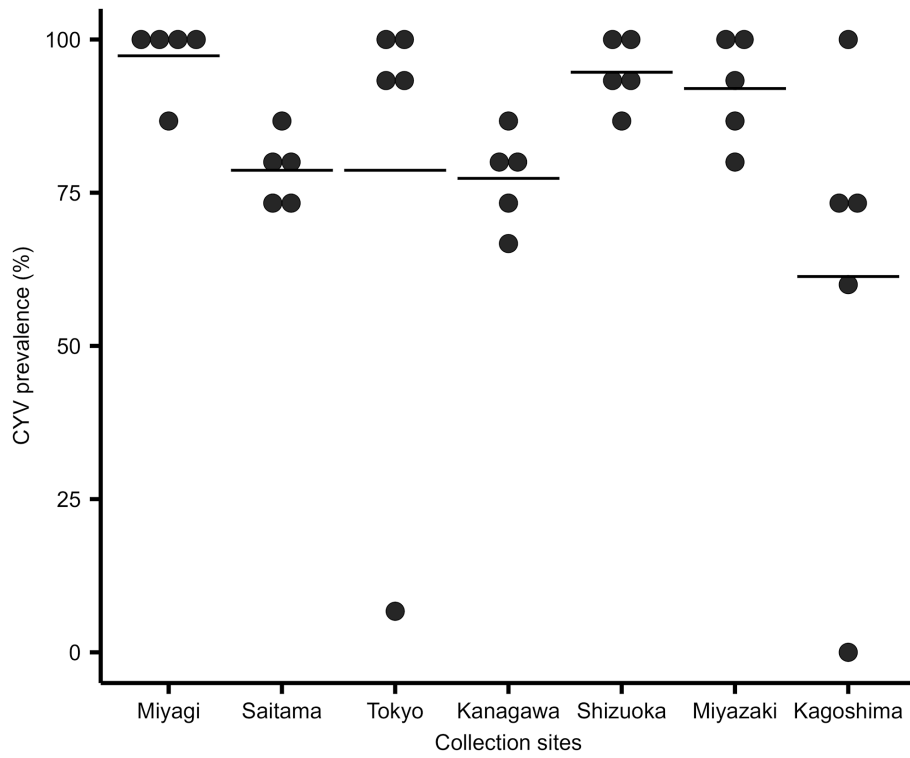
390

391

392

393

**Figure 3** CYV prevalence of each caste. The white bars indicate the prevalence in Tokyo, while the black bars indicate that in Kanagawa. The numbers within the bars represent the sample size.



394

395

396

397

398

399

**Figure 4** CYV prevalence at seven locations. Intra-colonial CYV prevalence was assessed in five nests per location. Fifteen minor workers from each colony were analyzed individually. Each point represents the prevalence within a single nest, while the bars indicate the average prevalence across the five nests in each location.

400 **Table 1** Infection status of *C. yamaokai* reared by *C. nawai*. Eggs of *C. yamaokai* were reared by  
401 workers of *C. nawai* that were not infected with CYV. The individuals that grew to adulthood were  
402 used for the investigation of CYV infection rates.

Eggs introduced	Workers emerged	CYV positive (%)
85	0	NA
71	4	3 (75)
111	8	6 (75)

403

404 **Table 2** The CYV infection of the offspring workers of a single queen.

Colony ID	n	CYV positive (%)
1	9	0 (0)
2	9	0 (0)
3	8	8 (100)
4	11	8 (91)
5	12	11 (92)
6	12	12 (100)

405

406 **Table 3** Infection status of *C. yamaokai* reared by individuals of the same species with different  
 407 CYV infection profiles. Infection status of the source colonies was determined before the fostering  
 408 experiment. The eggs of *C. yamaokai* were reared by workers with different CYV infection statuses.  
 409 The individuals that grew to adulthood were used for the investigation of CYV infection rates.

Infection status of the source colony		Eggs introduced	Emerged worker		CYV prevalence of nurse workers
Eggs	Nurse workers		n	CYV positive (%)	
Positive	Negative	21	5	5 (100)	0%
		40	10	7 (70)	0%
Negative	Positive	10	3	0 (0)	90%
		39	5	0 (0)	80%

410