1	Formicine ants swallow their highly acidic poison for gut microbial selection and control
2	Simon Tragust ^{1†*} , Claudia Herrmann ¹ , Jane Häfner ¹ , Ronja Braasch ¹ , Christina Tilgen ¹ , Maria
3	Hoock ¹ , Margarita Artemis Milidakis ¹ , Roy Gross ² , Heike Feldhaar ¹
4	
5	¹ Animal Ecology I, Bayreuth Center for Ecology and Environmental Research (BayCEER),
6	University of Bayreuth, Universitätsstraße 30, 95447 Bayreuth, Germany
7	² Microbiology, Biocenter, University of Würzburg, Am Hubland, 97074 Würzburg
8	[†] Present address: General Zoology, Hoher Weg 8, Martin-Luther University, 06120 Halle
9	(Saale), Germany
10	* Correspondence to: simon.tragust@zoologie.uni-halle.de
11	

12 Abstract

13 Animals continuously encounter microorganisms that are essential for health or cause disease. They are thus challenged to control harmful microbes while allowing acquisition of beneficial 14 15 microbes, a challenge that is likely especially important concerning microbes in food and in animals such as social insects that exchange food among colony members. Here we show that 16 17 formicine ants actively swallow their antimicrobial, highly acidic poison gland secretions after feeding. The ensuing creation of an acidic environment in the stomach, the crop, 18 improves individual survival in the face of pathogen contaminated food and limits disease 19 transmission during mutual food exchange. At the same time, crop acidification selectively 20 21 allows acquisition and colonization by known bacterial gut associates. The results of our study suggest that swallowing of acidic poison gland secretions acts as a microbial filter in 22 23 formicine ants and indicate a potentially widespread but so far underappreciated dual role of antimicrobials in host-microbe interactions. 24

25

26 Introduction

Animals commonly harbor gut associated microbial communities (Engel and Moran, 2013,
Moran et al., 2019). Patterns of recurring gut microbial communities have been described for
many animal groups (Brune and Dietrich, 2015, Kwong et al., 2017, Ochman et al., 2010).
The processes generating these patterns are however often not well understood. They might
result from host filtering (Mazel et al., 2018), codiversification between gut associated
microbes and their hosts (Moeller et al., 2016) or simply be the result of similar dietary
preferences (Anderson et al., 2012, Hammer et al., 2017).

Food is an important environmental source of bacterial gut associates (Blum et al., 2013,

Broderick and Lemaitre, 2012, David et al., 2014, Hammer et al., 2017, Perez-Cobas et al.,

2015) but also poses a challenge, the need to discriminate between harmful and beneficial 36 37 microbes, as food may contain microbes that produce toxic chemicals or that are pathogenic (Burkepile et al., 2006, Demain and Fang, 2000, Janzen, 1977, Trienens et al., 2010). In social 38 animals, control of harmful microbes in food while at the same time allowing the acquisition 39 40 and transmission of beneficial microbes from and with food, is likely especially important. Eusocial Hymenoptera not only transport and store food in their stomach, the crop, but also 41 distribute food to members of their colony via trophallaxis, i.e. the regurgitation of crop 42 content from donor individuals to receiver individuals through mouth-to-mouth feeding 43 (Gernat et al., 2018, Greenwald et al., 2018, LeBoeuf et al., 2016). While trophallaxis can 44 45 facilitate the transmission of beneficial microbes, from an epidemiological perspective it can 46 also entail significant costs, as it might open the door to unwanted microbial opportunists and pathogens that can take advantage of these transmission routes (Onchuru et al., 2018, Salem et 47 48 al., 2015).

49 Here we investigate how formicine ants, specifically the Florida carpenter ant *Camponotus* 50 floridanus, solve the challenge to control harmful microbes in their food while allowing acquisition and transmission of beneficial microbes from and with their food. Apart from 51 specialized intracellular endosymbionts associated with the midgut in the ant tribe 52 53 Camponotini (Degnan et al., 2004, Feldhaar et al., 2007, Russell et al., 2017, Williams and Wernegreen, 2015), formicine ant species have only low abundances of microbial associates 54 in their gut lumen but carry members of the bacterial family Acetobacteracea as a major part 55 56 of their gut microbiota (Brown and Wernegreen, 2016, Chua et al., 2018, He et al., 2011, Ivens et al., 2018). Some formicine gut associated Acetobacteracea show signs of genomic 57 58 and metabolic adaptations to their host environment indicating coevolution (Brown and Wernegreen, 2019). But the recurrent presence of Acetobacteracea in the gut of formicine ants 59 potentially also reflects direct transmission of bacteria among individuals, selective uptake on 60

the part of the ants, specific adaptation for colonizing ant guts on the part of the bacteria, orsome combination of all three (Engel and Moran, 2013).

Generally, the immune system together with physiochemical properties of the gut 63 64 environment maintains the homeostasis between gut associated microbes and the host (Chu 65 and Mazmanian, 2013, McFall-Ngai et al., 2013, Rakoff-Nahoum et al., 2004, Slack et al., 66 2009, Watnick and Jugder, 2020, Xiao et al., 2019, see also Foster et al., 2017). Highly acidic stomach lumens are ubiquitous in higher vertebrates, including amphibians, reptiles, birds and 67 mammals (Beasley et al., 2015, Koelz, 1992), while in insects, acidic regions have rarely been 68 described so far from midgut regions (Chapman, 2013, Holtof et al., 2019). However in both, 69 higher vertebrates, and the fruit fly Drosophila melanogaster, acidic gut compartments 70 71 together with the immune system serve microbial control and prevent infection by pathogens 72 (Giannella et al., 1972, Howden and Hunt, 1987, Martinsen et al., 2005, Overend et al., 2016, Rakoff-Nahoum et al., 2004, Slack et al., 2009, Tennant et al., 2008, Watnick and Jugder, 73 74 2020). Formicine ant species possess a highly acidic poison gland secretion containing formic 75 acid that is foremost used as a defensive weapon but is also distributed to the environment of 76 these ants as an external immune defence trait (sensu Otti et al., 2014), to protect their 77 offspring and the nest and to limit disease spread within the society (see references in Tragust, 78 2016, Brütsch et al., 2017, Pull et al., 2018). Thereby, ants can take up poison gland secretions from the acidopore, the opening of the poison gland at the gaster tip, into their 79 mouth during a specialized behaviour existing only in a subset of ant families among all 80 81 Hymenopterans (Basibuyuk and Quicke, 1999, Farish, 1972), termed acidopore grooming (Tragust et al., 2013). 82

Here we first investigate whether poison gland substances are also swallowed during
acidopore grooming in *C. floridanus* and seven other formicine ant species from three genera
in a comparative survey through measurement of pH levels in the crop and midgut lumen,

experimental manipulation of poison gland access, and behavioural observations. In loss of
poison gland function experiments, we then investigate whether analogous to acidic stomachs
of higher vertebrates and acidic midgut regions in the fruit fly, swallowing of poison gland
substances can serve gut microbial control and prevent bacterial pathogen infection and
transmission. Finally, we explore whether swallowing of poison gland substances acts as a
microbial filter that is permissible to gut colonization of bacteria from the family
Acetobacteracea.

93

94 Results and Discussion

To reveal whether poison gland secretions are swallowed during acidopore grooming, we 95 monitored acidity levels in the crop lumen of the Florida carpenter ant *Camponotus floridanus* 96 at different time points after feeding them 10% honey water (pH = 5). We found that over 97 time, the crop lumen became increasingly acidic, reaching highly acidic values 48h after 98 99 feeding (median pH = 2; 95% CI: 1.5-3.4), whilst renewed access to food after 48h restored the pH to levels recorded after the first feeding trial (Fig. 1a; LMM, LR-test, $\gamma^2 = 315.18$, df = 100 3, P < 0.001; Westfall corrected post-hoc comparisons: 0+4h vs. 48h+4h: P = 0.317, all other 101 102 comparisons: P < 0.001). This acidification was limited to the crop and did not extend to the midgut (Fig. 1 – figure supplement 1; pH-measurements at four points along the midgut 24h 103 after access to 10% honey-water; mean \pm se; midgut position $1 = 5.08 \pm 0.18$, midgut position 104 $2 = 5.28 \pm 0.17$, midgut position $3 = 5.43 \pm 0.16$, midgut position $4 = 5.31 \pm 0.19$). Prevention 105 of acidopore grooming in C. floridanus ants for 24h after feeding resulted in a significantly 106 diminished acidification of the crop lumen (Fig. 1b; LMM, LR-test, $\chi^2 = 44.68$, df = 1, P < 107 0.001), a result that was invariably obtained in a comparative survey across seven formicine 108 ant species (genera: Camponotus, Lasius and Formica) (Fig. 1c; two-sided Wilcoxon rank 109 sum tests, all comparisons: $P \le 0.036$). This indicates that after feeding, crop lumens of 110

formicine ants are acidified through swallowing of poison gland secretions during acidopore 111 112 grooming. Although venomous animals often bear a cost of venom production and express behavioural adaptations to limit venom expenditure (Casewell et al., 2013), C. floridanus 113 increases the frequency of acidopore grooming upon ingestion of food but also after ingestion 114 of water (Fig. 1 - figure supplement 2; GLMM, LR-test, $\chi^2 = 33.526$, df = 2, P <0.001; 115 Westfall corrected post-hoc pairwise comparisons, water vs. 10% honey-water: P = 0.634, 116 117 unfed vs water and unfed vs 10% honey-water: P < 0.001). This suggests a prophylactic acidification of crop lumens after fluid ingestion, irrespective of the fluids nutritional value. 118 119 To test whether crop lumen acidification serves microbial control and prevents infection by 120 pathogens, we prevented acidopore grooming in C. floridanus ants for 24h after feeding them either honey water contaminated with Serratia marcescens, an insect pathogenic bacterium 121 (Grimont and Grimont, 2006), or non-contaminated honey water. We found that acidopore 122 access after pathogen ingestion increased the survival probability of ants (Fig. 2a). The 123 survival of ants prevented from acidopore grooming and fed with pathogen contaminated food 124 125 was significantly lower than that of non-prevented ants fed with the same food source, the 126 latter not differing in survival to similarly manipulated ants that were fed a non-contaminated food source (COXME, LR-test, $\chi^2 = 20.95$, df = 3, P = 0.0001; Westfall corrected post-hoc 127 128 comparisons: FA - | Serratia presence + vs. all other ant groups: $P \le 0.027$, all other comparisons: $P \ge 0.061$). Food sanitation with antimicrobials that are either self-produced or 129 derived from the environment or symbiotic associations (Otti et al., 2014) is ubiquitous in 130 animals that provision food to their offspring or that store, cultivate, develop or live in food 131 (Cardoza et al., 2006, Currie et al., 1999, Herzner et al., 2013, Herzner and Strohm, 2007, 132 133 Joop et al., 2014, Milan et al., 2012, Mueller et al., 2005, Scott et al., 2008, Shukla et al., 2018, Vander Wall, 1990, Vogel et al., 2017). The results of our study indicate that formicine 134 ants not only distribute acidic poison gland secretions to the environment as an external 135

immune defence trait (see references in Tragust, 2016, Brütsch et al., 2017, Pull et al., 2018),
but also use them to sanitize ingested food.

Crop lumen acidification in formicine ants upon ingestion of pathogen contaminated food 138 139 may not only improve individual survival but might also limit oral disease transmission during food distribution via trophallaxis within a social insect society. To test an immune 140 functional role of crop lumen acidification during trophallaxis, we created two types of donor-141 receiver ant pairs. Donor ants in both pairs were directly fed S. marcescens contaminated 142 food, while receiver ants obtained food only through trophallaxis with their respective donor 143 ants. Receiver ants in both pairs were precluded from crop acidification through blockage of 144 145 their acidopore opening, while donor ants were blocked in one pair but only sham blocked in the other pair. We found that acidopore blockage per se had a significant negative effect on 146 the survival of donor as well as receiver ants (Fig. 2b; COXME, LR-test, $\gamma^2 = 66.68$, df = 3, P 147 < 0.001). Importantly however, although receiver ants that obtained food from donors with 148 the ability to acidify their crop lumen died at a higher rate than their respective donor 149 150 counterparts (hazard ratio: 1.81; Westfall corrected post-hoc comparison: P < 0.001) they 151 were approximately only half as likely to die compared to receiver ants that obtained pathogen contaminated food from blocked donors unable to acidify their crop lumen (hazard 152 ratio: 0.56; Westfall corrected post-hoc comparison: P < 0.001). Trophallactic behaviour 153 between the two donor-receiver ant pairs was not different (Fig. 2 – figure supplement 1; 154 LMM, LR-test, $\chi^2 = 1.23$, df = 1, P = 0.268). Although an antimicrobial activity of formicine 155 156 ant trophallactic fluids has been linked to the presence of proteins in previous studies (Hamilton et al., 2011, LeBoeuf et al., 2016), the results of our study suggest a major role of 157 158 crop lumen acidification through the ingestion of poison gland substances. Prophylactic acidification of the crop lumen after feeding in C. floridanus might therefore act as an 159 important barrier to disease spread within the colony and alleviate the cost of sharing 160

pathogen contaminated food (Onchuru et al., 2018, Salem et al., 2015). Together with other 161 162 parasite defence traits in social insect societies (Cremer et al., 2007, Stroeymeyt et al., 2018), acidification of crop lumens likely effectively counteracts the generally increased risk of 163 pathogen exposure and transmission associated with group-living (Alexander, 1974, 164 Boomsma et al., 2005, Kappeler et al., 2015) 165 In addition to pathogen control, the acidification of the crop lumen might act as a chemical 166 filter for gut associated microbial communities in formicine ants, similar to gut morphological 167 structures that can act as mechanical filters in ants and other insects (Itoh et al., 2019, Lanan 168 et al., 2016, Ohbayashi et al., 2015). To investigate the idea of a chemical filter, we tested the 169 170 ability of the pathogenic bacterium S. marcescens, and the insect gut associated bacterium Asaia sp. (family Acetobacteracea) to withstand acidic environments in vitro and in vivo. 171 172 Incubation of S. marcescens in 10% honey water acidified with formic acid for 2h resulted in a significantly reduced growth at pH 4 compared to 5, with zero growth at pH-levels less than 173 4 (Fig. 3 – figure supplement 1a; GLM, LR-test, $\chi^2 = 79.442$, df = 1, P < 0.001). Consistent 174 175 with this, when fed to C. floridanus, S. marcescens presence decreased sharply over time in the crop (Fig. 3a; GLMM, LR-test, $\chi^2 = 220.78$, df = 4, P < 0.001) with the proportion of 176 CFUs at 0.5h post-feeding relative to 0h in the crop diminishing from 48% (median, CI: 0-177 178 366%) to 0% at 4h (CI: 0-4%), 24h (CI: 0-2.7%), and 48h (CI: 0-21%) post-feeding. In addition, S. marcescens could only be detected at extremely low levels (median: 0%) in the 179 midgut at 0h (CI: 0-5%), 0.5h (CI: 0-1%) and 24h (CI: 0-1%) post-feeding relative to 0h in 180 the crop and not at all at 4h and 48h post-feeding (Fig. 3b; GLMM, LR-test, $\chi^2 = 1.044$, df = 181 2, P = 0.593). Taken together, *in vivo* and *in vitro* tests suggest that crop acidification results 182 183 in a quick and effective reduction of S. marcescens viability in the crop thus preventing further transport to the midgut. The same results were obtained in vivo for E. coli, a bacterium 184 that is not a gut associate of insects (Blount, 2015) (Fig. 3 – figure supplement 2; crop: 185

186	GLMM, LR-test, $\chi^2 = 156.74$, df = 4, $P < 0.001$; midgut: GLMM, LR-test, $\chi^2 = 14.898$, df = 3,
187	P = 0.002). In contrast to S. marcescens, Asaia sp. was able to grow in 10% honey water
188	acidified with formic acid to a pH of 3 for 2h in <i>in vitro</i> tests (Fig. 3 – figure supplement 1b;
189	GLM, overall LR-test $\chi^2 = 21.179$, df = 2, $P < 0.001$; Westfall corrected post hoc
190	comparisons: $pH = 5$ vs. $pH = 4$: $P = 0.234$, all other comparisons: $P < 0.001$). Moreover, in
191	in vivo tests, Asaia sp. only gradually diminished over time in the crop (Fig. 3c; GLMM; LR-
192	test, $\chi^2 = 124.01$, df = 4, $P < 0.001$) with 34% (median, CI: 3-85%) and 2% (CI: 0-7%)
193	relative to 0h in the crop still detectable at 4h and 24h post-feeding, respectively. At the same
194	time <i>Asaia</i> sp. steadily increased in the midgut (Fig. 3d; GLMM; LR-test, $\chi^2 = 59.94$, df = 3, <i>P</i>
195	< 0.001) from its initial absence at 0h post-feeding to 2% (median, CI: 0-5%) relative to 0h in
196	the crop at 48h post-feeding. This indicates that crop lumen acidification is permissible to gut
197	colonization by Asaia sp Given the ubiquitous presence of crop lumen acidification in our
198	comparative survey of formicine ant species (Fig. 1c) and the gut microbiota structuring
199	properties of acidic gut compartments in humans (Imhann et al., 2016) and fruit flies
200	(Overend et al., 2016), it is likely that host filtering (Mazel et al., 2018) through acidification
201	of crop lumens can explain the recurrent presence of Acetobacteracea in the gut of formicine
202	ants and the otherwise reduced microbial diversity and abundance of gut associated microbes
203	(Brown and Wernegreen, 2016, Chua et al., 2018, Ivens et al., 2018). On the other hand, some
204	formicine gut associated Acetobacteracea show signs of genomic and metabolic adaptations to
205	their host environment (Brown and Wernegreen, 2019), indicating coevolution and potentially
206	also mutual benefit, though this has not formally been established (see also Mushegian and
207	Ebert, 2016). The creation of a challenging gut environment through the ingestion of poison
208	gland substances that is easier to endure if colonizing microbes are mutualists agrees with the
209	theoretical concept of screening, as opposed to signalling, as a means of partner choice in
210	cross-kingdom mutualisms (Archetti et al., 2011a, Archetti et al., 2011b, Biedermann and
211	Kaltenpoth, 2014, Scheuring and Yu, 2012). Experimental evidence for screening is so far

limited in insect-microbe associations (Innocent et al., 2018, Itoh et al., 2019, Ranger et al., 212 213 2018), but the results of our study provide support for the prediction that screening is more 214 likely to evolve if a host's challenging environment is derived from defence traits against parasites (Archetti et al., 2011a, Archetti et al., 2011b). Altogether, our study provides 215 216 evidence that the well-established cross talk between the immune system and gut associated microbes in vertebrates and invertebrates (Chu and Mazmanian, 2013, Rakoff-Nahoum et al., 217 218 2004, Slack et al., 2009, Watnick and Jugder, 2020, Xiao et al., 2019) holds for a broader range of immune defence traits (sensu Otti et al., 2014) and might be realized not only 219 through signalling but also screening. 220

221

222 Conclusion

Overall our study provides evidence that swallowing of formic acid containing poison gland 223 secretions acts as a chemical filter for microbial selection and control of gut associated 224 225 microbes, protecting formicine ants from food borne bacterial pathogens and structuring gut associated microbial communities. In ants and other animals that lack acidic poison gland 226 secretions, acids produced by other exocrine glands (Fernández-Marín et al., 2015, Yek and 227 228 Mueller, 2011) or acidic derivatives produced by defensive symbionts (Florez et al., 2015) or other environmental bacteria (Ratzke and Gore, 2018) might provide functionally similar 229 roles to acidic poison gland secretions, as indicated in bees (Palmer-Young et al., 2018) and 230 termites (Inagaki and Matsuura, 2018). Antimicrobials as external immune defence traits (Otti 231 et al., 2014) may generally not only serve pathogen protection and microbial control but may 232 233 also act as microbial filters to manage host associated microbes, be it in food or the environment, and thus contribute to a host's ecological and evolutionary success. In the case 234 of social species by alleviating the increased risk of pathogen exposure and transmission 235

- associated with group living but allowing the acquisition and transmission of microbial
- 237 mutualists.

239 Methods

240	Ant species and maintenance. Colonies of the carpenter ant Camponotus floridanus were
241	collected in 2001 and 2003 in Florida, USA, housed in Fluon® (Whitford GmbH, Diez,
242	Germany) coated plastic containers with plaster ground and maintained at a constant
243	temperature of 25°C with 70% humidity and a 12h/12h light/dark cycle. They were given
244	water ad libitum and were fed three times per week with honey water (1:1 tap water and
245	commercial quality honey), cockroaches (Blaptica dubia) and an artificial diet (Bhatkar and
246	Whitcomb, 1971). For comparison, workers of one other Camponotus species (Camponotus
247	maculatus), collected close to Kibale Forest, Uganda in 2003 and housed under identical
248	conditions as Camponotus floridanus were used. Additionally, six other formicine ant species,
249	one Lasius and five Formica species (Lasius fuliginosus, Formica cinerea, Formica
250	cunicularia, Formica fuscocinerea, Formica pratensis and Formica rufibarbis) were collected
251	in Bayreuth, Germany in 2012 and 2018 and kept for approximately two weeks prior
252	experimental use at 20°C, 70% humidity and a 14h/10h light/dark cycle.
253	Acidification of crop lumen and pH measurements. To determine whether formicine ants

253 swallow poison gland secretions after feeding, we tracked changes in pH-levels of the crop 254 lumen over time. Before use in experimental settings, cohorts of 50-100 ants were taken out 255 256 of their natal colony (C. floridanus: n = 6 colonies) into small plastic containers lined with 257 Fluon® and starved for 24-48h. Thereafter, ants were put singly into small petri dishes (Ø 55 mm) with damp filter paper covered bottom, given access to a droplet of 10% honey water 258 259 (w/v) for 2h before removing the food source and measuring the pH of the crop lumen in C. *floridanus* after another 2h (group 0+4h: n = 60 workers), after 24h (group 0+24h: n = 59260 261 workers) or 48h (group 0+48h: n = 52 workers). To assess the effect of renewed feeding, a separate group of C. floridanus ants were given access to 10% honey water 48h after the first 262 feeding for 2h prior to measuring the pH of their crop lumen after another 2h (group 48h+4h: 263

n = 60 workers). To measure the pH, ants were first cold anesthetized on ice, then their gaster 264 265 was cut off with a fine dissection scissor directly behind the petiole and leaking crop lumen (1-3µl) collected with a capillary (5µl Disposable Micro Pipettes, Blaubrand intraMARK, 266 Brand, Wertheim). The collected crop lumen was then emptied on a pH sensitive paper to 267 268 assess the pH (Hartenstein, Unitest pH 1-11). We also measured the pH of 10% honey water on pH sensitive paper, which gave invariably pH = 5. In addition, we measured the pH in the 269 crop lumen and at four points in the lumen along the midgut (1st measurement directly behind 270 proventriculus to 4th measurement one mm apical from insertion point of malpighian tubules) 271 of C. floridanus workers that were fed 24 h prior to measurements with 10% honey-water. For 272 273 these measurements worker guts were dissected as a whole and pH was measured in the crop 274 (n = 2 workers from two colonies) and along the midgut (all midgut points n = 10, except point four with n = 9 workers from four different colonies) with a needle-shaped 275 276 microelectrode for pH measurements (UNISENSE pH-meter; microelectrode with needle tip 277 of 20µm diameter). In formicine ants, oral uptake of poison gland secretions into the mouth is performed via acidopore grooming (Tragust et al., 2013). During this behavior ants bend their 278 gaster forward between the legs and the head down to meet the acidopore, the opening of the 279 280 poison gland, at the gaster tip (Basibuyuk and Quicke, 1999, Farish, 1972). In an additional 281 experiment we therefore compared the crop lumen pH of C. floridanus workers from four 282 different colonies that were either prevented to reach their acidopore (FA- ants) or could reach their acidopore freely (FA+ ants). To do this, we again allowed single ants access to 10% 283 284 honey water for 2h after a starvation period, before cold anesthetizing them briefly on ice and immobilizing FA- ants (n = 22 workers) in a pipetting tip, while FA+ ants (n = 23 workers) 285 remained un-manipulated. After 24h we measured the pH of the crop lumen as before. To 286 investigate whether crop lumen acidification is widespread among formicine ants, the latter 287 experiment was repeated for six additional formicine ant species (FA- ants: n = 10 workers 288 except for *Formica pratensis* with n = 21; FA+ ants: n = 10 workers except for *Formica* 289

290 *pratensis* with n=20; all ants: n = 1 colony) in the same fashion as described before with the 291 exception that apart from *Formica pratensis* the crop lumen was collected through the mouth 292 by gently pressing the ants' gaster. Crop lumen of *Formica pratensis* ants was collected in the 293 same fashion as crop lumen of *C. floridanus* ants.

Bacterial strains and culture. As model entomopathogenic bacterium *Serratia marcescens*DSM12481 (DSMZ Braunschweig, Germany) was used. This bacterium is pathogenic in a
range of insects (Grimont and Grimont, 2006) and has been detected in formicine ants, i.e. *Anoplolepis gracilipes* (Cooling et al., 2018) and *Camponotus floridanus* (Ratzka et al.,

298 2011). While often non-lethal within the digestive tract, *S. marcescens* can cross the insect gut

wall (Mirabito and Rosengaus, 2016, Nehme et al., 2007) and is highly virulent upon entry

into the hemocoel (Flyg et al., 1980), not least due to the production of bacterial toxins

301 (Hertle, 2005). As a model bacterial gut-associate of ants Asaia sp. strain SF2.1 (Favia et al.,

2007), was used. *Asaia* sp. belongs to the family Acetobacteracea, members of which often

thrive in sugar-rich environments (Mamlouk and Gullo, 2013), such as honey-dew that ants

like *C. floridanus* predominantly feed on. *Asaia* sp. is capable of cross-colonizing insects of

phylogenetically distant genera and orders (Crotti et al., 2009, Favia et al., 2007) and can be a

306 component of the gut associated microbial community of formicine ants (Chua et al., 2018,

Kautz et al., 2013a, Kautz et al., 2013b). In addition to S. marcescens and Asaia sp.,

Escherichia coli DSM6897 (DSMZ Braunschweig, Germany) was used as a model bacterium
that is not a gut-associate of insects. *E. coli* bacteria are a principal constituent of mammalian

310 gut associated microbial communities but are commonly also found in the environment

311 (Blount, 2015).

Bacterial stocks of *S. marcescens, Asaia* sp., and *E. coli* were kept in 25% glycerol at -80°C

until use. For use, bacteria were plated on agar plates (LB-medium: 10g Tryptone, 5g Yeast

extract, 20g Agar in 1L MilliQ-water, and GLY-medium: 25g Gycerol, 10g Yeast extract, 20g

Agar in 1L MilliQ-water with pH adjusted to 5.0, for S. marcescens/E. coli and Asaia sp. 315 316 respectively), single colony forming units (CFUs) were picked after 24h (S. marcescens/E. 317 coli) or 48h (Asaia sp.) of growth at 30°C and transferred to 5ml liquid medium (LB-medium and GLY-medium minus agar for S. marcescens/E. coli and Asaia sp. respectively) for an 318 overnight culture (24h) at 30°C. The overnight culture was then pelleted by centrifugation at 319 3000g, the medium discarded and resolved in 10% (w/v) honey water to the respective 320 321 working concentration for the experiments. The concentration of a typical overnight culture was determined for *S. marcescens* and *Asaia* sp. by plating part of the overnight culture on 322 agar plates and counting CFUs after 24h or 48h of growth at 30°C, for S. marcescens and 323 Asaia sp. respectively. This yielded a concentration of $1.865 * 10^9 \pm 5.63 * 10^7$ (mean \pm sd) 324 bacteria per ml for S. marcescens and $5.13 \times 10^8 \pm 8.48 \times 10^6$ (mean \pm sd) bacteria for Asaia 325 326 sp.

Survival experiments. In a first survival experiment we tested whether the ability to perform 327 acidopore grooming within the first 24h after ingestion of pathogen contaminated food 328 329 provides a survival benefit for individual C. floridanus ants. Ants from eight colonies were starved as described before and single workers in small petri dishes were then either given 330 access to 5µl of S. marcescens contaminated 10% honey water $(9.33 * 10^9 \text{ bacteria/ml};$ 331 332 Serratia + ants: n = 127) or uncontaminated 10% honey water (Serratia- ants: n = 135) for 2 min. Thereafter, all ants were cold anaesthetized and approximately half of the Serratia+ and 333 the Serratia- ants (n = 65 and n = 69, respectively) immobilized in a pipetting tip, thus 334 335 preventing acidopore grooming (FA- ants: n = 134) while the other half remained fully mobile (FA+ ants: n = 128). After 24h, FA- ants were freed from the pipetting tip to minimize stress. 336 337 Mortality of the ants was monitored over 5 days (120h) every 12h.

In an additional survival experiment, we investigated whether the acidification of the croplumen has the potential to limit oral disease transmission during trophallactic food transfer.

To this end C. floridanus ants from seven colonies were again starved, divided randomly in 340 341 two groups (donor and receiver ants, each n = 322) and their gaster marked with one of two 342 colours (Edding 751). Additionally, to prevent uptake of poison gland secretion, the acidopore opening of all receiver ants (receiver FA-) and half of the donor ants (donor FA-) was sealed 343 344 with superglue, while the other half of the donor ants were sham treated (donor FA+) with a droplet of superglue on their gaster (Tragust et al., 2013). We then paired these ants into two 345 different donor-receiver ant pairs. Pairs with both donor and receiver ants having their 346 acidopore sealed (donor FA- | receiver FA-) and pairs with only receiver ants having their 347 acidopore sealed (donor FA+ | receiver FA-). Six hours after pairing, donor ants from both 348 349 pairs were isolated and given access to 5µl of S. marcescens contaminated 10% honey water $(1.865 * 10^9 \text{ bacteria/ml})$ for 12h. Thereafter donor ants were again paired with the respective 350 receiver ants for 12 h and all pairs filmed for the first 30min. (Logitech webcam c910). These 351 352 videos were then analyzed for the duration of trophallaxis events donor-receiver ant pairs engaged in. After this first feeding round, donor ants were fed in the same fashion, i.e. 353 isolation for 12h with access to S. marcescens contaminated 10% honey water, every 48h, 354 while they were maintained with the respective receiver ants for the rest of the time. This 355 356 experimental design ensured that receiver ants were fed only through the respective donor 357 ants with pathogen contaminated food. Survival of both, donor and receiver ants, was monitored daily for a total of 12 days. 358

Bacterial growth assays. We tested the ability of *S. marcescens* and *Asaia* sp. to withstand
acidic environments in the crop *in vitro* and *in vivo*, as well as their ability and the ability of *E. coli* to pass from the crop to the midgut *in vivo*. In ants, gut morphological structures, i.e.
the infrabuccal pocket, an invagination of the hypopharynx in the oral cavity (Eisner and
Happ, 1962), and the proventriculus, a valve that mechanically restricts passage of fluids from
the crop to the midgut (Eisner and Wilson, 1952), consecutively filter solid particles down to

365	2µm (Lanan et al., 2016) which would allow S. marcescens (Ø: 0.5-0.8µm, length: 0.9-2µm,
366	Grimont and Grimont, 2006), Asaia sp. (Ø: 0.4-1µm, length: 0.8-2.5µm, (Komagata et al.,
367	2014), and E. coli (length: 1µm, width: 0.35µm, Blount, 2015) to pass. For the in vitro tests
368	we incubated a diluted bacterial overnight culture (10^5 and 10^4 CFU/ml for S. marcescens and
369	Asaia sp., respectively) in 10% honey water ($pH = 5$) and in 10% honey water acidified with
370	commercial formic acid to a pH of 4, 3 or 2 for 2h at room temperature (S. marcescens: $n = 15$
371	for all pH-levels, except $pH = 4$ with $n = 13$; <i>Asaia</i> sp.: $n = 10$). Then we plated 100µl of the
372	bacterial solutions on agar-medium (LB-medium and GLY-medium for S. marcescens and
373	Asaia sp., respectively) and incubated them at 30°C for 24h (S. marcescens) or 48h (Asaia
374	sp.) before counting the number of formed CFUs. For the in vivo tests C. floridanus ants from
375	five (Asaia sp.), four (E. coli) or from six colonies (S. marcescens) were starved as before and
376	then individually given access to 5µl of bacteria contaminated 10% honey water (Asaia sp.
377	and E. coli: $1 * 10^7$ CFU/ml, S. marcescens: $1 * 10^6$ CFU/ml) for 2 min. To assess the number
378	of CFUs in the digestive tract, i.e. the crop and the midgut, ants were dissected either directly
379	after feeding (0h; <i>S. marcescens</i> : n = 60 workers; <i>Asaia</i> sp. and <i>E. coli</i> : n = 15 each), 0.5h (<i>S.</i>
380	<i>marcescens</i> : $n = 60$; <i>Asaia</i> sp. and <i>E. coli</i> : $n = 15$ each), 4h (<i>S. marcescens</i> : $n = 60$; <i>Asaia</i> sp.
381	and <i>E. coli</i> : $n = 15$ each), 24h (<i>S. marcescens</i> : $n = 53$; <i>Asaia</i> sp. and <i>E. coli</i> : $n = 15$ each) or
382	48h (S. marcescens: n = 19; Asaia sp. and E. coli: n = 15 each) after feeding. These timepoints
383	were chosen according to literature describing peak passage of food from the crop to the
384	midgut within 20h after food consumption in ants (Gösswald and Kloft, 1960, Howard and
385	Tschinkel, 1981). For dissection, ants were cold anesthetized, the gaster opened and the whole
386	gut detached. The crop and the midgut were then separated from the digestive tract, placed in
387	a reaction tube, mechanically crushed with a sterile pestle and dissolved in 100µl (Asaia sp.
388	and E. coli) or 150µl (S. marcescens) phosphate buffered saline (PBS-buffer: 8.74g NaCl,
389	1.78g Na ₂ HPO ₄ ,2H ₂ O in 1L MilliQ-water adjusted to a pH of 6.5). The resulting solutions
390	were then thoroughly mixed, 100µl streaked on agar-medium (LB-medium and GLY-medium

for *S. marcescens/E.coli* and *Asaia* sp., respectively) and incubated at 30°C for 24h (*S. marcescens* and *E. coli*) or 48h (*Asaia* sp.), before counting the number of formed CFUs. No
other bacteria (e.g. resident microbes) were growing on the agar plates which agrees with the
very low number of cultivable resident bacteria present in the midgut of *C. floridanus* (Stoll
and Gross, unpublished results).

Statistical analyses. All statistical analyses were performed with the R statistical 396 397 programming language (version 3.6.1, R Core Team, 2019). All (zero-inflated) General(ized) linear and mixed models and Cox mixed-effects models were compared to null (intercept 398 only) or reduced models (for those with multiple predictors) using Likelihood Ratio (LR) tests 399 400 to assess the significance of predictors. Pairwise comparisons between factor levels of a significant predictor were performed using pairwise post-hoc tests adjusting the family-wise 401 error rate according to the method of Westfall (package "multcomp", Bretz et al., 2011). We 402 checked necessary model assumptions of (zero-inflated) General(ised) linear and mixed 403 404 models using model diagnostic tests and plots implemented in the package "DHARMa" 405 (Hartig, 2019). Acidification of the crop lumen (log transformed pH to normalize data) and 406 midgut lumen in C. floridanus was analyzed using linear mixed models (LMM, package "lme4", Bates et al., 2015) including time since feeding (four levels: 0+4h, 0+24h, 0+48h, 407 408 48h+4h; Fig. 1a), ant manipulation (two levels: FA+ and FA-, i.e. ants with and without acidopore access; Fig. 1b) or digestive tract part (four levels: crop, midgut position 1, midgut 409 position 2, midgut position 3, midgut position 4; Fig.1 – supplementary figure 1) as predictors 410 411 and natal colony as a random effect. Due to non-normality and heteroscedasticity, the acidification of crop lumen in the seven formicine ant species other than C. floridanus (Fig. 412 413 1c) was analysed using per species Wilcoxon Rank Sum tests with ant manipulation (FA+ and FA-) as predictor. The frequency of acidopore grooming in C. floridanus upon feeding 414 different types of fluids was analyzed using Generalized linear mixed models (GLMM, 415

package "lme4", Bates et al., 2015) with negative binomial errors and type of fluid (three
levels: unfed, water-fed or 10% honey water fed) as predictor and natal colony as random
effect (Fig. 1 – supplementary figure 2).

419 Survival data were analysed with Cox mixed effects models (COXME, package "coxme", Therneau, 2019). For the survival of individual ants (Fig. 2a), ant treatment (four levels: 420 Serratia- | FA-, Serratia- | FA+, Serratia+ | FA-, Serratia+ | FA+) was added as a predictor 421 422 and the three "blocks", in which the experiment was run and the colony, ants originated from, were included as two random intercept effects. For the survival of donor-receiver ant pairs 423 (Fig. 2b), ant treatment (four levels: donor FA+, donor FA-, receiver FA+, receiver FA-) was 424 425 included as a predictor and the three "blocks", in which the experiment was run, the colony, ants originated from, and petri dish, in which donor and receiver ants were paired, were 426 included as three random intercept effects. Survival of receiver ants was right censored if the 427 corresponding donor ant died at the next feeding bout (right censoring of both donor and 428 429 receiver ants in one pair upon death of one of the ants yielded statistically the same result: COXME, overall LR χ^2 = 60.202, df = 3, P < 0.001; post-hoc comparisons: receiver FA- vs 430 431 donor FA-: P = 0.388, all other comparisons: P < 0.001). The duration of trophallaxis events (square-root transformed to normalize data) between donor-receiver ant pairs was analysed 432 using a linear mixed model with ant pair type (two levels: donor FA+ | receiver FA- and 433 donor FA- | receiver FA-) as predictor and the three "blocks", in which the experiment was 434 run and the colony ants originated from as random effect (Fig. 2 - supplementary figure 1). 435 436 Bacterial growth in vitro was analysed separately for Asaia sp. and S. marcescens using Generalized linear models (GLM) with negative binomial errors and pH as predictor, 437 excluding pH levels with zero bacterial growth due to complete data separation (Fig. 3 -438 supplementary figure 1). Relative values shown in Fig. 3 -supplementary figure 1 were 439 calculated by dividing single CFU numbers through the mean of CFU numbers at pH 5. 440

Bacterial growth in vivo within the digestive tract of C. floridanus over time was analysed 441 442 separately for the crop and midgut for both Asaia sp. and S. marcescens (Fig. 3) and for E. coli (Fig. 3 – figure supplement 2). Zero-inflated generalized linear mixed models with 443 negative binomial errors (package "glmmTMB", Brooks et al., 2017) were used to model 444 CFU number, with time after feeding as fixed predictor and ant colony as random effect, 445 except for *E. coli* growth in the crop were colony was included as fixed factor as the model 446 447 did not converge with colony as a random factor. Time points with zero bacterial growth were again excluded from the model. Relative values shown in Fig. 3 and Fig. 3 – supplementary 448 figure 2 and reported in the main text were calculated by dividing single CFU numbers 449 450 through the mean of CFU numbers at timepoint 0h in the crop.

452 Acknowledgements

453	We would like to	thank Robert Paxton	for English grammar	and style check of a pre-
-55	we would like to	mank Robert I anton	for English Stamma	and style encert of a pre

- 454 submission version of the manuscript, Franziska Vogel and Marvin Gilliar for part of the data
- 455 collection, Elena Crotti and Daniele Daffonchio for providing the Asaia strain and Martin
- 456 Kaltenpoth for access to the pH microelectrode.

457

458 Author contributions

- 459 S.T. and H.F. conceived the experiments. S.T. and M.A.M. performed the survival assays and
- the behavioral observations. C. H., C. T., R. B. and J. H. measured crop lumen acidification.
- 461 H. F. measured pH in the midgut. M. H. and C. H. performed *in vivo* bacterial growth
- 462 measurements. C. T. performed the *in vitro* bacterial growth measurements. S.T. analyzed the
- data and prepared the manuscript. S.T., C.H., J.H., R.B., C.T., M.H., M.A.M., R.G. and H.F.
- 464 edited the manuscript.

465

466 **Competing interests**

467 The authors declare no competing interests.

468

469 Data and code availability

470 The authors declare that all data supporting the findings of this study and that all code

471 required to reproduce the analyses and figures of this study are available within the article and

its supplementary information and will be made publicly available at a digital repository upon

473 acceptance.

474 **References**

- ALEXANDER, R. D. 1974. The evolution of social behavior. *Annual Review of Ecology and Systematics*, 5, 325-383.
- ANDERSON, K. E., RUSSELL, J. A., MOREAU, C. S., KAUTZ, S., SULLAM, K. E., HU,
 Y., BASINGER, U., MOTT, B. M., BUCK, N. & WHEELER, D. E. 2012. Highly
 similar microbial communities are shared among related and trophically similar ant
 species. *Molecular Ecology*, 21, 2282-2296.
- 481 ARCHETTI, M., SCHEURING, I., HOFFMAN, M., FREDERICKSON, M. E., PIERCE, N.
 482 E. & YU, D. W. 2011a. Economic game theory for mutualism and cooperation.
 483 *Ecology Letters*, 14, 1300-12.
- 484 ARCHETTI, M., UBEDA, F., FUDENBERG, D., GREEN, J., PIERCE, N. E. & YU, D. W.
 485 2011b. Let the right one in: a microeconomic approach to partner choice in 486 mutualisms. *American Naturalist*, 177, 75-85.
- 487 BASIBUYUK, H. H. & QUICKE, D. L. J. 1999. Grooming behaviours in the Hymenoptera
 488 (Insecta): Potential phylogenetic significance. *Zoological Journal of the Linnean*489 Society, 125, 349-382.
- BATES, D., MAECHLER, M., BOLKER, B. & WALKER, S. 2015. Fitting Linear mixedeffects models using lme4. *Journal of Statistical Software*, 67, 1-48.
- BEASLEY, D. E., KOLTZ, A. M., LAMBERT, J. E., FIERER, N. & DUNN, R. R. 2015. The
 evolution of stomach acidity and its relevance to the human microbiome. *PloS One*,
 10, e0134116.
- BHATKAR, A. & WHITCOMB, W. H. 1971. Artificial diet for rearing various species of
 ants. *Florida Entomologist*, 53, 229-232.
- BIEDERMANN, P. H. & KALTENPOTH, M. 2014. New synthesis: the chemistry of partner
 choice in insect-microbe mutualisms. *Journal of Chemical Ecology*, 40, 99.
- BLOUNT, Z. D. 2015. The unexhausted potential of *E. coli. eLife*, 4.
- BLUM, J. E., FISCHER, C. N., MILES, J. & HANDELSMAN, J. 2013. Frequent
 replenishment sustains the beneficial microbiome of *Drosophila melanogaster. mBio*,
 4, e00860-13.
- BOOMSMA, J. J., SCHMID-HEMPEL, P. & HUGHES, W. O. H. 2005. Life histories and
 parasite pressure across the major groups of social insects. *In:* FELLOWES, M. H. G.
 & ROLFF, J. (eds.) *Insect Evolutionary Ecology*. Oxon, UK: CABI.
- BRETZ, F., HOTHORN, T. & WESTFALL, P. 2011. *Multiple Comparisons using R.*, Boca
 Raton, FL, CRC Press.
- 508 BRODERICK, N. A. & LEMAITRE, B. 2012. Gut-associated microbes of *Drosophila* 509 *melanogaster*. *Gut Microbes*, 3, 307-21.
- BROOKS, M. E., KRISTENSEN, K., VAN BENTHEM, K. J., MAGNUSSON, A., BERG,
 C. W., NIELSEN, A., SKAUG, H. J., MAECHLER, M. & BOLKER, B. M. 2017.
 glmmTMB balances speed and flexibility among packages for zero-inflated
 generalized linear mixed modeling. *The R Journal*, 9, 378-400.
- 514 BROWN, B. P. & WERNEGREEN, J. J. 2016. Deep divergence and rapid evolutionary rates 515 in gut-associated Acetobacteraceae of ants. *BMC Microbiology*, 16.
- 516 BROWN, B. P. & WERNEGREEN, J. J. 2019. Genomic erosion and extensive horizontal
 517 gene transfer in gut-associated Acetobacteraceae. *BMC Genomics*, 20.
- BRUNE, A. & DIETRICH, C. 2015. The gut microbiota of termites: Digesting the diversity
 in the light of ecology and evolution. *Annual Review of Microbiology*, 69, 145-166.
- BRÜTSCH, T., JAFFUEL, G., VALLAT, A., TURLINGS, T. C. & CHAPUISAT, M. 2017.
 Wood ants produce a potent antimicrobial agent by applying formic acid on treecollected resin. *Ecology and Evolution*, 7, 2249-2254.

BURKEPILE, D. E., PARKER, J. D., WOODSON, C. B., MILLS, H. J., KUBANEK, J., 523 524 SOBECKY, P. A. & HAY, M. E. 2006. Chemically mediated competition between microbes and animals: Microbes as consumers in food webs. *Ecology*, 87, 2821-2831. 525 CARDOZA, Y. J., KLEPZIG, K. D. & RAFFA, K. F. 2006. Bacteria in oral secretions of an 526 527 endophytic insect inhibit antagonistic fungi. Ecological Entomology, 31, 636-645. CASEWELL, N. R., WUSTER, W., VONK, F. J., HARRISON, R. A. & FRY, B. G. 2013. 528 Complex cocktails: The evolutionary novelty of venoms. Trends in Ecology & 529 Evolution, 28, 219-229. 530 531 CHAPMAN, R. F. 2013. The insects: Structure and function., Cambridge, United Kingdom, Cambridge University Press. 532 CHU, H. & MAZMANIAN, S. K. 2013. Innate immune recognition of the microbiota 533 promotes host-microbial symbiosis. Nature Immunology, 14, 668-75. 534 CHUA, K. O., SONG, S. L., YONG, H. S., SEE-TOO, W. S., YIN, W. F. & CHAN, K. G. 535 536 2018. Microbial community composition reveals spatial variation and distinctive core microbiome of the weaver ant Oecophylla smaragdina in Malaysia. Scientific Reports, 537 538 8, 10777. COOLING, M. D., HOFFMANN, B. D., GRUBER, M. A. M. & LESTER, P. J. 2018. 539 540 Indirect evidence of pathogen-associated altered oocyte production in queens of the 541 invasive yellow crazy ant, Anoplolepis gracilipes, in Arnhem Land, Australia. Bulletin of Entomological Research, 108, 451-460. 542 543 CREMER, S., ARMITAGE, S. A. & SCHMID-HEMPEL, P. 2007. Social immunity. Current 544 Biology, 17, R693-702. CROTTI, E., DAMIANI, C., PAJORO, M., GONELLA, E., RIZZI, A., RICCI, I., NEGRI, I., 545 SCUPPA, P., ROSSI, P., BALLARINI, P., RADDADI, N., MARZORATI, M., 546 547 SACCHI, L., CLEMENTI, E., GENCHI, M., MANDRIOLI, M., BANDI, C., FAVIA, G., ALMA, A. & DAFFONCHIO, D. 2009. Asaia, a versatile acetic acid bacterial 548 549 symbiont, capable of cross-colonizing insects of phylogenetically distant genera and orders. Environmental Microbiology, 11, 3252-3264. 550 CURRIE, C. R., SCOTT, J. A., SUMMERBELL, R. C. & MALLOCH, D. 1999. Fungus-551 growing ants use antibiotic-producing bacteria to control garden parasites. Nature, 552 553 398, 701-704. 554 DAVID, L. A., MAURICE, C. F., CARMODY, R. N., GOOTENBERG, D. B., BUTTON, J. E., WOLFE, B. E., LING, A. V., DEVLIN, A. S., VARMA, Y., FISCHBACH, M. A., 555 BIDDINGER, S. B., DUTTON, R. J. & TURNBAUGH, P. J. 2014. Diet rapidly and 556 557 reproducibly alters the human gut microbiome. Nature, 505, 559-63. 558 DEGNAN, P. H., LAZARUS, A. B., BROCK, C. D. & WERNEGREEN, J. J. 2004. Hostsymbiont stability and fast evolutionary rates in an ant-bacterium association: 559 560 cospeciation of *Camponotus* species and their endosymbionts, *candidatus* Blochmannia. Systematic Biology, 53, 95-110. 561 DEMAIN, A. L. & FANG, A. 2000. The Natural Functions of Secondary Metabolites. In: 562 563 FIECHTER, A. (ed.) History of Modern Biotechnology I. Berlin, Heidelberg: Springer Berlin Heidelberg. 564 EISNER, T. & HAPP, G. M. 1962. The infrabuccal pocket of a formicine ant: a social 565 566 filtration device. Psyche, 69, 107-116. EISNER, T. & WILSON, E. O. 1952. The morphology of the porventriculus of a formicine 567 ant. Psyche, 59, 47-60. 568 ENGEL, P. & MORAN, N. A. 2013. The gut microbiota of insects - diversity in structure and 569 570 function. FEMS Microbiology Reviews, 37, 699-735. FARISH, D. J. 1972. The evolutionary implications of qualitative variation in the grooming 571 behaviour of the Hymenoptera (Insecta). Animal Behaviour, 20, 662-76. 572

573	FAVIA, G., RICCI, I., DAMIANI, C., RADDADI, N., CROTTI, E., MARZORATI, M.,
574	RIZZI, A., URSO, R., BRUSETTI, L., BORIN, S., MORA, D., SCUPPA, P.,

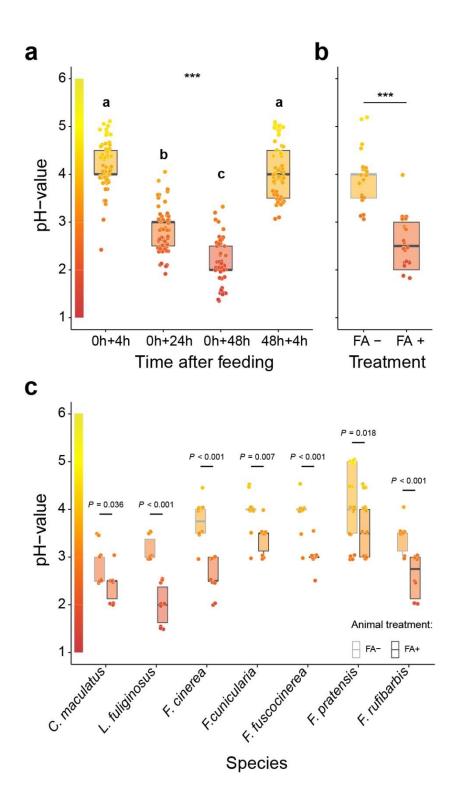
- 575 PASQUALINI, L., CLEMENTI, E., GENCHI, M., CORONA, S., NEGRI, I.,
- GRANDI, G., ALMA, A., KRAMER, L., ESPOSITO, F., BANDI, C., SACCHI, L. &
 DAFFONCHIO, D. 2007. Bacteria of the genus *Asaia* stably associate with *Anopheles stephensi*, an Asian malarial mosquito vector. *Proceedings of the National Academy of Sciences of the United States of America*, 104, 9047-9051.
- FELDHAAR, H., STRAKA, J., KRISCHKE, M., BERTHOLD, K., STOLL, S., MUELLER,
 M. J. & GROSS, R. 2007. Nutritional upgrading for omnivorous carpenter ants by the
 endosymbiont *Blochmannia*. *BMC Biology*, 5, 48.
- FERNÁNDEZ-MARÍN, H., NASH, D. R., HIGGINBOTHAM, S., ESTRADA, C., VAN
 ZWEDEN, J. S., D'ETTORRE, P., WCISLO, W. T. & BOOMSMA, J. J. 2015.
 Functional role of phenylacetic acid from metapleural gland secretions in controlling
 fungal pathogens in evolutionarily derived leaf-cutting ants. *Proceedings of the Royal Society of London. Series B, Biological Sciences*, 282, 20150212.
- FLOREZ, L. V., BIEDERMANN, P. H. W., ENGL, T. & KALTENPOTH, M. 2015.
 Defensive symbioses of animals with prokaryotic and eukaryotic microorganisms.
 Natural Product Reports, 32, 904-936.
- FLYG, C., KENNE, K. & BOMAN, H. G. 1980. Insect pathogenic properties of *Serratia marcescens*: Phage-resistant mutants with a decreased resistance to *Cecropia* immunity and a decreased virulence to *Drosophila*. *Journal of General Microbiology*,
 120, 173-181.
- FOSTER, K. R., SCHLUTER, J., COYTE, K. Z. & RAKOFF-NAHOUM, S. 2017. The
 evolution of the host microbiome as an ecosystem on a leash. *Nature*, 548, 43-51.
- GERNAT, T., RAO, V. D., MIDDENDORF, M., DANKOWICZ, H., GOLDENFELD, N. &
 ROBINSON, G. E. 2018. Automated monitoring of behavior reveals bursty interaction
 patterns and rapid spreading dynamics in honeybee social networks. *Proceedings of the National Academy of Sciences of the United States of America*, 115, 1433-1438.
- GIANNELLA, R. A., ZAMCHECK, N. & BROITMAN, S. A. 1972. Gastric-acid barrier to
 ingested microorganisms in man studies in-vivo and in-vitro. Gut, 13, 251-256.
- GÖSSWALD, K. & KLOFT, W. 1960. Untersuchungen mit radioaktiven Isotopen an
 Waldameisen. *Entomophaga*, 5, 33-41.
- 605 GREENWALD, E. E., BALTIANSKY, L. & FEINERMAN, O. 2018. Individual crop loads
 606 provide local control for collective food intake in ant colonies. *eLife*, 7, e31730.
- 607 GRIMONT, F. & GRIMONT, P. A. D. 2006. The genus Serratia. In: DWORKIN, M.,
 608 FALKOW, S., ROSENBERG, E., SCHLEIFER, K.-H. & STACKEBRANDT, E.
 609 (eds.) The Prokaryotes: Volume 6: Proteobacteria: Gamma Subclass. New York, NY:
 610 Springer New York.
- HAMILTON, C., LEJEUNE, B. T. & ROSENGAUS, R. B. 2011. Trophallaxis and
 prophylaxis: social immunity in the carpenter ant *Camponotus pennsylvanicus*. *Biology Letters*, 7, 89-92.
- HAMMER, T. J., JANZEN, D. H., HALLWACHS, W., JAFFE, S. P. & FIERER, N. 2017.
 Caterpillars lack a resident gut microbiome. *Proc Natl Acad Sci U S A*, 114, 96419646.
- HARTIG, F. 2019. DHARMa: Residual diagnostics for hierarchical (multi-level/mixed)
 regression models. R package version 0.2.4. *https://CRAN.R- project.org/package=DHARMa*.
- HE, H., CHEN, Y. Y., ZHANG, Y. L. & WEI, C. 2011. Bacteria associated with gut lumen of
 Camponotus japonicus Mayr. *Environmental Entomology*, 40, 1405-1409.
- HERTLE, R. 2005. The family of *Serratia* type pore forming toxins. *Current Protein and Peptide Science*, 6, 313-325.

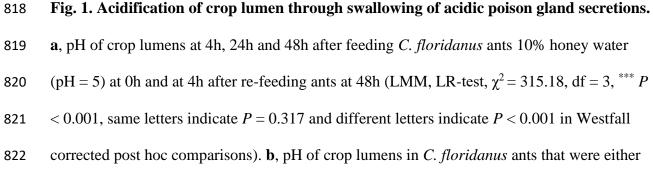
624	HERZNER, G., SCHLECHT, A., DOLLHOFER, V., PARZEFALL, C., HARRAR, K.,
625	KREUZER, A., PILSL, L. & RUTHER, J. 2013. Larvae of the parasitoid wasp
626	Ampulex compressa sanitize their host, the American cockroach, with a blend of
627	antimicrobials. Proceedings of the National Academy of Sciences of the United States
628	of America, 110, 1369-1374.
629	HERZNER, G. & STROHM, E. 2007. Fighting fungi with physics: food wrapping by a
630	solitary wasp prevents water condensation. Current Biology, 17, R46-7.
631	HOLTOF, M., LENAERTS, C., CULLEN, D. & VANDEN BROECK, J. 2019. Extracellular
632	nutrient digestion and absorption in the insect gut. <i>Cell and Tissue Research</i> , 377,
633	397-414.
634	HOWARD, D. F. & TSCHINKEL, W. R. 1981. The flow of food in colonies of the fire ant,
635	Solenopsis invicta: a multifactorial study. Physiological Entomology, 6, 297-306.
636	HOWDEN, C. W. & HUNT, R. H. 1987. Relationship between gastric-secretion and
637	infection. <i>Gut</i> , 28, 96-107.
638	IMHANN, F., BONDER, M. J., VICH VILA, A., FU, J., MUJAGIC, Z., VORK, L.,
639	TIGCHELAAR, E. F., JANKIPERSADSING, S. A., CENIT, M. C., HARMSEN, H.
640	J., DIJKSTRA, G., FRANKE, L., XAVIER, R. J., JONKERS, D., WIJMENGA, C.,
641	WEERSMA, R. K. & ZHERNAKOVA, A. 2016. Proton pump inhibitors affect the
641 642	
	gut microbiome. Gut, 65, 740-8.
643	INAGAKI, T. & MATSUURA, K. 2018. Extended mutualism between termites and gut
644	microbes: Nutritional symbionts contribute to nest hygiene. <i>The Science of Nature</i> ,
645	105, 52.
646	INNOCENT, T., HOLMES, N., AL BASSAM, M., SCHIØTT, M., SCHEURING, I.,
647	WILKINSON, B., HUTCHINGS, M. I., BOOMSMA, J. J. & YU, D. W. 2018.
648	Experimental demonstration that screening can enable the environmental recruitment
649	of a defensive microbiome. <i>bioRxiv</i> .
650	ITOH, H., JANG, S., TAKESHITA, K., OHBAYASHI, T., OHNISHI, N., MENG, X. Y.,
651	MITANI, Y. & KIKUCHI, Y. 2019. Host-symbiont specificity determined by
652	microbe-microbe competition in an insect gut. Proceedings of the National Academy
653	of Sciences of the United States of America, 116, 22673-22682.
654	IVENS, A. B. F., GADAU, A., KIERS, E. T. & KRONAUER, D. J. C. 2018. Can social
655	partnerships influence the microbiome? Insights from ant farmers and their
656	trophobiont mutualists. <i>Molecular Ecology</i> , 27, 1898-1914.
657	JANZEN, D. H. 1977. Why fruits rot, seeds mold, and meat spoils. American Naturalist, 111,
658	691-713.
659	JOOP, G., ROTH, O., SCHMID-HEMPEL, P. & KURTZ, J. 2014. Experimental evolution of
660	external immune defences in the red flour beetle. Journal of Evolutionary Biology, 27,
661	1562-1571.
662	KAPPELER, P. M., CREMER, S. & NUNN, C. L. 2015. Sociality and health: impacts of
663	sociality on disease susceptibility and transmission in animal and human societies.
664	Philosophical Transactions of the Royal Society of London. Series B, Biological
665	Sciences, 370, 20140116.
666	KAUTZ, S., RUBIN, B. E. R. & MOREAU, C. S. 2013a. Bacterial infections across the ants:
667	Frequency and prevalence of Wolbachia, Spiroplasma, and Asaia. Psyche, e936341.
668	KAUTZ, S., RUBIN, B. E. R., RUSSELL, J. A. & MOREAU, C. S. 2013b. Surveying the
669	microbiome of ants: Comparing 454 pyrosequencing with traditional methods to
670	uncover bacterial diversity. Applied and Environmental Microbiology, 79, 525-534.
671	KOELZ, H. R. 1992. Gastric-acid in vertebrates. Scandinavian Journal of Gastroenterology,
672	27, 2-6.
673	KOMAGATA, K., IINO, T. & YAMADA, Y. 2014. The family Acetobacteraceae. In:
674	ROSENBERG, E., DELONG, E. F., LORY, S., STACKEBRANDT, E. &

675	THOMPSON, F. (eds.) The Prokaryotes: Alphaproteobacteria and
676	Betaproteobacteria. Berlin, Heidelberg: Springer Berlin Heidelberg.
677	KWONG, W. K., MEDINA, L. A., KOCH, H., SING, K. W., SOH, E. J. Y., ASCHER, J. S.,
678	JAFFE, R. & MORAN, N. A. 2017. Dynamic microbiome evolution in social bees.
679	Science Advances, 3.
680	LANAN, M. C., RODRIGUES, P. A. P., AGELLON, A., JANSMA, P. & WHEELER, D. E.
681	2016. A bacterial filter protects and structures the gut microbiome of an insect. The
682	ISME Journal, 10, 1866-1876.
683	LEBOEUF, A. C., WARIDEL, P., BRENT, C. S., GONCALVES, A. N., MENIN, L.,
684	ORTIZ, D., RIBA-GROGNUZ, O., KOTO, A., SOARES, Z. G., PRIVMAN, E.,
685	MISKA, E. A., BENTON, R. & KELLER, L. 2016. Oral transfer of chemical cues,
686	growth proteins and hormones in social insects. <i>eLife</i> , 5, e20375.
687	MAMLOUK, D. & GULLO, M. 2013. Acetic acid bacteria: Physiology and carbon sources
688	oxidation. Indian Journal of Microbiology, 53, 377-384.
689	MARTINSEN, T. C., BERGH, K. & WALDUM, H. L. 2005. Gastric juice: A barrier against
690	infectious diseases. Basic & Clinical Pharmacology & Toxicology, 96, 94-102.
691	MAZEL, F., DAVIS, K. M., LOUDON, A., KWONG, W. K., GROUSSIN, M. & PARFREY,
692	L. W. 2018. Is host filtering the main driver of phylosymbiosis across the tree of life?
693	mSystems, 3.
694	MCFALL-NGAI, M., HADFIELD, M. G., BOSCH, T. C., CAREY, H. V., DOMAZET-
695	LOSO, T., DOUGLAS, A. E., DUBILIER, N., EBERL, G., FUKAMI, T., GILBERT,
696	S. F., HENTSCHEL, U., KING, N., KJELLEBERG, S., KNOLL, A. H., KREMER,
697	N., MAZMANIAN, S. K., METCALF, J. L., NEALSON, K., PIERCE, N. E.,
698	RAWLS, J. F., REID, A., RUBY, E. G., RUMPHO, M., SANDERS, J. G., TAUTZ,
699	D. & WERNEGREEN, J. J. 2013. Animals in a bacterial world, a new imperative for
700	the life sciences. Proceedings of the National Academy of Sciences of the United
701	<i>States of America</i> , 110, 3229-36.
702	MILAN, N. F., KACSOH, B. Z. & SCHLENKE, T. A. 2012. Alcohol consumption as self-
703	medication against blood-borne parasites in the fruit fly. Current Biology, 22, 488-
704	493.
705	MIRABITO, D. & ROSENGAUS, R. B. 2016. A double-edged sword? The cost of
706	proctodeal trophallaxis in termites. Insectes Sociaux, 63, 135-141.
707	MOELLER, A. H., CARO-QUINTERO, A., MJUNGU, D., GEORGIEV, A. V.,
708	LONSDORF, E. V., MULLER, M. N., PUSEY, A. E., PEETERS, M., HAHN, B. H.
709	& OCHMAN, H. 2016. Cospeciation of gut microbiota with hominids. Science, 353,
710	380-382.
711	MORAN, N. A., OCHMAN, H. & HAMMER, T. J. 2019. Evolutionary and Ecological
712	Consequences of Gut Microbial Communities. Annual Review of Ecology, Evolution,
713	and Systematics, 50, 451-+.
714	MUELLER, U. G., GERARDO, N. M., AANEN, D. K., SIX, D. L. & SCHULTZ, T. R.
715	2005. The evolution of agriculture in insects. Annual Review of Ecology Evolution and
716	Systematics, 36, 563-595.
717	MUSHEGIAN, A. A. & EBERT, D. 2016. Rethinking "mutualism" in diverse host-symbiont
718	communities. <i>Bioessays</i> , 38, 100-108.
719	NEHME, N. T., LIEGEOIS, S., KELE, B., GIAMMARINARO, P., PRADEL, E.,
720	HOFFMANN, J. A., EWBANK, J. J. & FERRANDON, D. 2007. A model of bacterial
721	intestinal infections in <i>Drosophila melanogaster</i> . <i>PLoS Pathogens</i> , 3, 1694-1709.
722	OCHMAN, H., WOROBEY, M., KUO, C. H., NDJANGO, J. B. N., PEETERS, M., HAHN,
723	B. H. & HUGENHOLTZ, P. 2010. Evolutionary relationships of wild hominids
724	recapitulated by gut microbial communities. <i>PloS Biology</i> , 8.

725	OHBAYASHI, T., TAKESHITA, K., KITAGAWA, W., NIKOH, N., KOGA, R., MENG, X.
726	Y., TAGO, K., HORI, T., HAYATSU, M., ASANO, K., KAMAGATA, Y., LEE, B.
727	L., FUKATSU, T. & KIKUCHI, Y. 2015. Insect's intestinal organ for symbiont
728	sorting. Proceedings of the National Academy of Sciences of the United States of
729	America, 112, E5179-E5188.
730	ONCHURU, T. O., MARTINEZ, A. J., INGHAM, C. S. & KALTENPOTH, M. 2018.
731	Transmission of mutualistic bacteria in social and gregarious insects. Current Opinion
732	in Insect Science, 28, 50-58.
733	OTTI, O., TRAGUST, S. & FELDHAAR, H. 2014. Unifying external and internal immune
734	defences. Trends in Ecology & Evolution, 29, 625-634.
735	OVEREND, G., LUO, Y., HENDERSON, L., DOUGLAS, A. E., DAVIES, S. A. & DOW, J.
736	A. 2016. Molecular mechanism and functional significance of acid generation in the
737	Drosophila midgut. Scientific Reports, 6, 27242.
738	PALMER-YOUNG, E. C., RAFFEL, T. R. & MCFREDERICK, Q. S. 2018. pH-mediated
739	inhibition of a bumble bee parasite by an intestinal symbiont. <i>Parasitology</i> , 146, 380-
740	388.
741	PEREZ-COBAS, A. E., MAIQUES, E., ANGELOVA, A., CARRASCO, P., MOYA, A. &
742	LATORRE, A. 2015. Diet shapes the gut microbiota of the omnivorous cockroach
743	Blattella germanica. FEMS Microbiology Ecology, 91.
744	PULL, C. D., UGELVIG, L. V., WIESENHOFER, F., GRASSE, A. V., TRAGUST, S.,
745	SCHMITT, T., BROWN, M. J. & CREMER, S. 2018. Destructive disinfection of
746	infected brood prevents systemic disease spread in ant colonies. <i>eLife</i> , 7.
747	RAKOFF-NAHOUM, S., PAGLINO, J., ESLAMI-VARZANEH, F., EDBERG, S. &
748	MEDZHITOV, R. 2004. Recognition of commensal microflora by toll-like receptors
749	is required for intestinal homeostasis. <i>Cell</i> , 118, 229-41.
750	RANGER, C. M., BIEDERMANN, P. H. W., PHUNTUMART, V., BELIGALA, G. U.,
751	GHOSH, S., PALMQUIST, D. E., MUELLER, R., BARNETT, J., SCHULTZ, P. B.,
752	REDING, M. E. & BENZ, J. P. 2018. Symbiont selection via alcohol benefits fungus
753	farming by ambrosia beetles. <i>Proceedings of the National Academy of Sciences of the</i>
754	United States of America, 115, 4447-4452.
755	RATZKA, C., LIANG, C., DANDEKAR, T., GROSS, R. & FELDHAAR, H. 2011. Immune
756	response of the ant <i>Camponotus floridanus</i> against pathogens and its obligate
757	mutualistic endosymbiont. Insect Biochemistry and Molecular Biology, 41, 529-36.
758	RATZKE, C. & GORE, J. 2018. Modifying and reacting to the environmental pH can drive
759	bacterial interactions. <i>PloS Biology</i> , 16, e2004248.
760	R CORE TEAM 2019. R: A language and environment for statistical computing. Vienna,
761	Austria: R Foundation for Statistical Computing.
762	RUSSELL, J. A., SANDERS, J. G. & MOREAU, C. S. 2017. Hotspots for symbiosis:
763	function, evolution, and specificity of ant-microbe associations from trunk to tips of
764	the ant phylogeny (Hymenoptera: Formicidae). <i>Myrmecological News</i> , 24, 43-69.
765	SALEM, H., FLOREZ, L., GERARDO, N. & KALTENPOTH, M. 2015. An out-of-body
766	experience: the extracellular dimension for the transmission of mutualistic bacteria in
767	insects. Proceedings of the Royal Society B-Biological Sciences, 282, 20142957.
768	SCHEURING, I. & YU, D. W. 2012. How to assemble a beneficial microbiome in three easy
769	steps. <i>Ecology Letters</i> , 15, 1300-1307.
770	SCOTT, J. J., OH, D. C., YUCEER, M. C., KLEPZIG, K. D., CLARDY, J. & CURRIE, C. R.
771	2008. Bacterial protection of beetle-fungus mutualism. <i>Science</i> , 322, 63-63.
772	SHUKLA, S. P., PLATA, C., REICHELT, M., STEIGER, S., HECKEL, D. G.,
773	KALTENPOTH, M., VILCINSKAS, A. & VOGEL, H. 2018. Microbiome-assisted
774	carrion preservation aids larval development in a burying beetle. <i>Proceedings of the</i>
775	National Academy of Sciences of the United States of America, 115, 11274-11279.
	manonal frequency of sciences of the Onlieu States of America, 115, 112/4-112/9.

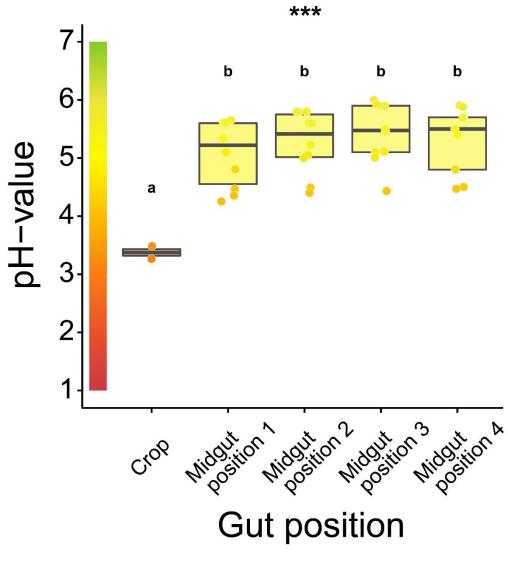
776	SLACK, E., HAPFELMEIER, S., STECHER, B., VELYKOREDKO, Y., STOEL, M.,
777	LAWSON, M. A., GEUKING, M. B., BEUTLER, B., TEDDER, T. F., HARDT, W.
778	D., BERCIK, P., VERDU, E. F., MCCOY, K. D. & MACPHERSON, A. J. 2009.
779	Innate and adaptive immunity cooperate flexibly to maintain host-microbiota
780	mutualism. Science, 325, 617-20.
781	STROEYMEYT, N., GRASSE, A. V., CRESPI, A., MERSCH, D. P., CREMER, S. &
782	KELLER, L. 2018. Social network plasticity decreases disease transmission in a
783	eusocial insect. Science, 362, 941-945.
784	TENNANT, S. M., HARTLAND, E. L., PHUMOONNA, T., LYRAS, D., ROOD, J. I.,
785	ROBINS-BROWNE, R. M. & VAN DRIEL, I. R. 2008. Influence of gastric acid on
786	susceptibility to infection with ingested bacterial pathogens. Infection and Immunity,
787	76, 639-645.
788	THERNEAU, T. 2019. coxme: Mixed Effects Cox Models. R package version 2.2-14.
789	http://CRAN.R-project.org/package=coxme.
790	TRAGUST, S. 2016. External immune defence in ant societies (Hymenoptera: Formicidae):
791	The role of antimicrobial venom and metapleural gland secretion. Myrmecological
792	News, 23, 119-128.
793	TRAGUST, S., MITTEREGGER, B., BARONE, V., KONRAD, M., UGELVIG, L. V. &
794	CREMER, S. 2013. Ants disinfect fungus-exposed brood by oral uptake and spread of
795	their poison. Current Biology, 23, 76-82.
796	TRIENENS, M., KELLER, N. P. & ROHLFS, M. 2010. Fruit, flies and filamentous fungi -
797	experimental analysis of animal-microbe competition using Drosophila melanogaster
798	and Aspergillus mould as a model system. Oikos, 119, 1765-1775.
799	VANDER WALL, S. B. 1990. Food hoarding in animals, Chicago, Illinois, USA, University
800	of Chicago Press.
801	VOGEL, H., SHUKLA, S. P., ENGL, T., WEISS, B., FISCHER, R., STEIGER, S.,
802	HECKEL, D. G., KALTENPOTH, M. & VILCINSKAS, A. 2017. The digestive and
803	defensive basis of carcass utilization by the burying beetle and its microbiota. <i>Nature</i>
804	Communications, 8, 15186.
805	WATNICK, P. I. & JUGDER, B. E. 2020. Microbial control of intestinal homeostasis via
806	enteroendocrine cell innate immune signaling. Trends in Microbiology, 28, 141-149.
807	WILLIAMS, L. E. & WERNEGREEN, J. J. 2015. Genome evolution in an ancient bacteria-
808	ant symbiosis: parallel gene loss among <i>Blochmannia</i> spanning the origin of the ant
809	tribe Camponotini. <i>PeerJ</i> , 3, e881.
810	XIAO, R., WANG, X., XIE, E., JI, T., LI, X., MUHAMMAD, A., YIN, X., HOU, Y. & SHI,
811	Z. 2019. An IMD-like pathway mediates the intestinal immunity to modulate the
812	homeostasis of gut microbiota in <i>Rhynchophorus ferrugineus</i> Olivier (Coleoptera:
813	Dryophthoridae). Developmental & Comparative Immunology, 97, 20-27.
814	YEK, S. H. & MUELLER, U. G. 2011. The metapleural gland of ants. <i>Biological Reviews of</i>
815	the Cambridge Philosophical Society, 86, 774-91.





prevented to ingest formic acid containing poison gland secretions (FA-) or not (FA+) for 24h after feeding (LMM, LR-test, $\chi^2 = 44.68$, df = 1, ****P* < 0.001). **c**, pH-value of crop lumens 24h after feeding in seven formicine ant species that were either prevented to ingest formic acid containing poison gland secretions (FA-) or not (FA+). Wilcoxon rank sum tests (twosided). Lines and shaded boxes show median and interquartile range; points show all data. Colours in shaded boxes and points correspond to universal indicator pH colours. Border of shaded boxes represents animal treatment (light grey: prevention of poison ingestion, FA-;

830 dark grey: poison ingestion not prevented, FA+).



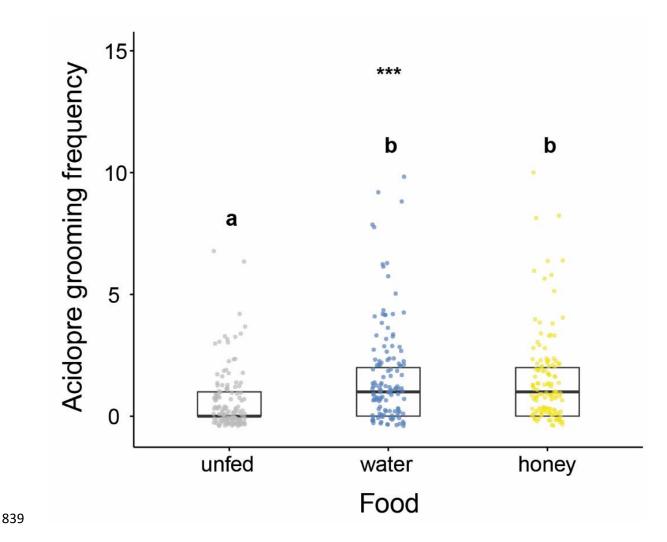
832

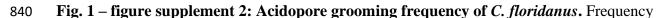
Fig. 1 – figure supplement 1: Acidification along the gastrointestinal tract of *C*.

834 *floridanus*. pH-measurements 24h after access to 10% honey-water in the crop (N = 2) and

directly after the proventriculus at four points along the midgut (N = 10 except position 4 with

- 836 N = 9) (LMM, LR-test, χ^2 =22.152, df=4, *** *P* <0.001, same letters indicate *P* ≥ 0.443 and
- 837 different letters indicate P < 0.001 in Westfall corrected post hoc comparisons).





of acidopore grooming within 30 min. after fluid ingestion (water or 10% honey water)

compared to ants that did not receive any fluid (unfed) (GLMM, LR-test, χ^2 =33.526, df=2, ***

843 P < 0.001, same letters indicate P = 0.634 and different letters indicate P < 0.001 in Westfall

844 corrected post hoc comparisons).

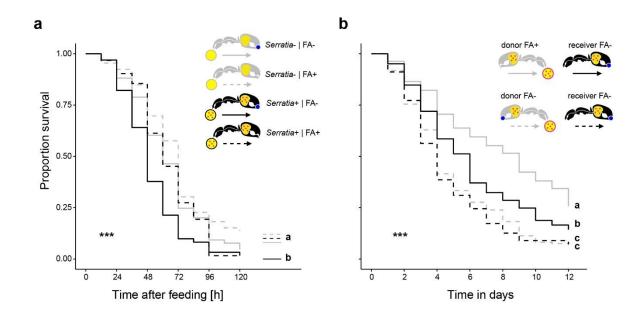


Fig. 2. Survival after ingestion of pathogen contaminated food. a, Survival of individual 847 ants that were either prevented to ingest formic acid containing poison gland secretions (FA-; 848 ant outlines with blue dot) or not (FA+) after feeding on either honey water contaminated 849 850 with Serratia marcescens (Serratia+, yellow circle with pink dots and black ant outlines) or non-contaminated honey water (*Serratia*-) (COXME, LR-test, $\gamma^2 = 20.95$, df=3, ***P = 0.0001, 851 same letters indicate $P \ge 0.061$ and different letters indicate $P \le 0.027$ in Westfall corrected 852 post hoc comparisons). **b**, Survival of donor ants (light grey ant outlines) that were directly 853 fed with pathogen contaminated food (yellow circle with pink dots in insert) and were either 854 prevented to ingest formic acid containing poison gland secretions (FA-; ant outlines with 855 blue dot) or not (FA+) and survival of receiver ants (black ant outlines) that received 856 pathogen contaminated food only through trophallaxis with donor ants and were always 857 858 prevented to ingest formic acid containing poison gland secretions (FA-) (COXME, LR-test, $\chi^2 = 66.68$, df = 3, *** P < 0.001, same letters indicate P = 0.309 and different letters indicate P 859 ≤ 0.002 in Westfall corrected post hoc comparisons). 860

861

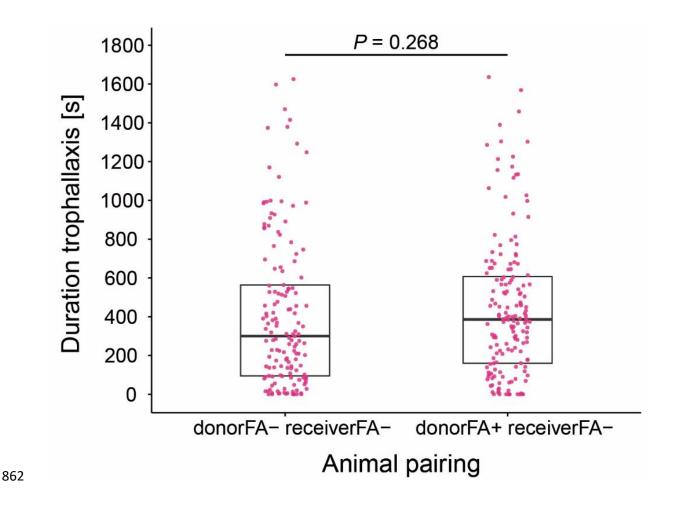


Fig. 2 – figure supplement 1: Duration of trophallaxis in donor-receiver ant pairs. Total 863 duration of trophallaxis events within 30 min. of the first bout of food exchange between 864 donor-receiver ant-pairs (LMM, LR-test, $\chi^2 = 1.23$, df = 1, P = 0.268). Donor ants in both 865 866 pairs were directly fed with Serratia marcescens contaminated 10% honey water and were either prevented to ingest formic acid containing poison gland secretions (FA-) or not (FA+), 867 while receiver ants received pathogen contaminated food only through trophallaxis with the 868 respective donor ants and were always prevented to ingest formic acid containing poison 869 gland secretions (FA-). 870

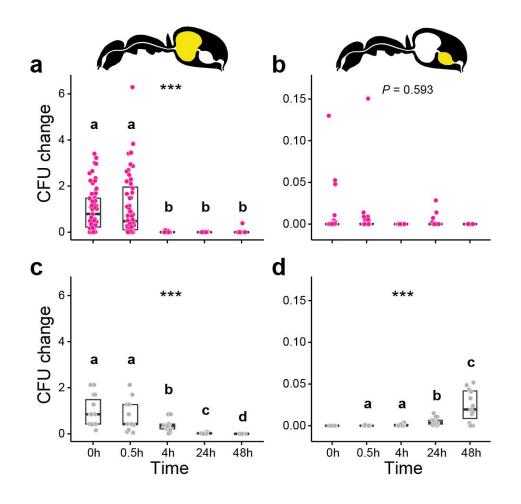




Fig. 3. Bacterial passage through the digestive tract of C. floridanus over time. Change in 873 the number of colony forming units (CFUs) in the crop (**a**,**c**) and midgut (**b**,**d**) part of the 874 digestive tract (vellow colour in insert) relative to 0h in the crop at 0h, 0.5h, 4h, 24h, and 48h 875 876 after feeding ants 10% honey water contaminated with Serratia marcescens (a,b) or Asaia sp. (c,d). a, Change of S. marcescens in the crop (GLMM, LR-test, $\chi^2 = 220.78$, df = 4, *** P 877 <0.001, same letters indicate $P \ge 0.623$ and different letters indicate P < 0.001 in Westfall 878 879 corrected post hoc comparisons). b, Change of S. marcescens in the midgut (GLMM, LR-test, $\chi^2 = 1.044$, df = 2, P = 0.593). **c**, Change of *Asaia* sp. in the crop (GLMM; LR-test, $\chi^2 =$ 880 124.01, df = 4, *** P < 0.001, same letters indicate P = 0.488 and different letters indicate $P \le$ 881 0.013 in Westfall corrected post hoc comparisons). d, Change of Asaia sp. in the midgut 882 (GLMM; LR-test, $\chi^2 = 59.94$, df = 3, ***P < 0.001, same letters indicate P = 0.116 and 883 different letters indicate $P \le 0.005$ in Westfall corrected post hoc comparisons). 884

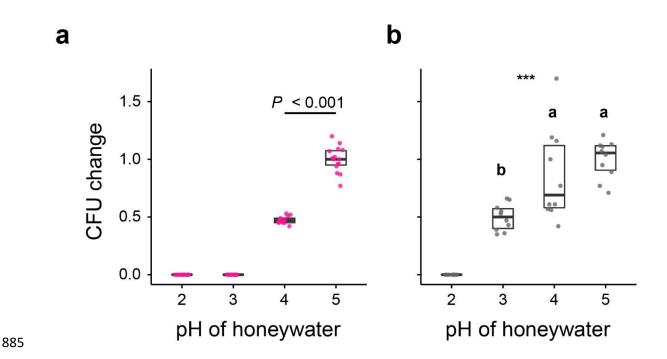
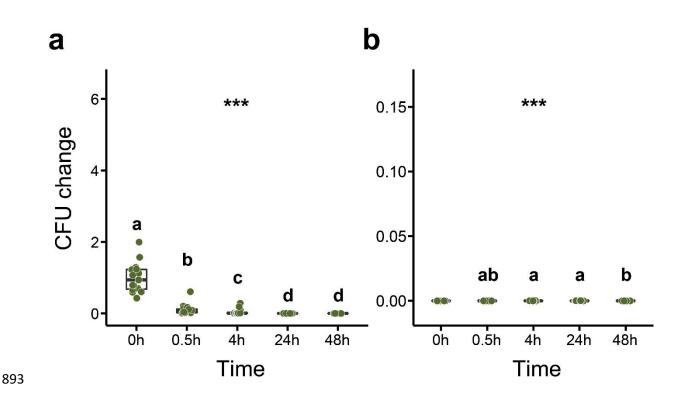
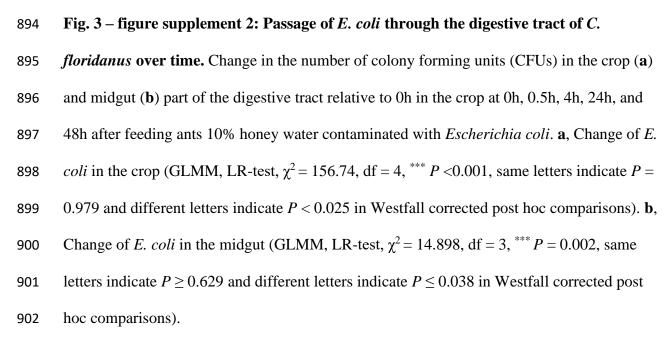


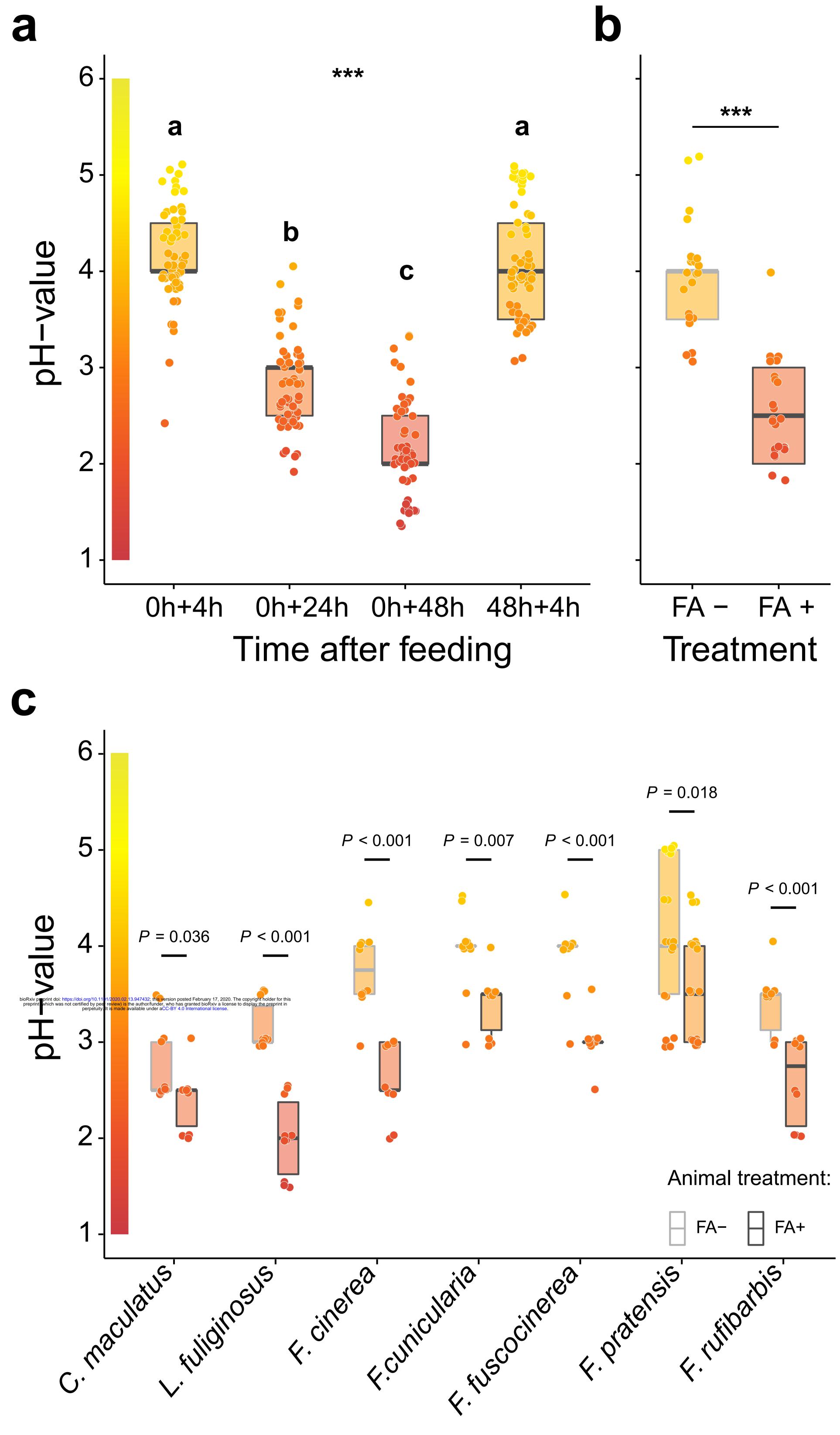
Fig. 3 – figure supplement 1: Bacterial growth *in vitro*. Change in the number of CFUs relative to pH 5 after incubation of *Serratia marcescens* (**a**) and *Asaia* sp. (**b**) in 10% honey water (pH = 5) or in 10% honey water acidified with commercial formic acid to a pH of 4, 3 or 2 for 2h (*S. marcescens*: GLM, LR-test, $\chi^2 = 79.442$, df = 1, *P* < 0.001; *Asaia* sp.: GLM,

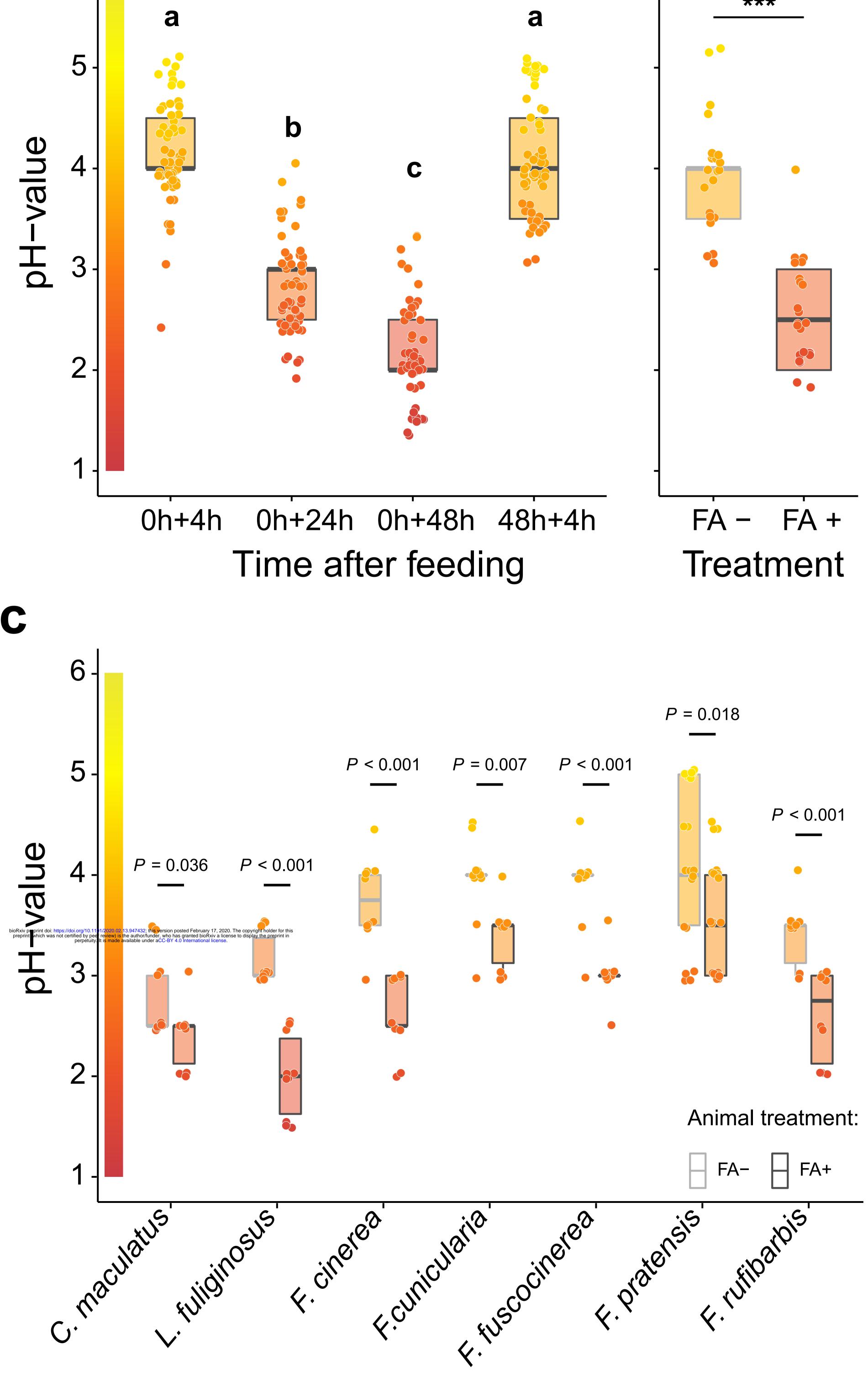
890 LR-test $\chi^2 = 21.179$, df = 2, P < 0.001, same letters indicate P = 0.234, and different letters

indicate P < 0.001 in Westfall corrected post hoc comparisons).

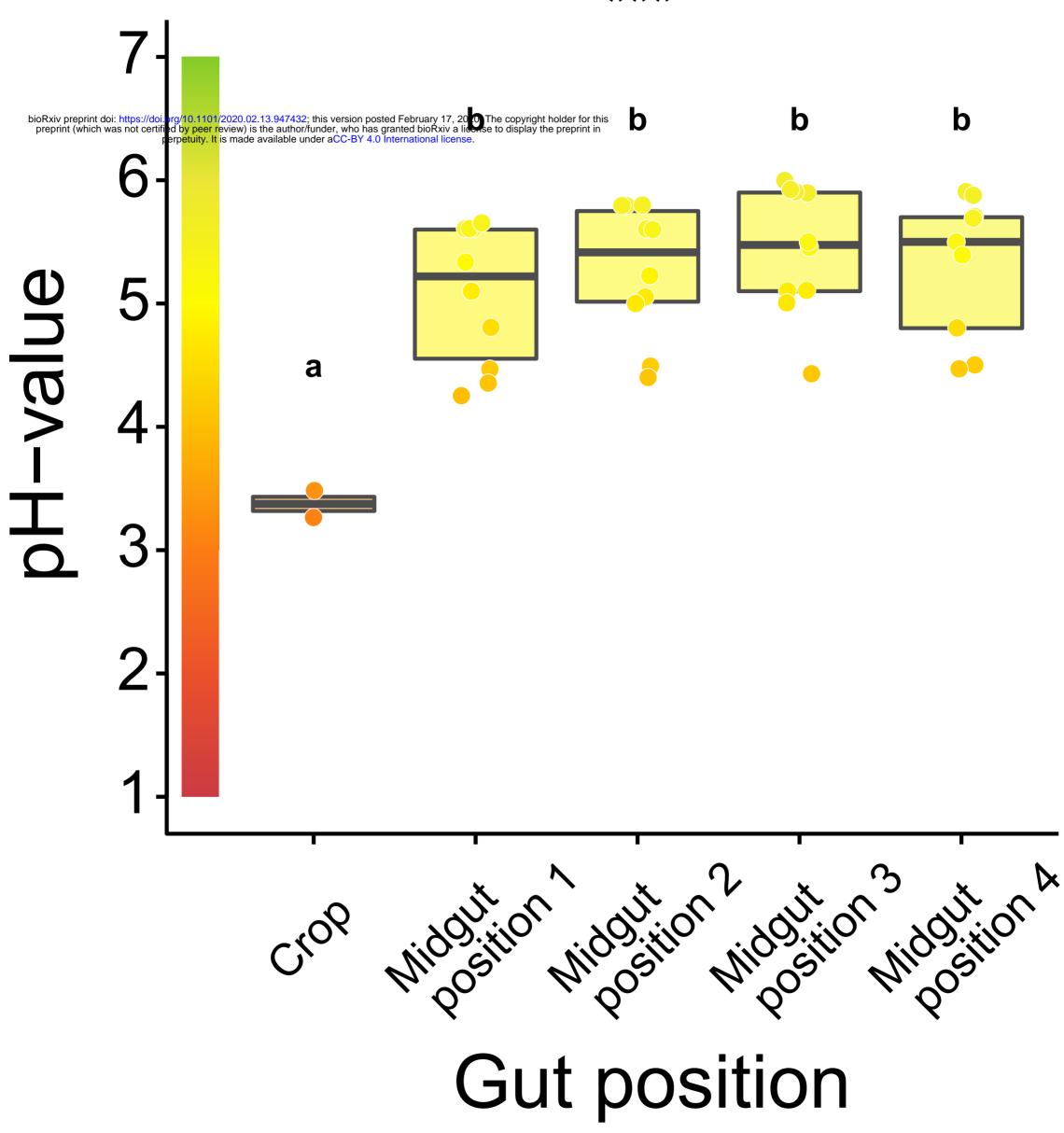


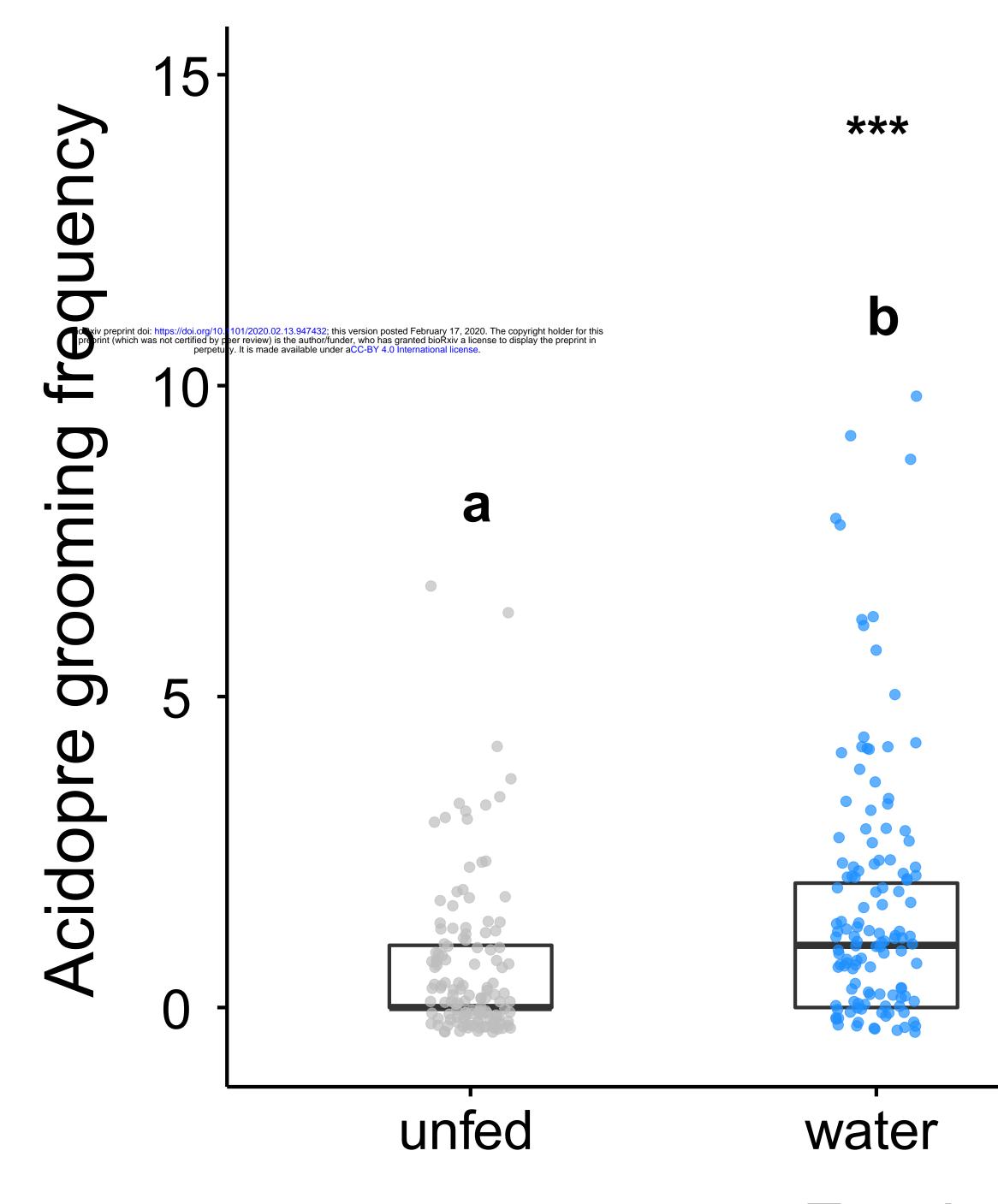






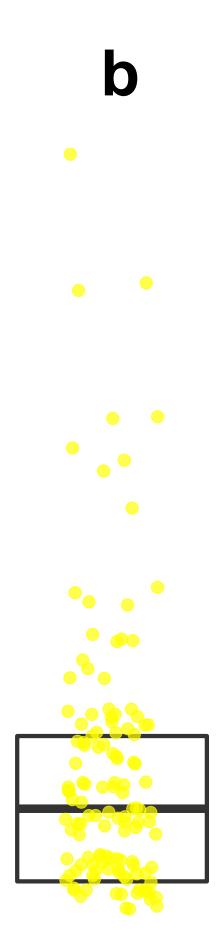
Species

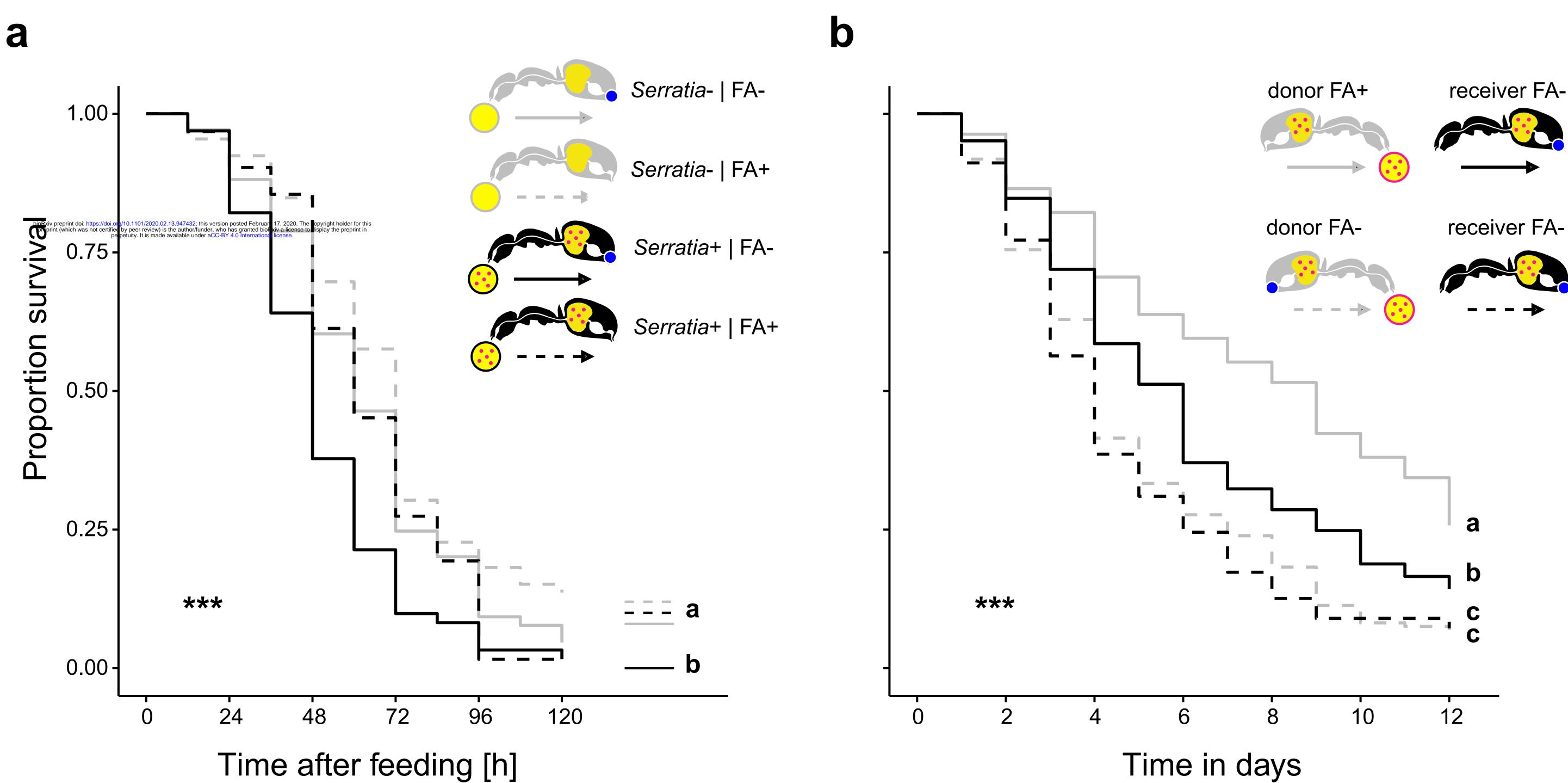


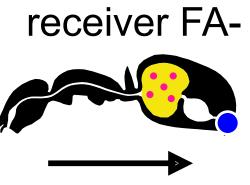


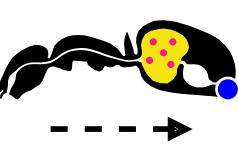
Food

honey

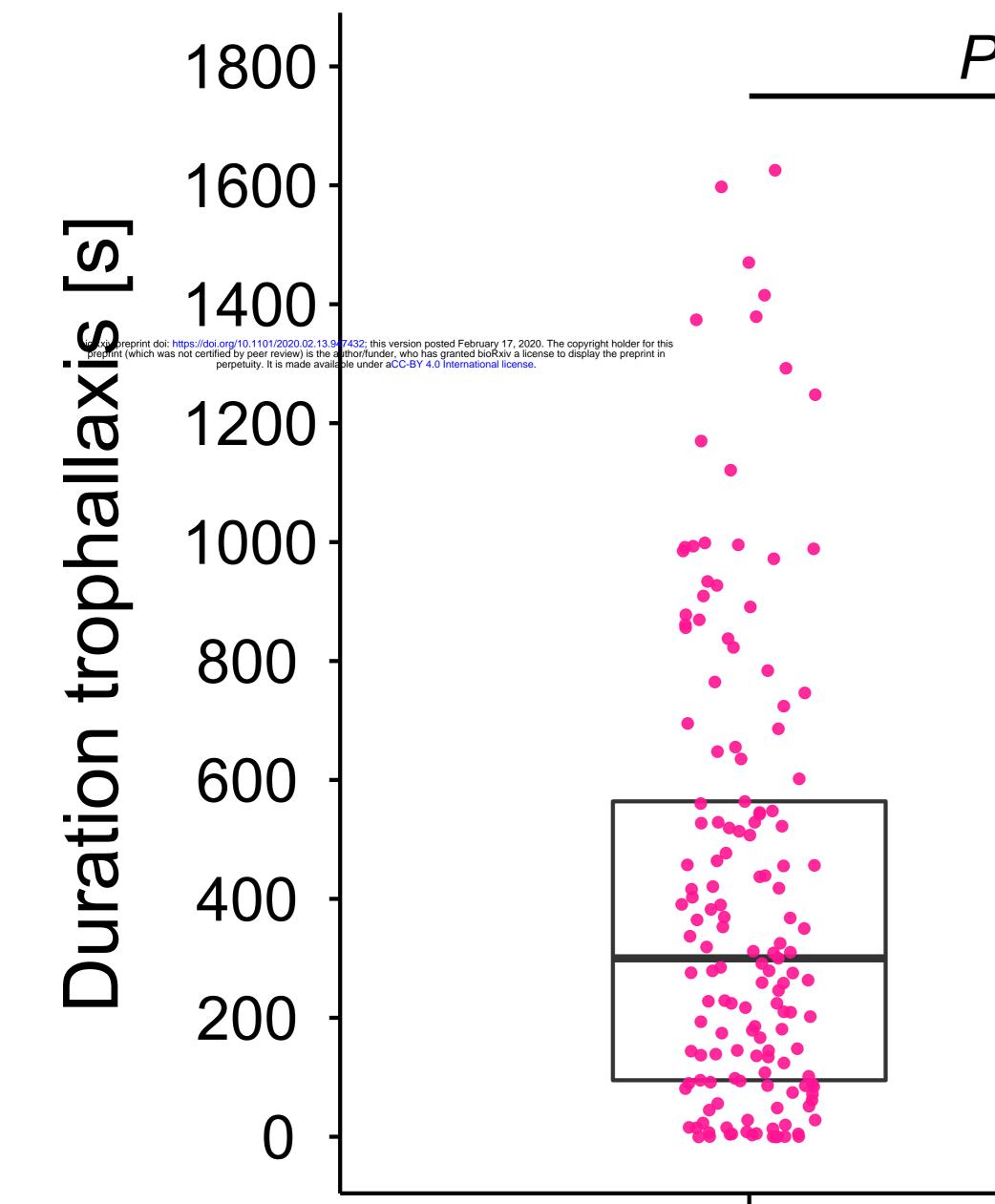






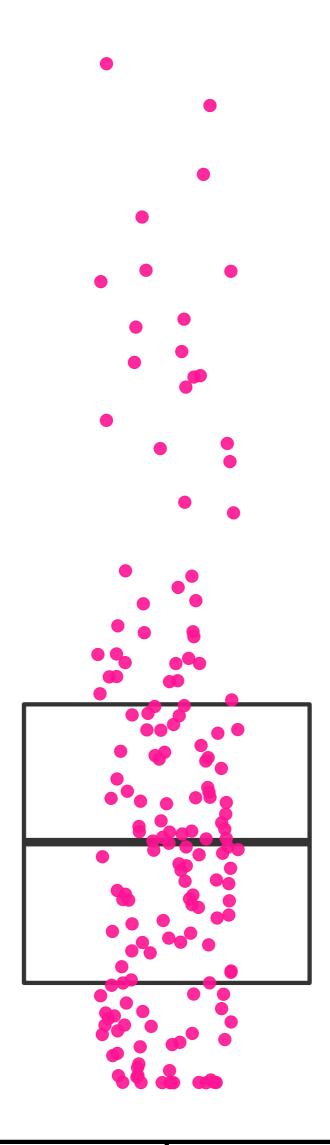




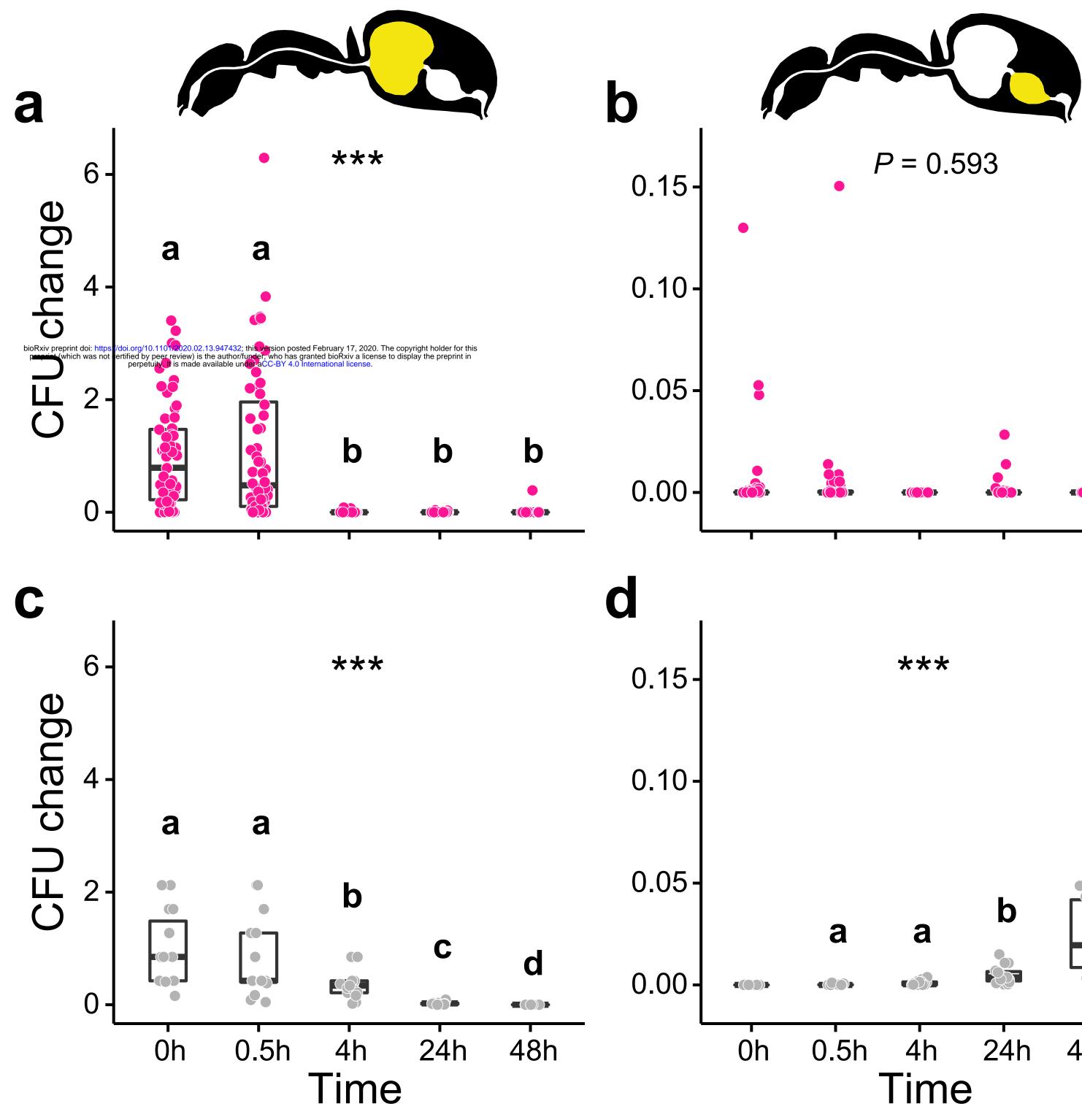


donorFA- receiverFA- donorFA+ receiverFA-

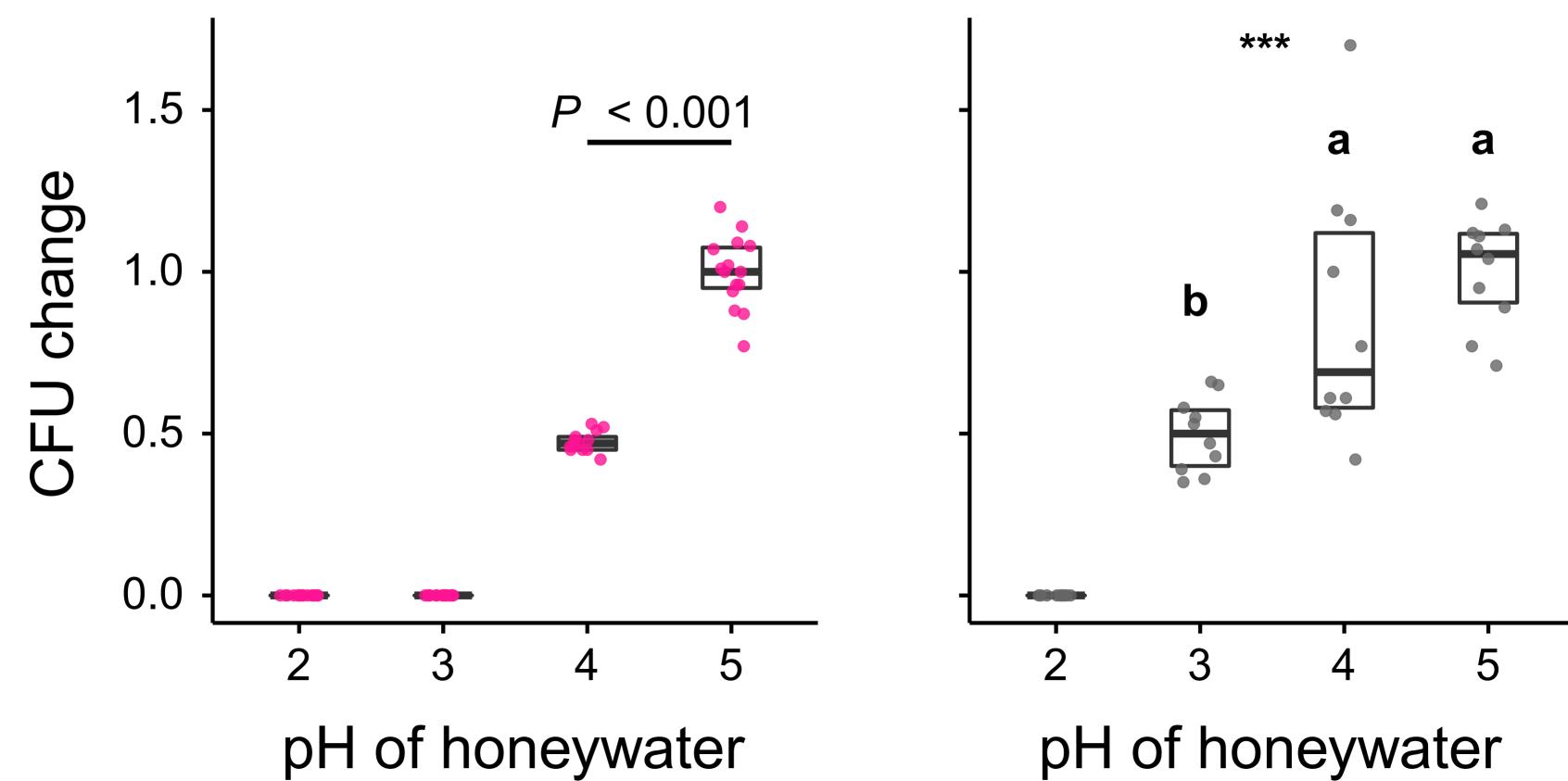
P = 0.268



Animal pairing



С 48h 8



b

