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1 **Microbial impacts on insect evolutionary diversification: from patterns to**
2 **mechanisms**

3

4 **Fabrice Vavre & Natacha Kremer**

5

6 **Abstract**

7 Symbiosis can favor rapid shifts in host phenotypic traits, particularly through the
8 contribution of symbionts to the host's physiology. In addition, variations in the
9 microbiota composition between individuals can be associated with pre- and post-
10 zygotic barriers. All together, these phenomena may contribute to insect diversification
11 and speciation. Recent advances have also shown that the host-microbiota molecular
12 dialogue, mediated notably by host immune and developmental pathways, is critical for
13 the acquisition and control of the microbiota, and could also contribute to reproductive
14 isolation. While still a controversial hypothesis, adaptation through symbiosis could
15 thus trigger host-symbiont coevolution and accelerate differentiation.

16

17

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21

22

23 **Highlights**

- 24 - Symbiotic communities in insects are shaped by host and environmental cues
25 - Recruitment and control of symbionts involve host immunity and development
26 - Symbionts can affect host niche exploitation and modulate pre-mating isolation
27 - Host-symbiont coevolution can lead to specificity and trigger post-mating
28 isolation

29

30 **Introduction**

31 Biology is undergoing a paradigm shift. An individual should no longer be considered as
32 a single organism, but as a chimera composed of a community of interacting organisms,
33 including the host itself, but also a wealth of microbial partners that are associated with
34 it. Microbial partners can be extracellular or intracellular, vertically or horizontally
35 transmitted, beneficial or detrimental, but all contribute to the phenotype of the
36 symbiotic individual. This phenotype is thus an 'extended phenotype' resulting from the
37 expression of multiple genomes and their interactions [1].

38 At a macro-evolutionary scale, there is no doubt that symbiosis has played a major role
39 in the evolution and diversification of entire clades of insects by allowing the
40 exploitation and/or colonization of new niches [2-6]. For instance, symbionts can
41 physiologically contribute to the provision of essential nutrients to hosts that feed on
42 unbalanced food (*e.g.*, plant sap or blood), or to the exploitation of recalcitrant food
43 sources (*e.g.*, wood) [7,8]. Nonetheless, our understanding of the micro-evolutionary
44 processes involved in diversification is surprisingly still very limited.

45 The picture is however changing. First, microbiota are described in a growing number of
46 insect species, which makes now possible the study of the biotic and abiotic factors
47 shaping their composition. Second, the molecular dialogue between hosts and symbionts
48 starts to be deciphered, highlighting notably a crucial role of host immune and
49 developmental pathways in the acquisition of the microbiota and its control. Third,
50 rapid shifts in microbiota composition have recently been associated with physiological
51 traits, potentially favoring niche diversification and reproductive isolation. After
52 reviewing these different aspects, we propose that mechanisms involved in the control
53 of symbionts (immunity, development) and effects of microbial partners on their host
54 (niche expansion, reproductive isolation) can reinforce each other and facilitate insect
55 diversification.

56

57 **Within- and between-species variation in the composition of microbial** 58 **communities.**

59 With the development of high throughput sequencing technologies, symbiotic
60 communities - and notably gut microbiota - have recently been characterized in a
61 number of insect species (review in [8]). While descriptive, these approaches constitute

62 a first hint to elucidate factors involved in the variation of symbiotic communities and
63 their adaptive value within and between phylogenetically related species.

64 Environment has a clear influence on symbiotic composition. For instance, changes in
65 diet during life or during development are associated with important variations in the
66 gut microbiota composition (*e.g.*, *Drosophila* or *Cephalotes* ant microbiota [9,10]), but
67 other factors, like parasite infection, can also modulate it [11]. Interestingly, a
68 comparison of 62 insect species from various orders highlighted convergence in the
69 microbiota composition between distantly related species sharing the same diet [12].
70 This convergence could partly result from adaptation for optimal exploitation of the
71 environment. Together with the fact that host-associated communities are highly
72 different from environmental ones (*e.g.*, [10,13]), and that an important predictor of the
73 symbiotic composition of individuals is the species they belong to (*e.g.*, [14,15]), these
74 host-microbiota association patterns suggest a fundamental filtering process during the
75 stable colonization of the host. This filtering can also occur during symbiont
76 transmission, as recently shown in beewolf wasps, where inoculation of non-native
77 protective *Streptomyces* symbionts led to normal colonization, but to an absence of
78 transmission [16]. Different studies have even evidenced that variations detected in the
79 composition of the microbiota recapitulate host phylogeny, a phenomenon now referred
80 as phylosymbiosis [17]. For example, different species of the ant genus *Cephalotes*
81 display a species-specific microbiota, although individuals from a single species were
82 collected in highly different environments [18]. Similarly, a phylosymbiotic signal was
83 found in the wasp genus *Nasonia*, albeit all species were reared on the same
84 environment [19]. Both species-specificity and phylosymbiosis suggest an influence of
85 the host-microbiota dialogue on the microbiota composition, with possible co-
86 divergence in the case of phylosymbiosis.

87 While these studies show that both environmental and host factors influence the
88 composition of the microbiota, they also underline that host factors are of prime
89 importance in filtering environmental bacterial communities (figure 1). Evident
90 directions of research are to determine the contribution of the microbiota to the host
91 phenotype and the adaptive value of its composition, which remain unknown in most
92 cases.

93

94 **Immunity and development shape bacterial microbiota.**

95 Within the host, the microbiota resides in specific tissues (*e.g.*, the intestine) that
96 constitute a specific niche. This host niche is shaped by biotic and abiotic factors (*e.g.*,
97 temperature, pH, oxygen, metabolites, secreted molecules) that may be under the
98 control of host and bacterial genes. Recent advances have started to elucidate the
99 proximate mechanisms involved in the construction of this niche and how these
100 mechanisms regulate the composition and abundance of bacterial communities.

101 Recent findings on *D. melanogaster* indicate that the immune system plays a central role:
102 it does not only participate in the regulation of pathogens, but also to the regulation of
103 resident bacteria and to the homeostasis between resident and pathogenic bacteria
104 (review in [20]). For instance, the repression of NFκB-dependent antimicrobial peptides
105 (AMPs) controls the commensal microbial community in the fly gut and limits the
106 density of the pathogenic *Gluconobacter morbifer* [21]. Indeed, RNAi-silencing of the
107 negative regulator *Caudal* (IMD pathway), specifically expressed in the posterior midgut,
108 results in a decrease of commensal *Acetobacteraceae*. This process is followed by the
109 overgrowth of *G. morbifer*, the induction of apoptosis, and the death of the fly [21].
110 Interestingly, the microbiota itself can directly modify the niche [22]. For example, uracil
111 produced by opportunists, but not by resident bacteria, activates the Dual oxidase that
112 regulates the production of microbicidal Reactive Oxygen Species (ROS) [23,24].

113 In the midgut of the majority of arthropod species, epithelial cells secrete a peritrophic
114 membrane (PM) which constitutes a critical interface with the microbiota, protecting
115 the host against pathogenic infections [8,20]. Remarkably, transcription factors and
116 toxic molecules, by modulating immune pathways (*e.g.*, IMD/relish, JAK-STAT or JNK),
117 also have a pleiotropic role in host developmental processes [25–28]. Indeed, JAK-STAT
118 or JNK pathways, which are activated by microbicidal ROS, facilitate the epithelium
119 renewal [25]. The PM integrity is also directly impacted by gut microbiota in the tick
120 *Ixodes scapularis*. Indeed, dysbiosed larvae exhibit a reduced expression of STAT that
121 lowers the expression of the peritrophin, a major glycoprotein structuring the PM [29].
122 In this case however, the reduced thickness of the PM limits the colonization of the
123 pathogenic spirochete *Borrelia burgdorferi* [29].

124 A differential regulation of microbial populations can be supported by the development
125 of anatomical structures where a specific immune regulation is locally triggered. For
126 instance, the evolution of compartmentalization together with the important anatomical
127 variation of gut structures and immune regulations between species may be the

128 consequence of the intense selection imposed by symbiosis (reviews in [8,20]). Another
129 striking example is the confinement of *Sitophilus* primary endosymbiont (SPE) within
130 the weevil's bacteriocyte (*i.e.*, cells specialized in hosting symbionts) in response to
131 secretion of AMPs. Indeed, the localized secretion of coleoptericin-A within the
132 bacteriocytes regulates bacterial growth, initiating the development of giant filamentous
133 endosymbionts that are not able to spread into insect tissues [30].

134 All these studies highlight the fundamental role of the host-microbiota dialogue in
135 shaping both immune and developmental homeostasis (Figure 2). This suggests that
136 coevolution between partners favors the maintenance of specific microbes in a
137 particular niche, a process which could underlie the establishment of phylosymbiosis
138 (Figure 1).

139

140 **Symbiont-induced mechanisms favoring diversification and speciation.**

141 While symbionts play an important role in numerous insect functions (review in [31]),
142 only a few studies directly link the variation of the microbiota - within or between
143 closely related species - to phenotypic traits potentially involved in diversification and
144 speciation.

145 The first category of phenotypic traits relates to symbiont-mediated exploitation of the
146 host ecological niche (review in [32]). The acquisition of symbionts has been associated
147 with rapid niche shifts in a few cases. For instance, experimental switching of the
148 *Ishikawaella* symbionts between *Megacopta punctatissima* and *M. cribraria* led to a
149 complete reversal of the performances of the plataspid stinkbugs on different host
150 plants, *i.e.* soybean and pea [33]. Another example is the evolution of a variant of the
151 western corn rootworm *Diabrotica virgifera* in response to the pest control crop
152 rotation (corn *vs.* non-host soybean). This variant exhibits a shifted microbiota
153 composition with an increase in *Klebsiella* sp. and *Stenotrophomonas* sp., which could
154 favor tolerance to anti-herbivory defenses of the new host plant through the increase of
155 cysteine proteases activity [34]. In these cases, provision of novel traits by symbionts
156 can support access and/or adaptation to new environments and favor adaptive
157 radiation.

158 The second category of traits potentially involved in differentiation relates to the impact
159 of symbionts on the interruption of gene flows between individuals harboring different
160 microbiota, *i.e.* on host reproductive isolation. Individuals harboring similar

161 extracellular or intracellular microbiota exhibit kin recognition and mate preferentially
162 together in several *Drosophila* species [35–37]. For instance, the different microbiota
163 composition of *D. melanogaster* flies fed on different food sources, and particularly the
164 presence/absence of *Lactobacillus plantarum*, influences the sexual isolation pattern
165 [35]. In the *D. paulistorum* species complex, infection by *Wolbachia* also influences
166 mating preference of males and females [37]. These preferences could directly rely on
167 the modification of pheromonal profiles through the participation of symbionts to the
168 synthesis of cuticular hydrocarbons or volatile compounds [35], but other mechanisms,
169 such as a modification in the neuronal integration of the signal, remain to be explored. In
170 addition, both vertically- and horizontally-transmitted symbionts may participate to
171 post-mating isolation by inducing hybrid sterility. In the *Drosophila paulistorum* and
172 *Nasonia* species complexes, sterility is associated with the over-proliferation of
173 symbionts in the testes of hybrid males [37,38]. While the mechanisms involved are not
174 known, proliferation of symbionts in hybrids may result from the perturbation of the
175 genetic interactions between symbionts and host genes involved in the control of the
176 symbiotic population. Supporting this hypothesis, Brucker et al. (2013) showed that
177 hybrid viability is restored when gut bacteria are removed from *Nasonia* wasps [17].
178 Dead hybrids show an altered microbiota, a strong melanization coupled with an
179 activation of the immune system, suggesting that ‘control’ mechanisms may diverge
180 rapidly between closely related species, and be involved in post-zygotic barrier to
181 hybrid formation. This hypothesis has recently been convincingly exposed in [17].
182 Finally, microbe-microbe interactions can also participate to post-mating isolation. The
183 most studied example is the hybrid mortality resulting from bidirectional
184 incompatibility in crosses between individuals infected with different *Wolbachia* strains
185 [reviewed in 39,40].

186

187 **Symbiosis as a driver of insect diversification.**

188 Modifications of symbiotic communities can be extremely rapid both within individuals
189 and populations. These shifts can reflect selection for symbiont-mediated traits that
190 allow adaptation to the local environment. For example, *Spiroplasma* has rapidly spread
191 within *Drosophila neotestacea* populations, owing to the protection it confers against
192 sterilizing nematodes. These adaptive processes can also be coupled to processes that
193 are not adaptive for the host. For example, *Rickettsia* rapidly spread in populations of

194 *Bemisia tabaci* in the United States as a result of the benefit it provides on some traits
195 (e.g., fecundity, developmental time), but also because of the reproductive manipulation
196 it induces (i.e., female-bias in the progeny) [42]. Whatever the mechanisms involved,
197 these examples highlight that symbiont frequencies can dramatically change over short
198 periods of time. Importantly, these rapid changes can dramatically affect the selective
199 pressures acting on the host to acquire, control and tolerate beneficial and/or prevalent
200 symbionts [43]. For example, tolerance evolution has been proposed as the fundamental
201 force that led to the evolution of host dependence in the *Wolbachia* - *Asobara tabida*
202 symbiosis, as a consequence of the accommodation of the host to the modification of
203 ROS homeostasis by the symbiont [44–46]. This coevolutionary dynamics of hosts and
204 symbionts following rapid changes in microbiota composition could have dramatic
205 consequences on hybrid viability, as shown in *Nasonia*.

206 All together, symbiosis could thus trigger insect differentiation through a variety of
207 mechanisms. Symbionts, by providing new physiological capabilities to their hosts, can
208 allow niche expansion, a first step towards adaptive radiation. In addition, acquisition
209 and spread of a new symbiont may be accompanied by side effects that facilitate or
210 trigger host differentiation. First, facilitation can occur when individuals harboring the
211 same microbiota exhibit mate preference. Second, host genes underlying local
212 adaptation may not only encode traits directly involved in niche exploitation, but also
213 genes involved in the adaptation to the symbiotic partner, such as immune and
214 developmental genes. Rapid evolution of these genes may favor the emergence of post-
215 zygotic barriers and increase host-symbiont specificity, thus allowing niche segregation
216 and rapid differentiation.

217

218 **Conclusion**

219 For a long time, global phylogenetic patterns have suggested that symbiosis is an
220 important driver of insect diversification. Recent advances in symbiont-mediated
221 behavioral modifications and in the mechanisms involved in symbiotic homeostasis now
222 highlight proximate mechanisms through which this could occur. Studies of symbiosis
223 diversification at a short time-scale are needed to get a better picture of the selective
224 pressures and processes involved in the evolution of symbiotic relationships, and of
225 their role in the diversification of insects. A full understanding of these processes
226 requires to expand our documentation on the variations of community composition, but

227 more importantly on the mechanisms underlying host-symbiont interactions within
228 species, between biotypes/host races or closely related species. New methodologies are
229 offering a unique opportunity to tackle these questions, providing a full description of
230 the composition and the functioning of these interactions and facilitating the detection
231 of host genes involved in local adaptation. Are those genes frequently associated with
232 the regulation of the symbiotic compartment? How do they influence hybrid
233 performance and viability? Studying the mechanisms of host-symbiont interactions and
234 their micro-evolutionary dynamics is thus a crucial step for the field of insect symbiosis
235 in particular, but more importantly for the entire field of entomology.

236

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238

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243 **Figure legend:**

244

245 **Figure 1: Processes of variation in microbiota composition.** When symbionts are
246 environmentally acquired, bacterial composition within the host depends on the
247 microbial composition of environmental communities. A plastic composition of the
248 microbiota may be adaptive when the environment fluctuates rapidly and without
249 predictability. This could for example be the case in *Drosophila melanogaster*, where the
250 local environment, among which diet, has an extreme influence on the composition of
251 the microbiota [9,47]. Numerous examples also indicate an active filtering process,
252 which results in the selection of a subset of the environmental community and an
253 increase in the host/microbiota specificity. The phylosymbiotic signal observed in some
254 instances may reflect (co)evolution of the host-symbiont interactions. Circles of different
255 colors represent bacterial strains/species and rectangles host genotypes.

256

257 **Figure 2: Host-microbiota dialogue shapes both immune and developmental**
258 **homeostasis to control the microbiota composition.** Molecular pathways (*italics*)
259 exhibiting a pleiotropic role in immunity and development must play a particularly
260 important role in defining and maintaining the specificity of the interaction in a
261 particular host niche.

262

263 **Figure 3: Model for the role of symbiosis in the reinforcement of differentiation**
264 **between populations.** Symbionts can promote rapid adaptation to local conditions.
265 Rapid shifts in microbiota can also generate selective pressures on the partners for
266 optimization of symbiont acquisition and/or for tolerance. As a consequence, host-
267 microbiota specificity should increase, leading to a reduction in hybrid performance.
268 Furthermore, host-symbiont coevolution can lead to symbiont-mediated
269 incompatibilities between hosts adapted to different microbiota, reinforcing specificity
270 and thus niche segregation between hosts harboring different microbiota. This scenario
271 can be applied when microbiota diversification occurs in allopatric populations. In the
272 case of sympatric/parapatric populations, reinforcement mechanisms possibly
273 mediated by symbionts, such as niche fidelity or mate choice would be required.

274

275

276 **References:**

- 277 1. McFall-Ngai M, Hadfield MG, Bosch TCG, Carey H V, Domazet-Loso T, Douglas AE,
278 Dubilier N, Eberl G, Fukami T, Gilbert SF, *et al.*: **Animals in a bacterial world, a**
279 **new imperative for the life sciences.** *Proc. Natl. Acad. Sci. USA* 2013, **110**:3229–
280 3236.
- 281 2. Moran NA, Tran P, Gerardo NM: **Symbiosis and Insect Diversification: an**
282 **Ancient Symbiont of Sap-Feeding Insects from the Bacterial Phylum**
283 **Bacteroidetes.** *Appl Env. Microbiol* 2005, **71**:8802–10.
- 284 3. Russell JA, Moreau CS, Goldman-Huertas B, Fujiwara M, Lohman DJ, Pierce NE:
285 **Bacterial gut symbionts are tightly linked with the evolution of herbivory in**
286 **ants.** *Proc Natl Acad Sci USA* 2009, **106**:21236–41.
- 287 4. Moran NA, McCutcheon JP, Nakabachi A: **Genomics and Evolution of Heritable**
288 **Bacterial Symbionts.** *Annu Rev Genet.* 2008, **42**:165–190.
- 289 5. Feldhaar H: **Bacterial symbionts as mediators of ecologically important traits**
290 **of insect hosts.** *Ecol. Entomol.* 2011, **36**:533–543.
- 291 6. Ferrari J, Vavre F: **Bacterial symbionts in insects or the story of communities**
292 **affecting communities.** *Philos. Trans. R. Soc. Lond. B. Biol. Sci.* 2011, **366**:1389–
293 400.
- 294 7. Douglas AE: **The microbial dimension in insect nutritional ecology.** *Funct.*
295 *Ecol.* 2009, **23**:38–47.
- 296 8. Engel P, Moran NA: **The gut microbiota of insects - diversity in structure and**
297 **function.** *FEMS Microbiol. Rev.* 2013, **37**:699–735.
- 298 ** A thorough review adressing the diversity of host-microbiota interactions in the gut
299 in terms of gut anatomy and physiochemical properties; host-microbe molecular
300 dialogue; microbiota composition, function and transmission.
- 301 9. Chandler JA, Lang JM, Bhatnagar S, Eisen JA, Kopp A: **Bacterial communities of**
302 **diverse *Drosophila* species: ecological context of a host-microbe model**
303 **system.** *PLoS Genet.* 2011, **7**:e1002272.
- 304 10. Hu Y, Łukasik P, Moreau CS, Russell JA: **Correlates of gut community**
305 **composition across an ant species (*Cephalotes varians*) elucidate causes and**
306 **consequences of symbiotic variability.** *Mol. Ecol.* 2014, **23**:1284–300.
- 307 11. Koch H, Cisarovsky G, Schmid-Hempel P: **Ecological effects on gut bacterial**
308 **communities in wild bumblebee colonies.** *J. Anim. Ecol.* 2012, **81**:1202–10.
- 309 12. Colman DR, Toolson EC, Takacs-Vesbach CD: **Do diet and taxonomy influence**
310 **insect gut bacterial communities?** *Mol. Ecol.* 2012, **21**:5124–37.

- 311 * Using a comparative analysis of the microbiota of 62 insect species belonging to five
312 different orders, the authors highlight that microbiota composition is determined
313 both by phylogenetic and environmental factors at this large phylogenetic scale.
- 314 13. Duguma D, Rugman-Jones P, Kaufman MG, Hall MW, Neufeld JD, Stouthamer R,
315 Walton WE: **Bacterial communities associated with culex mosquito larvae**
316 **and two emergent aquatic plants of bioremediation importance.** *PLoS One*
317 2013, **8**:e72522.
- 318 14. Jones RT, Sanchez LG, Fierer N: **A cross-taxon analysis of insect-associated**
319 **bacterial diversity.** *PLoS One* 2013, **8**:e61218.
- 320 15. Dietrich C, Köhler T, Brune A: **The cockroach origin of the termite gut**
321 **microbiota: patterns in bacterial community structure reflect major**
322 **evolutionary events.** *Appl. Environ. Microbiol.* 2014, **80**:2261–9.
- 323 16. Kaltenpoth M, Roeser-Mueller K, Koehler S, Peterson A, Nechitaylo TY,
324 Stubblefield JW, Herzner G, Seger J, Strohm E: **Partner choice and fidelity**
325 **stabilize coevolution in a Cretaceous-age defensive symbiosis.** *Proc Natl Acad*
326 *Sci USA* 2014, **111**:6359–64.
- 327 17. Brucker RM, Bordenstein SR: **The hologenomic basis of speciation: gut**
328 **bacteria cause hybrid lethality in the genus *Nasonia*.** *Science.* 2013, **341**:667–
329 9.
- 330 ** This article presents evidence that bacterial communities in the guts of closely related
331 species of the genus *Nasonia* form species-specific phylosymbiotic assemblages
332 that cause lethality in interspecific hybrids. In particular, hybrid viability can be
333 rescued by removing gut bacteria.
- 334 18. Sanders JG, Powell S, Kronauer DJC, Vasconcelos HL, Frederickson ME, Pierce NE:
335 **Stability and phylogenetic correlation in gut microbiota: lessons from ants**
336 **and apes.** *Mol. Ecol.* 2014, **23**:1268–83.
- 337 19. Brucker RM, Bordenstein SR: **The roles of host evolutionary relationships**
338 **(genus: *Nasonia*) and development in structuring microbial communities.**
339 *Evolution.* 2012, **66**:349–62.
- 340 20. Buchon N, Broderick NA, Lemaitre B: **Gut homeostasis in a microbial world:**
341 **insights from *Drosophila melanogaster*.** *Nat Rev Microbiol* 2013, **11**:615–26.
- 342 * A must-read review on the interplay between host and microbes in shaping gut
343 homeostasis, highlighting the importance of immune and developmental
344 pathways, and the mechanisms allowing the host to eliminate pathogens while
345 tolerating indigenous symbionts.
- 346 21. Ryu J-H, Kim S-H, Lee H-Y, Bai JY, Nam Y-D, Bae J-W, Lee DG, Shin SC, Ha E-M, Lee
347 W-J: **Innate immune homeostasis by the homeobox gene *caudal* and**
348 **commensal-gut mutualism in *Drosophila*.** *Science.* 2008, **319**:777–82.

- 349 22. Wong AC-N, Dobson AJ, Douglas AE: **Gut microbiota dictates the metabolic**
350 **response of *Drosophila* to diet.** *J. Exp. Biol.* 2014, **217**:1894-1901.
- 351 23. Ha E-M, Lee K-A, Seo YY, Kim S-H, Lim J-H, Oh B-H, Kim J, Lee W-J: **Coordination**
352 **of multiple dual oxidase-regulatory pathways in responses to commensal**
353 **and infectious microbes in drosophila gut.** *Nat. Immunol.* 2009, **10**:949-957.
- 354 24. Lee K-A, Kim S-H, Kim E-K, Ha E-M, You H, Kim B, Kim M-J, Kwon Y, Ryu J-H, Lee
355 W-J: **Bacterial-derived uracil as a modulator of mucosal immunity and gut-**
356 **microbe homeostasis in *Drosophila*.** *Cell* 2013, **153**:797-811.
- 357 ** This very complete study shows that bacterial-derived uracil acts as a ligand for Dual
358 oxidase-dependent production of ROS. Because the production of uracil by
359 resident bacteria is limited, uracil concentration constitutes a 'signal' that guides
360 the host to discriminate between pathogenic and resident bacteria.
- 361 25. Buchon N, Broderick NA, Chakrabarti S, Lemaitre B: **Invasive and indigenous**
362 **microbiota impact intestinal stem cell activity through multiple pathways in**
363 ***Drosophila*.** *Genes Dev.* 2009, **23**:2333-44.
- 364 26. Jones R, Luo L, Ardita C, Richardson A, Kwon Y, Mercante J, Alam A, Gates C, Wu H,
365 Swanson P, et al.: **Symbiotic *lactobacilli* stimulate gut epithelial proliferation**
366 **via Nox-mediated generation of reactive oxygen species.** *EMBO J* 2013,
367 **32**:3017-28.
- 368 27. Guo L, Karpac J, Tran SL, Jasper H: **PGRP-SC2 promotes gut immune**
369 **homeostasis to limit commensal dysbiosis and extend lifespan.** *Cell* 2014,
370 **156**:109-22.
- 371 28. Broderick NA, Buchon N, Lemaitre B: **Microbiota-Induced Changes in**
372 ***Drosophila melanogaster* Host Gene Expression and Gut Morphology.** *MBio*
373 2014, **5**:e01117-14.
- 374 29. Narasimhan S, Rajeevan N, Liu L, Zhao YO, Heisig J, Pan J, Eppler-Epstein R,
375 Deponte K, Fish D, Fikrig E: **Gut microbiota of the tick vector *Ixodes scapularis***
376 **modulate colonization of the lyme disease spirochete.** *Cell Host Microbe* 2014,
377 **15**:58-71.
- 378 * This study highlights that gut homeostasis, notably the integrity of the peritrophic
379 membrane, depends on the presence of the microbiota that activates the immune
380 and developmental STAT signaling pathway. As a consequence of altered
381 peritrophic membrane, colonization by *Borrelia* bacteria is reduced in the tick.
- 382 30. Login FH, Balmand S, Vallier A, Vincent-Monégat C, Vigneron A, Weiss-Gayet M,
383 Rochat D, Heddi A: **Antimicrobial peptides keep insect endosymbionts under**
384 **control.** *Science.* 2011, **334**:362-5.

- 385 ** Using FISH and RNAi technologies, the authors demonstrate the role of the
386 antimicrobial peptide ColaA, specifically expressed within the bacteriome, in the
387 gigantism of endosymbionts and their sequestration within specific cells.
- 388 31. Douglas AE: **The Molecular Basis of Bacterial-Insect Symbiosis.** *J. Mol. Biol.*
389 2014, doi:10.1016/j.jmb.2014.04.005.
- 390 32. Douglas AE: **Microbial brokers of insect-plant interactions revisited.** *J. Chem.*
391 *Ecol.* 2013, **39**:952–61.
- 392 33. Hosokawa T, Kikuchi Y, Shimada M, Fukatsu T: **Obligate symbiont involved in**
393 **pest status of host insect.** *Proc R Soc L. B Biol Sci* 2007, **274**:1979–84.
- 394 34. Chu C-C, Spencer JL, Curzi MJ, Zavala JA, Seufferheld MJ: **Gut bacteria facilitate**
395 **adaptation to crop rotation in the western corn rootworm.** *Proc Natl Acad Sci*
396 *USA* 2013, **110**:11917–22.
- 397 ** This article highlights that rapid adaptation of insects to a new host plant can be
398 linked to a modification of the composition of the microbiota. In the species under
399 study, an enrichment in bacteria favoring tolerance to the anti-herbivory defenses
400 of the plant was detected.
- 401 35. Sharon G, Segal D, Ringo JM, Hefetz A, Zilber-Rosenberg I, Rosenberg E:
402 **Commensal bacteria play a role in mating preference of *Drosophila***
403 ***melanogaster*.** *Proc Natl Acad Sci USA* 2010, **107**:20051–20056.
- 404 36. Lizé A, McKay R, Lewis Z: **Kin recognition in *Drosophila*: the importance of**
405 **ecology and gut microbiota.** *ISME J.* 2014, **8**:469–77.
- 406 37. Miller WJ, Ehrman L, Schneider D: **Infectious speciation revisited: impact of**
407 **symbiont-depletion on female fitness and mating behavior of *Drosophila***
408 ***pauistorum*.** *PLoS Pathog.* 2010, **6**:e1001214.
- 409 38. Chafee ME, Zecher CN, Gourley ML, Schmidt VT, Chen JH, Bordenstein SR, Clark
410 ME, Bordenstein SR: **Decoupling of host-symbiont-phage coadaptations**
411 **following transfer between insect species.** *Genetics* 2011, **187**:203–215.
- 412 39. Engelstädter J, Hurst GDD: **The Ecology and Evolution of Microbes that**
413 **Manipulate Host Reproduction.** *Annu. Rev. Ecol. Evol. Syst.* 2009, **40**:127–149.
- 414 40. Serbus LR, Casper-Lindley C, Landmann F, Sullivan W: **The genetics and cell**
415 **biology of *Wolbachia*-host interactions.** *Annu. Rev. Genet.* 2008, **42**:683–707.
- 416 41. Jaenike J, Unckless R, Cockburn SN, Boelio LM, Perlman SJ: **Adaptation via**
417 **symbiosis: recent spread of a *Drosophila* defensive symbiont.** *Science.* 2010,
418 **329**:212-5.
- 419 42. Himler AG, Adachi-Hagimori T, Bergen JE, Kozuch A, Kelly SE, Tabashnik BE, Chiel
420 E, Duckworth VE, Dennehy TJ, Zchori-Fein E, *et al.*: **Rapid spread of a bacterial**

- 421 **symbiont in an invasive whitefly is driven by fitness benefits and female**
422 **bias.** *Science*. 2011, **332**:254–6.
- 423 43. Brucker RM, Bordenstein SR: **Speciation by symbiosis.** *Trends Ecol. Evol.* 2012,
424 **27**:443–51.
- 425 ** This opinion article notably presents the idea that including the microbiota in
426 classical Bateson-Dobzhansky-Muller models of speciation increases considerably
427 the number of possible hybrid incompatibilities.
- 428 44. Kremer N, Voronin D, Charif D, Mavingui P, Mollereau B, Vavre F: **Wolbachia**
429 **interferes with ferritin expression and iron metabolism in insects.** *PLoS*
430 *Pathog.* 2009, **5**:e1000630.
- 431 45. Kremer N, Dedeine F, Charif D, Finet C, Allemand R, Vavre F: **Do variable**
432 **compensatory mechanisms explain the polymorphism of the dependence**
433 **phenotype in the *Asobara tabida*-*Wolbachia* association?** *Evolution.* 2010,
434 **64**:2969–2979.
- 435 46. Kremer N, Charif D, Henri H, Gavory F, Wincker P, Mavingui P, Vavre F: **Influence**
436 **of *Wolbachia* on host gene expression in an obligatory symbiosis.** *BMC*
437 *Microbiol.* 2012, **12 Suppl 1**:S7.
- 438 47. Wong AC-N, Chaston JM, Douglas AE: **The inconsistant gut microbiota of**
439 ***Drosophila* species revealed by 16S rRNA gene analysis.** *ISME J* 2013, **7**:1922–
440 32.
- 441

Figure 1:

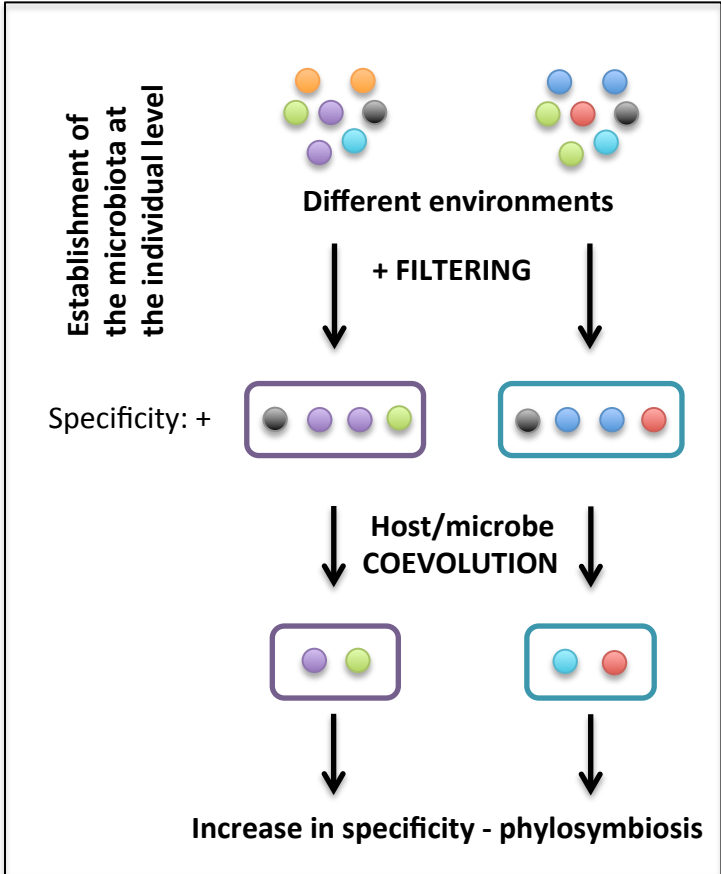


Figure 2:

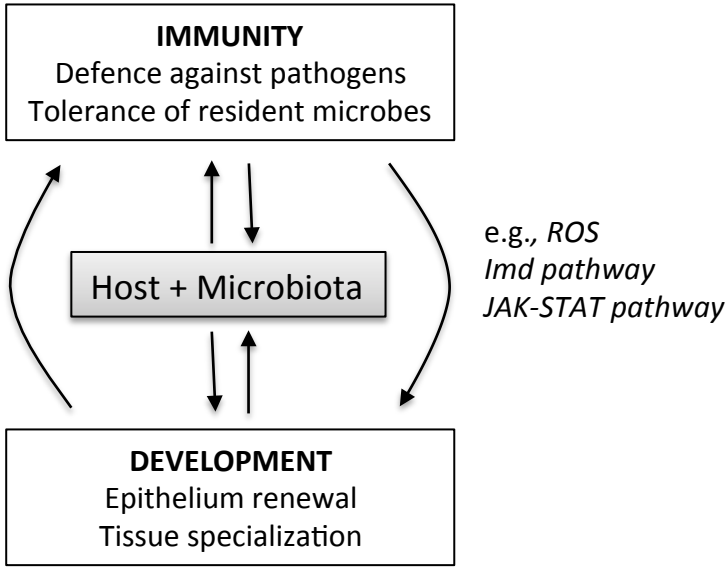


Figure 3:

