Selection for outbreeding in Varroa parasitising resistant honey bee (Apis mellifera) colonies

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INTRODUCTION

The conflicting fitness optima between hosts and parasites means the evolution of a beneficial adaptation in one is expected to select for a counter-adaptation in the other: driving a co-evolutionary arms race (Bell, 1982). The Red Queen Hypothesis predicts that a co-evolutionary arms race will drive oscillations in haplotype frequencies in hosts and parasites influenced by the relative frequency and fitness of matching alleles: selecting for increased genetic diversity, recombination, and evolutionary rates (Bell, 1982; Hamilton, Axelrod, &
The typically short reproductive cycles of parasites, compared to their hosts, are expected to increase their rate of evolution. However, the highly inbred lifestyles of some parasites (Beaurepaire, Krieger, & Moritz, 2017) may make it difficult for a population to evolve when their host develops a new defense. This could be the case for the brood-parasitic mite Varroa destructor, Anderson & Trueman: a devastating parasite of honey bees (Apis mellifera, L.). Managed honey bee colonies, untreated with acaricides, typically die within 3 years of Varroa infestation. However, management practices can hinder the evolution of Varroa resistance in many honey bee populations.

Varroa mothers infest honey bee pupal cells shortly before capping. They then lay one male and up to four female eggs in the pupal cell (Rosenkranz, Aumeier, & Ziegelmann, 2010). The offspring hatch, feed on the developing pupa (Donzé & Guerin, 1994), and mate inside the natal cell. This is the only time in their lives when Varroa will mate. Mature, mated, daughter mites leave the cell with their mother and the eclosing bee, carrying all the stored sperms they will ever have for future reproduction. The male and any immature daughter mites desiccate inside the cell (Rosenkranz et al., 2010). The frequent occurrence of full-sibling mating between Varroa means populations can rapidly become highly inbred, with low proportions of heterozygotes, particularly in the middle of the brood season (June–July in Europe (Calis, Fries, & Ryrie, 1999)). This is when Varroa females are most likely to singly infest a cell and therefore cannot outbreed (Beaurepaire et al., 2017; Fuchs, 1992). This means alleles can rapidly become fixed in a Varroa population (Beaurepaire et al., 2017), a potential disadvantage in a co-evolutionary arms race. With the vast majority of Varroa infestations in managed honey bee colonies treated with acaricides (Rosenkranz et al., 2010), there is strong positive selection for the evolution of Varroa resistance to these chemicals (Beaurepaire et al., 2017; González-Cabrera et al., 2016). However, there has been little research into how Varroa can adapt when host resistance traits are allowed to coevolve through natural selection, causing dynamic shifts in Varroa’s fitness optimum.

We investigated the potential for the evolution of counter resistance traits and selection for outbreeding in Varroa infesting resistant honey bee colonies near Toulouse, France (Kefuss, Vanpoucke, Bolt, & Kefuss, 2015). Colonies in this population have survived over 20 years of Varroa infestation without treatment using acaricides (Kefuss et al., 2015). Instead, natural selection has resulted in the evolution of a honey bee population with a greatly reduced rate of Varroa population growth (Kefuss et al., 2015). This reduced rate of Varroa population growth has been linked to the inhibition of Varroa’s reproduction in pupal cells; particularly the drone brood where Varroa normally produces the most offspring (Conlon et al., 2019; Kefuss et al., 2015; Rosenkranz et al., 2010). We focus on the inhibition of Varroa’s reproduction by infested drone pupae. Having identified colonies which exhibited unusually high rates of nonreproducing Varroa, we investigated the reproductive success of Varroa between singly and multiply infested cells. We then used genetic analyses to test if reproductive success was linked to genetic polymorphism in founding females. Selection for increased recombination, via outbreeding, could increase evolutionary rates in this Varroa population and indicate it is engaged in a co-evolutionary arms race with its host (Beaurepaire, Ellis, Krieger, & Moritz, 2019; Beaurepaire et al., 2017; Bell, 1982; Hamilton et al., 1990).

2 | MATERIALS AND METHODS

2.1 | Honey bee colony screening

Colony screening took place using a Varroa-resistant honey bee population near Villemur-sur-Tarn, Haute Garonne, France (Conlon et al., 2019; Kefuss et al., 2015; Rosenkranz et al., 2010). All drone pupal cells in the screened colonies were opened. Cells containing pupae from the white-eyed stage onwards were phenotyped using the number of infesting Varroa foundresses and the presence of male and female offspring. By this age, male and female Varroa offspring were easily visible to the naked eye. Only cells where Varroa had produced male and female offspring were classified as successfully reproducing as this would imply at least one mature, mated, daughter, capable of reproducing herself, will leave the cell with the emerging bee. Cells with no offspring or only sons, which desiccate in the natal cell after the bee has emerged, were classified as nonreproducing. Cells where the mite had died were included when calculating the expected and actual proportions of multiply infested cells, as the mite was presumed to have been alive when entering the cell, but not in the analysis of reproductive success. All mites were collected and stored in ethanol at −20°C until the DNA extraction.

To minimize the effect of the host, we sampled from closely related (one mother queen and three daughter queens) colonies found at four different sites within a 5 km radius. Colonies were considered resistant if >30% of infesting Varroa failed to reproduce and susceptible if <15% failed to reproduce. (Martin, Holland, & Murray, 1997). As resistance in the mother colony had been linked to a single locus (Conlon et al., 2019), we also calculated variation from a 50:50 distribution of resistant to nonresistant for all infested drone pupae using a chi-squared test for equal proportions in R (R Core Team, 2017). As we were interested in the potential for coevolution between Varroa and resistant honey bee hosts, and a single susceptible colony is too low a number to produce a statistically sound test of resistant versus susceptible colonies, only those colonies classified as resistant were included in subsequent analyses.

2.2 | Mite density and distribution

Using the screening data, we calculated the expected proportion of multiply infested drone cells, if mites were distributed randomly, using a Poisson distribution:

\[ p_i = \frac{L_i}{N} \times e^{-1} \]
where $p$ is the probability that a mite will enter a cell already infested by $i$ mites and $L$ is the mean infestation calculated from the number of mites ($V$) and the number of available drone cells ($C$) (Fuchs, 1992).

$$L = \frac{V}{C}$$

The difference between the expected and observed proportions was tested using a chi-squared test in R (R Core Team, 2017). As the calculation for the expected proportion of multiply infested drone cells is a function of the number of available drone cells in a colony, we calculated the observed and expected proportions separately for each colony.

2.3 | Reproductive success

We tested for a link between the number of infesting Varroa and reproductive success in the drone pupae of resistant honey bee colonies using a binomial GLMM in the lme4 package (Bates, Mächler, Bolker, & Walker, 2015) for R (R Core Team, 2017). We used reproductive success as a binary response variable, genetic polymorphism between the founding Varroa as a fixed variable, and colony as a random effect.

2.4 | Genetic polymorphism

For each resistant colony, DNA for mites from multiply infested drone cells ($n = 34$) was isolated by washing the mites twice with double-distilled H$_2$O and dried before being crushed in a PCR plate containing 100 μl of 5% Chelex solution. 5 μl of Proteinase K was then added to each sample. Total mite DNA was isolated from the individuals using standard Chelex thermocycling conditions (Walsh, Metzger, & Higuchi, 1991) for genotyping at LMU Biozentrum (Munich, Germany). Seven microsatellite markers (Vdes01, Vdes04, VD112, VD152, VD307, VJ292, and VJ294) (Cornman et al., 2010; Evans, 2000; Solignac et al., 2003) were tested.

The minimum number of haplotypes across all sampled mites was inferred for multiply infested drone cells. We counted the number of drone cells where only one haplotype was identified (monomorphic; i.e., genetically identical foundresses) and those with at least two haplotypes identified (polymorphic). For missing data or heterozygous alleles, we assumed the minimum possible number of genotypes were present; we therefore risked underestimating, rather than overestimating, genetic diversity within a cell.

Table 1: Screening data for honey bee colonies with the number of uninfested cells, singly infested cells, multiply infested cells, the number of cells in which the Varroa had died and the total number of Varroa collected (Resistant colonies: Mother, Daughter 1, and Daughter 2; Susceptible colony: Daughter 3)

<table>
<thead>
<tr>
<th>Colony</th>
<th>Uninfested cells</th>
<th>Infested cells</th>
<th>Number of mites</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mother</td>
<td>385</td>
<td>78</td>
<td>119</td>
</tr>
<tr>
<td>Daughter 1</td>
<td>41</td>
<td>13</td>
<td>30</td>
</tr>
<tr>
<td>Daughter 2</td>
<td>117</td>
<td>15</td>
<td>35</td>
</tr>
<tr>
<td>Daughter 3</td>
<td>22</td>
<td>14</td>
<td>61</td>
</tr>
</tbody>
</table>

We tested whether the number of polymorphic cells was significantly different than expected if the mites were distributed randomly using a chi-squared test. The expected number of polymorphic cells was calculated by randomly permuting the observed genotypes between cells in each colony and averaging the number of polymorphic cells obtained over 10,000 permutations. We then tested whether Varroa in polymorphic cells were more likely to reproduce than Varroa in monomorphic cells using a GLMM in the lme4 package (Bates et al., 2015) for R (R Core Team, 2017). We used reproductive success as a binary response variable, genetic polymorphism between the founding Varroa as a fixed variable, and colony as a random effect.

3 | RESULTS

3.1 | Colony screening

We screened four honey bee colonies, three (Mother; Daughter 1; and Daughter 2) resistant and one (Daughter 3) susceptible (Table 1). The mother colony was produced in 2015 while the 3 daughters came from 2016. None of the resistant colonies varied significantly from a 50:50 distribution of resistant:susceptible pupae (Mother: resistant= 32, susceptible = 38, $\chi^2 = 0.357$, $df = 1$, $p = .550$; Daughter 1:resistant = 8, susceptible = 5, $\chi^2 = 0.308$, $df = 1$, $p = .579$; Daughter 2:resistant = 4, susceptible = 9, $\chi^2 = 1.231$, $df = 1$, $p = .267$) while the susceptible colony exhibited significant variation (resistant = 1, susceptible = 12, $\chi^2 = 7.692$, $df = 1$, $p = .006$). In total, we identified 140 infested drone cells in resistant colonies; of which 34 (24%) were multiply infested. Of these 13 Varroa foundresses had died after infesting the cell leaving 127 cells for further analyses.

3.2 | Reproductive success and mite density

Varroa were significantly more likely to reproduce successfully in multiply infested drone cells in the resistant honey bee colonies (Figure 1a; Multiple 80% success, Single 54% success; GLMM, Multiple versus Single infestation: $\chi^2 = 7.396$, $df = 1$, $p = .007$). However, we identified no significant differences in the expected versus observed rates of singly infested cells in resistant colonies (Figure 1b; Mother: $\chi^2 = 0.045$, $df = 1$, $p = .833$; Daughter 1: $\chi^2 = 0.206$, $df = 1$, $p = .650$; Daughter 2: $\chi^2 = 1.475$, $df = 1$, $p = .225$). The number of sons in cells classified as successfully reproducing always matched...
the number of foundresses. As Varroa mothers lay only one male egg per reproductive episode (Rosenkranz et al., 2010), this indicates all mothers laid at least one egg in multiply infested cells where Varroa successfully reproduced (Colony screening data, available on Dryad).

3.3 | Genetic polymorphism

Across the 3 resistant colonies, DNA extraction and microsatellite amplification was successful for 31 multiply infested pupal cells. Three microsatellites were identified as polymorphic (VJ294, VD307, and Vdes02; two alleles per locus) and retained for further analyses.

While there was a trend for increased reproductive success in polymorphic cells, it was not significant (Figure 2a; 77.8% success in polymorphic cells, 58.3% in monomorphic cells; GLMM-Monomorphic vs. polymorphic: $\chi^2 = 1.667, df = 1, p = .197$). The number of polymorphic cells in each colony was slightly higher than expected (Figure 2b), except for Daughter 1, although the difference was not significant ($\chi^2 = 0.49, df = 3, p = .92$). While the nonsignificant result could be due to sample size, it was not possible to collect more samples as every drone cell in the colonies was opened during screening.

4 | DISCUSSION

We investigated the potential for the evolution of counter-adaptations and selection for outbreeding in Varroa parasitising Varroa-resistant honey bee colonies: focusing on the inhibition of Varroa’s reproduction by host drone pupa. During our initial colony screening, we identified 3 resistant colonies (1 mother, 2 daughter) and 1 nonresistant colony (Daughter 3). That only the
nonresistant colony exhibited significant variation from a 50:50 ratio of Resistant:Susceptible pupae, with no intermediate levels of resistance, supported the previous identification of a single resistance-linked locus in this population (Conlon et al., 2019) and suggests Mendelian inheritance of the resistance trait.

Varroa were significantly more likely to successfully reproduce when multiply infesting drone pupal cells in a resistant honey bee colony, with a nonsignificant trend for this to increase further when foundresses were polymorphic. This could suggest that Varroa can overcome the host resistance trait by multiply infecting a resistant drone cell. However, Varroa’s distribution between multiply and singly infested drone cells was not significantly different from random. This suggests the mites either cannot identify or do not preferentially enter already-infested cells and cannot discriminate between co-foundresses based on relatedness.

The increased reproductive success for Varroa when foundresses co-infest a cell could suggest selection for an increased evolutionary rate, through outbreeding and recombination, in Varroa (Bell, 1982; Hamilton et al., 1990). This could be particularly important in our colonies where the evolution of host defenses means successful reproduction is less likely in singly infested cells but still possible in multiply infested cells. By contrast, the artificial selection pressure of human-applied acaricide treatments, where Varroa’s reduced reproductive success is not a trait of the infested pupa, means resistant haplotypes can rapidly approach fixation in a largely inbred population (Beaurepaire et al., 2017; González-Cabrera et al., 2016). As the distribution of Varroa in our colonies was not significantly different from random, it appears Varroa cannot detect or does not preferentially enter already-infested cells. However, particularly when mite density is low, a prospective foundress faces several trade-offs in deciding whether or not to infest a cell.

Varroa foundresses were more likely to reproduce successfully when multiply infesting a cell. However, the increased likelihood of mortality and reduced fertility after a long phoretic phase, outside of the honey bee pupal cell (Nazzi & Le Conte, 2016; Rosenkranz et al., 2010), could explain why mite-distribution was not significantly different from random in our colonies. When mite density in a colony is low, the search time for an already-infested cell increases (Fuchs, 1992). Eventually, it could be expected that the fitness cost of entering an uninfested cell, and undergoing an inbred or failed reproductive cycle, will become less than that of continuing the search and risking reduced fertility or mortality (Charnov, 1976; Nazzi & Le Conte, 2016; Parker & Maynard Smith, 1990; Rosenkranz et al., 2010). This could explain why we detected significant differences in Varroa’s reproductive success between singly and multiply infested cells but not in the distribution of Varroa among cells; any mechanism to detect and preferentially enter already-infested cells may not be used often enough to warrant its maintenance by selection. Therefore, the only criterion Varroa uses when deciding to enter a cell is whether it is of the right age, although this leaves open the question of why Varroa is still more likely to successfully reproduce when infesting a cell with other foundresses, that could be the result of local mate competition (Hamilton, 1967).

It has previously been shown that the number of Varroa daughters per-mite decreases as the number of infesting mites per-cell increases; a consequence of fewer eggs per-foundress rather than complete nonreproduction by some mites (Fuchs & Langenbach, 1989). With Varroa’s first egg being male, this shifts the sex ratio from 22:78 toward 50:50 (Fuchs & Langenbach, 1989; Hamilton, 1967). It has been hypothesized that Varroa require the presence of specific host compounds, above a minimum threshold, in their diet in order to successfully initiate a reproductive cycle (Conlon et al., 2019). However, the presence of another female mite may reduce this threshold. Varroa could then invest the limited resources at its disposal in at least one unfertilized egg, a haploid male, in an attempt to benefit from the reproductive investment of another female. This reduced investment in offspring could be an adaptation to overcome the fitness costs associated with increased competition for food, and valuable host compounds, when co-infecting a cell. Reduced individual investment in a reproductive cycle, when co-infesting pupal cells, could therefore help Varroa overcome host resistance when mite density is high.

Acaricide treatment prevents Varroa resistance from evolving in many managed honey bee colonies, thereby preventing the evolution of a stable host–parasite relationship (Bell, 1982; Hamilton et al., 1990). Our results show that, when Varroa resistance is allowed to develop by natural selection (Fries & Bommarco, 2007; Kefuss et al., 2015), it is possible for a host–parasite relationship to evolve. The increased reproductive success we identify when Varroa co-infests the drone pupae of resistant honey bee colonies means that, in contrast to acaricide-treated colonies (Beaurepaire et al., 2017; González-Cabrera et al., 2016), there may be selection for outbred offspring. This, combined with a small proportion of Varroa reproducing in each generation, could reduce the selective pressure for the evolution of more virulent counter resistance traits and result in a more stable host–parasite relationship.

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Conflict of Interest

None declared.

Author Contributions

Benjamin H. Conlon: Conceptualization (equal); data curation (equal); formal analysis (equal); investigation (equal); methodology (equal); writing – original draft (lead); writing – review & editing (equal). Chedly Kastally: Data curation (equal); formal analysis (equal); investigation (equal); methodology (equal); writing – review & editing (equal). Marina Kardell: Investigation (supporting); writing – review & editing (supporting). John Kefuss: Investigation (supporting); methodology (supporting); writing – review & editing (supporting).
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Robin F. A. Moritz: Conceptualization (equal); methodology (equal); resources (equal); supervision (supporting); writing – review & editing (supporting). Jarkko Routtu: Conceptualization (equal); funding acquisition (equal); methodology (equal); project administration (equal); supervision (lead); writing – review & editing (equal).

DATA AVAILABILITY STATEMENT
Colony screening and microsatellite data are available from Dryad: https://doi.org/10.5061/dryad.15dv41ntz.

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