Addicted? Reduced host resistance in populations with defensive symbionts

Julien Martinez1,†, Rodrigo Cogni1,2,†, Chuan Cao1, Sophie Smith1, Christopher J. R. Illingworth1 and Francis M. Jiggins1

1Department of Genetics, University of Cambridge, Cambridge, UK
2Departamento de Ecologia, Instituto de Biociências, Universidade de São Paulo, 05508 900 São Paulo, SP, Brazil

†First authors.

Heritable symbionts that protect their hosts from pathogens have been described in a wide range of insect species. By reducing the incidence or severity of infection, these symbionts have the potential to reduce the strength of selection on genes in the insect genome that increase resistance. Therefore, the presence of such symbionts may slow down the evolution of resistance. Here we investigated this idea by exposing Drosophila melanogaster populations to infection with the pathogenic Drosophila C virus (DCV) in the presence or absence of Wolbachia, a heritable symbiont of arthropods that confers protection against viruses. After nine generations of selection, we found that resistance to DCV had increased in all populations. However, in the presence of Wolbachia the resistant allele of pastrel—a gene that has a major effect on resistance to DCV—was at a lower frequency than in the symbiont-free populations. This finding suggests that defensive symbionts have the potential to hamper the evolution of insect resistance genes, potentially leading to a state of evolutionary addiction where the genetically susceptible insect host mostly relies on its symbiont to fight pathogens.

1. Introduction

Pathogens impose strong selection on populations leading to the evolution of numerous adaptations to resist attack, as exemplified by the diversity of immune defences. In addition to resistance mechanisms encoded by the nuclear genome, organisms can also be associated with symbionts that protect them against infection. These defensive symbionts have been found in a diverse array of taxa [1–6]. Many of the best-studied examples are vertically transmitted bacterial symbionts in arthropods, such as Hamiltonella defensa that protects the pea aphid against hymenopteran parasitoids [7] or Wolbachia that protects Drosophila and mosquitoes against viruses [4,8,9].

The evolution of resistance through symbionts likely differs from the evolution of resistance provided by host genes in several important ways. Although rare on an ecological timescale, over evolutionary times these host–symbiont associations are characterized by extensive horizontal transmission, with frequent gains and losses of the symbiont [10,11]. The acquisition of a defensive symbiont may be a fast way to immediately gain complex adaptations encoded by many genes [10]. This allows the horizontal transfer of adaptations between species, in an analogous way to plasmid transfers in bacteria [12]. On the other hand, these defensive symbionts can be a very costly form of defence [13–17]. For example, the Wolbachia strains that provide the strongest antiviral protection are associated with substantial reductions in other fitness-related traits, such as fecundity, male fertility, egg viability or lifespan [15,18,19]. This trade-off between protection and cost is thought to be mediated by Wolbachia density, as strong antiviral protection requires a high symbiont density [19–21].

The presence of a defensive symbiont may affect the evolution of resistance mechanisms encoded by the nuclear genome. The acquisition of a defensive...
symbiont can lead to a redundancy of function where both host and symbiont genes contribute to the same biological process. Therefore, the presence of a symbiont may reshape the fitness landscape of host nuclear genes by changing the strength of selection on these genes. This may be especially important because pathogens are continually evolving to evade or suppress host defences. Therefore, hosts may become more susceptible over time unless they are also evolving novel forms of defence. Potentially, a defensive symbiont could slow down the evolution of host-encoded defences. Indeed, by relaxing the selection on host genes, the presence of the symbiont may prevent the spread of new resistance alleles, resulting in a population composed of hosts genetically susceptible to pathogens. In an analogous example, resistance to parasitoid wasps was lost in Drosophila sechellia, likely as the result of this species feeding on fruit that contain a toxin that kills the parasitoids [22]. A similar loss of host-gene originated defences in host–symbiont associations would potentially leave the host population with an evolutionary addiction to its symbiont, as symbiont-free individuals would be vulnerable to infection.

The dynamics of host resistance genes, defensive symbionts and pathogens may be complex, as changes in the frequency of any one of these players may alter the frequency of the others. For example, the spread of a protective symbiont may reduce the prevalence of the pathogen, leading to negative frequency-dependent selection [3,23]. However, this will not always be the case. For example, Wolbachia bacteria commonly cause a reproductive manipulation called cytoplasmic incompatibility [24], and this could result in them being fixed within populations regardless of whether viruses are present. Similarly, some pathogens may have broad host ranges and be frequently transmitted between different species. In this case, the presence of a protective symbiont in a host species may have little effect on the rate at which this host is exposed to the pathogen if the dynamics of the pathogen is mostly influenced by its epidemiology in other species.

We have investigated these processes using the common insect symbiont Wolbachia. Many strains of Wolbachia can protect insects against viral infection, both increasing survival and reducing viral titres [4,8,20,21]. In most natural populations, Drosophila melanogaster is infected with a strain of Wolbachia that protects it against a wide range of RNA viruses, including a naturally occurring and highly pathogenic virus called Drosophila C virus (DCV) [25,26]. There is also considerable genetic variation in susceptibility to DCV that is caused by the insect genome, and 47% of this genetic variance can be explained by a single amino acid polymorphism in a gene called pastrel [27]. This was confirmed when flies from a different population were artificially selected for DCV resistance, which caused the resistant allele of pastrel to increase in frequency [28]. A number of other genes affecting DCV resistance have also been mapped [27,28] (C. Cao 2015, unpublished data), but these have always been of relatively small effect and the same gene has never been found by different studies.

Here we tested whether the defensive symbiont Wolbachia can slow down the rate at which insects evolve resistance to viruses. We exposed populations of D. melanogaster to DCV in the presence or absence of a protective Wolbachia strain for nine generations. We then measured DCV resistance in our populations after selection and followed changes in the frequency of the pastrel resistant allele. Our findings suggest that Wolbachia has the potential to slow down the evolution of host resistance.

### 2. Material and methods

#### (a) Fly population and Wolbachia infection

We used an outbred population of D. melanogaster that was founded from 1526 isofemale lines collected in 2014 in Coventry (UK) using traps baited with bananas. This original population was kept in the laboratory in large numbers for five generations at 25°C on a standard cornmeal diet (1% agar, 8.75% dextrose, 7.5% maize, 2% yeast, 3% nipagin). In order to control for Wolbachia infection, we introgressed the nuclear background of the outbred population into a cytotype infected with the Wolbachia strain wMelCs. For this, 100 males of the outbred population were crossed to 100 females of the wMelCs,b DrosDel w1118 isogenic line described elsewhere [15,19]. This backcross was repeated for six generations (assuming no selection this would lead to an average of 98% of the nuclear genome being replaced). Three independent introgression replicates were performed (1WC, 2WC and 3WC, table 1). Wolbachia-cured counterparts of these introgressed populations (1TC, 2TC and 3TC, table 1) were generated by raising them on Ready Mix Dried Food (Philip Harris) supplemented with 0.03% w/v tetracycline for two generations. After introgression and tetracycline treatment, the Wolbachia infection status was checked by PCR on 30 females per population (electronic supplementary material, S1). In order to homogenize the gut microbiota between Wolbachia-infected populations and their uninfected counterparts, the tetracycline-treated populations were then raised for one generation on standard cornmeal food on which 50 males of the Wolbachia-infected populations had been kept for 1 day and removed. Experiments were all performed more than two generations after tetracycline treatment.

#### (b) Virus production and infection

The DCV was produced in Schneider Drosophila line 2 (DL2) cells as described in [29] (see protocol in electronic supplementary material, S1). To infect flies with DCV, 3–6 day old flies were anaesthetized with CO2, then were stabbed in the left pleural suture on the thorax with a 0.15 mm diameter anodized steel needle (Austerlitz Insect Pins) bent 0.25 mm from the end and dipped into viral solution. The DCV solution was prepared on Ringer’s solution [30] to a viral dose of $7.7 \times 10^7$ TCID50 ml$^{-1}$. Following infection flies were placed at 18°C.
(c) Effect of Drosophila C virus infection with and without the symbiont

Within the gene pastrel the variant that is most strongly associated with resistance is a non-synonymous single nucleotide polymorphism (SNP) at position 521 (exon 6) that replaces Ala with Thr (named C521T [27]). We, therefore, used this SNP as a marker for the resistant allele of pastrel and measured the effect of DCV infection on the frequency of this SNP in our Wolbachia-free and Wolbachia-infected populations. We compared three treatments (100 female flies in each): no stabbing, stabbing with Ringer’s solution and stabbing with DCV solution (see the infection procedure described earlier). Flies were placed at 18°C in a vial (20 females per vial) of standard cornmeal food and transferred to fresh vials every 3 days. Dead flies were counted every day for 15 days. At the end, the flies that survived were frozen for DNA extraction and genotyping (see methods in electronic supplementary material, S1).

(d) Selection for virus resistance with and without the symbiont

Four different treatments were performed in parallel for nine generations with three replicate populations in each treatment: absence or presence of Wolbachia, infection with DCV or no viral infection (table 1). Populations were kept at 18°C in cages (90 mm diameter × 200 mm height) containing a 90 mm Petri dish of standard cornmeal food replaced every 3 days. For the DCV treatment, male and female flies were stabbed with DCV (as described above) at each generation. The experiment above showed that DCV infection led to strong selection favouring the resistant allele of pastrel, but not stabbing with DCV-free Ringer’s solution (see Results). Therefore, no stabbing was performed for the control populations during selection. Our finding that pastrel confers resistance to DCV and not wounding is supported by previous work. It was shown that pastrel is specifically associated with increased survival after stabbing with DCV infection [27], and did not increase survival after flies were stabbed with other viruses. Similarly, no differences were found in DCV resistance over 34 generations of experimental evolution between populations that were stabbed with sterile medium and non-stabbed populations [28].

For each population, a given generation was started with 150 males and 150 females 3–6 day old flies placed in a cage. Given the high DCV-induced mortality in the Wolbachia-cured populations, two cages were prepared in order to obtain a sufficient number of offspring, leading to a population size of 300 males and 300 females for these populations (1TDCV, 2TDCV and 3TDCV, table 1). After 13 days, adult flies were discarded and the eggs kept for the next generation. At the start of the selection (generation 0), the DCV-induced mortality 13 days post-infection (dpi) was 50% and 20% for 3TDCV, table 1). After 13 days, adult flies were discarded and the eggs kept for the next generation. At the start of the selection (generation 0), the DCV-induced mortality 13 days post-infection (dpi) was 50% and 20% for 3TDCV, and 0% for 2TDCV and 1TDCV. At the end of the selection experiment, the within-host Wolbachia density of the Wolbachia-infected populations was quantified by quantitative PCR on DNA extracted from 10 pools of 10 females per population (electronic supplementary material, S1).

(e) Drosophila C virus resistance assay

The level of resistance to virus infection was measured five generations after the selection experiment (see protocol above). Dead flies were recorded every day for 39 days after infection. For each infection treatment (DCV or Ringer control) and each replicate population, five independent vials were performed (100 flies in total). The same phenotypic assay was performed in parallel on the same populations but that were treated with tetracycline (for two generations, see protocol above) at the end of the selection experiment. Sixteen females per population from the same cohorts were genotyped and their Wolbachia infection status checked (electronic supplementary material, S1).

(f) Selection and dominance coefficient estimates

An inference model was applied in order to estimate selection and dominance coefficients from the data. We first derive an expression for the relative fitness of the C allele at locus 521. We describe the fitness of the heterozygote and homozygote genotypes as

\[ w_{CC} = 1 + s; \quad w_{CT} = 1 + hs; \quad w_{TT} = 1, \]

where \( s \) and \( h \) are, respectively, the selection and dominance coefficients. Assuming random mating, and that the C allele exists in the population with frequency \( p \) at some generation, the mean fitness of an individual genotype containing the C allele is given by

\[ w_C = p(1 + s) + (1 - p)(1 + hs), \]

while the mean fitness of an individual genotype containing the T allele is

\[ w_T = p(1 + hs) + (1 - p). \]

The ratio between these values is then given by

\[ \frac{w_C}{w_T} = \frac{1 + s(h + p - hp)}{1 + hsp}. \]

Expressing this in an alternative way, we then note that, if the mean fitness of an individual containing the T allele is rescaled to equal 1, the mean fitness of an individual containing the C allele may be expressed as \( 1 + S \), where

\[ S = \frac{s(h + p - 2hp)}{1 + hsp}. \]

Using this result, we described the propagation of the system in terms of \( p \) using the delta method described in [31]. Where the mean and variance of \( p \) are given at generation \( t \) by \( \mu_t \) and \( \sigma_t^2 \), then ignoring mutation, the values of the equivalent parameters at generation \( t + 1 \) are approximated by

\[ \mu_{t+1} = \frac{(1 + S)\mu_t}{1 + S\mu_t} \]

and

\[ \sigma_{t+1}^2 = \frac{1}{N} \left( \frac{(1 + S)\mu_t}{1 + S\mu_t} \right)^2 \left( \frac{(1 + S)\mu_t}{1 + S\mu_t} \right)^2 \sigma_t^2, \]

where \( N \) is the population size. Observed values of the different genotype frequencies at times \( t \) were denoted as

\[ \{n_{CC}^t, n_{CT}^t, n_{TT}^t\}. \]

Setting \( \sigma_t^2 = 0 \) the parameters \( \mu_t, s \) and \( h \) were optimized in order to fit the genotype frequency observations. A multinomial model was used for fitting, integrating over the distribution of
values of the frequency \( p \). Parameters were thus optimized to 
maximize the likelihood 
\[
\sum_{t} \log \left( \frac{N_{t}}{p_{t}} \right) (1-p_{t})^{N_{t}}
\]
where \( N_{t} \) was the total number of observations collected at time \( t \), and 
\( p_{t} \sim N(\mu, \sigma_{t}^{2}) \).

The integral was calculated via numerical approximation. 
Selection parameters were jointly inferred across replicate lines 
with or without Wolbachia; initial allele frequencies were learnt 
indeed independently for each experimental replicate. Given maximum-
likelihood estimates of \( \mu_{s} \) and \( h \), the frequency \( p_{t} \) of the C 
allele at time \( t \) is normally distributed with mean \( \mu_{s} \) and variance \( \sigma_{t}^{2} \); corresponding diploid allele frequencies may be estimated as 
\( p_{t}^{2}, 2p_{t}(1-p_{t}) \) and \( (1-p_{t})^{2} \).

In order to measure uncertainty in the inferred parameters, repeated 
sampling of the evolutionary models for lines with and without Wolbachia was conducted, generating likelihood 
surfaces for the distributions of \( s \) and \( h \) in each circumstance. 
In order to evaluate the extent to which each evolved population 
was adapted to an environment without Wolbachia, approximate 
estimates of the final fitness of each population, under these con-
ditions were calculated, being expressed relative to the final 
fitness of the line 1TDCV. Via repeated sampling, and considering 
the data without Wolbachia, we obtained sets of values 
\( \{s_{0}, h_{0}, \mu_{0}, L_{0}\} \) where \( s_{0} \) and \( h_{0} \) are proposed selection parameters, 
\( \mu_{0} \) are optimal mean allele frequencies at time \( t = 9 \) in 
each of three lines \( l \), conditional on \( s_{0} \) and \( h_{0} \) and \( L_{0} \) are the 
associated log likelihoods. Given these values, we can calculate the 
approximate fitness values 
\[
f_{(i,j)} = \mu_{(i,j)}^{2}(1 + s_{i}) + 2\mu_{(i,j)}(1 - \mu_{(i,j)})(1 + h_{i}p_{(i,j)}) + (1 - \mu_{(i,j)})^{2},
\]
which can be expressed relative to those values obtained from 
the line 1TDCV as 
\[
F_{(i,j)} = \frac{f_{(i,j)}}{f_{(1TDCV)}}.
\]

Denoting the value of \( i \) corresponding to the maximum-
likelihood value \( L_{i} \) as \( i^{*} \), and the log-likelihood difference 
\( \Delta_{i}(\gamma) = L_{i} - L_{0} \) then for lines grown without Wolbachia, relative 
fitness likelihood surfaces were calculated as the range \( [\min F_{(i,j)}, \max F_{(i,j)}] \) across the set of points \( i \) for which \( \Delta_{i}(\gamma) \geq \varepsilon \) for variable 
log-likelihood difference cut-offs \( \varepsilon \). To perform an 
equivalent calculation for lines grown with Wolbachia, multiple 
sets of selection parameters \( s_{0} \) and \( h_{0} \) were sampled from the no-
Wolbachia data, along with log-likelihood differences \( \Delta_{i}(\gamma) \). 
Final mean frequencies \( \mu_{(i,j)} \) were then sampled from the with-
Wolbachia data, along with their corresponding differences 
\( \Delta_{i}(\gamma) \), where \( j \) denotes the optimal parameter set derived from 
the within Wolbachia data. Next, where 
\[
F_{(i,j)} = \frac{f_{(i,j)}}{f_{(1TDCV)}}
\]
relative fitness likelihood surfaces were calculated as the range 
\( [\min F_{(i,j)}, \max F_{(i,j)}] \) across the set of points \( i, j \) for which 
\( \Delta_{i}(\gamma) + \Delta_{j}(\gamma) \geq \varepsilon \) for variable log-likelihood difference cut-offs \( \varepsilon \).

### Statistical analyses

Statistical analyses were performed in the R software package [32]. 
Survival rates after DCV infection were analysed using Cox’s 
proportional hazard mixed models (package coxme). The hazard ratio 
for a given replicate population is the probability of death occur-
rning at a given timepoint divided by the probability of death in 
the control population. Flies that were alive at the end of the 
experiment were treated as censored data. Following the tests of the 
fixed effects, pairwise comparisons between selection treatments 
were performed with Tukey honest significance tests (Tukey HSD) using the package multcomp. The changes in allele 
frequency during the selection experiment were tested separately 
for the selected and control populations using a generalized 
linear model (package lme4) with a binomial distribution. Wolbachia 
densities were analysed using a linear mixed-effect model 
(package lme4), with the data being log-transformed to reach the 
assumptions of normality and homoscedasticity.

In all analyses, the selection treatment and the Wolbachia 
infection status were treated as fixed effects and the replicate 
population and/or vial of flies as random effects.

### 3. Results

(a) The benefit conferred by host resistant allele 
depends on the symbiotic infection status

In natural \( D. \) melanogaster populations, most genetic variation 
in DCV resistance is caused by a polymorphism in a gene 
called pastrel [27]. We, therefore, assessed the effect of DCV 
infection on the survival of flies bearing the resistant 
and susceptible alleles of pastrel in our Wolbachia-free and 
Wolbachia-infected populations. Over 15 days post-infection 
we observed no mortality in non-stabbed flies, whereas stab-
bbing with Ringer’s solution induced around 5% mortality in 
both Wolbachia-free and Wolbachia-infected flies (figure 1a,b). 
The frequency of the pastrel resistant allele in the flies that 
survived was not significantly different between the Ringer 
and the ‘no stabbing’ treatments (figure 1c,d), indicating 
that the stabbing procedure does not select for or against 
the pastrel resistant allele.

By contrast, more than 60% of the flies stabbed with DCV 
died over 15 days in the absence of Wolbachia, whereas with 
Wolbachia only around 5% died (figure 1a,b), thus confirming 
the protective effect of Wolbachia. Moreover, the frequency of 
the pastrel resistant allele was significantly higher in flies 
surviving the virus infection in the absence of Wolbachia, 
whereas no significant change was detected in the presence 
of Wolbachia (figure 1c,d). Therefore, the benefit of the resis-
tant allele of pastrel to DCV-infected flies is weaker in the presence 
of Wolbachia.

(b) Artificial selection increases \( Drosophila \) C virus 
resistance

Over nine generations we infected Wolbachia-infected and 
Wolbachia-free populations of \( D. \) melanogaster with DCV, 
and then measured whether resistance to the virus had 
increased. Upon DCV infection, the survival of the selected 
populations had increased relative to the controls, regardless 
of whether they were infected with Wolbachia (figure 2a and 
table 2a; Tukey HSD, both \( p < 0.0001 \)). As expected, the 
populations that were infected with Wolbachia also had sub-
stantially higher survival rates (figure 2a and table 2a; 
Tukey HSD, both \( p < 0.0001 \)). To check whether the change 
in survival reflected a change in DCV resistance, we also 
mock-infected flies with saline solution. These control flies 
all showed high survival, and there was no effect of the selec-
tion treatment or Wolbachia on their mortality rate (electronic 
supplementary material, figure S1a; table 2b).
To investigate how Wolbachia affected the strength of selection on pastrel, we followed the frequency of the pastrel resistant allele across the nine generations of selection. The resistant allele was initially at intermediate frequencies and increased in frequency across generations in all DCV-exposed populations (electronic supplementary material, table S1a; figure 3a). However, the rate of increase was slower in the Wolbachia-infected populations (electronic supplementary material, table S1a; figure 3a). In the absence of Wolbachia the resistant allele was fixed, but it only reached a mean frequency of 77% in the Wolbachia-infected populations. In control populations that were not exposed to DCV there was a slight overall decrease in pastrel resistant allele frequency between the beginning and the end of the selection experiment (electronic supplementary material, table S1b) but no effect of Wolbachia (electronic supplementary material, table S1b).

(c) Host-resistant allele reaches a lower frequency in populations infected with Wolbachia

To quantify the effect of Wolbachia on the strength of selection, we estimated the selection coefficient $s$ and the dominance coefficient $h$ of the pastrel resistant allele. We modelled the average fitness of the three genotypes $\tilde{w}$ as:

$$\tilde{w}_{CC} = 1 + s,$$

$$\tilde{w}_{CT} = 1 + hs,$$

and $$\tilde{w}_{TT} = 1,$$

where $T$ is the susceptible allele and $C$ the resistant allele.

Using this model to estimate changes in genotype frequency during selection, there is a striking effect of Wolbachia. In populations with the symbiont, 50% or less of the population is homozygous for the resistant allele (figure 3d). However, in the symbiont-free populations approximately 90% or more of the populations are homozygous resistant (figure 3d). Plotting the likelihood surface for our estimates of $s$ and $h$ from the model clearly highlighted a difference in the mode of selection between the two populations (figure 3b).

Figure 1. Effect of DCV infection on fly survival and the frequency of the resistant allele of pastrel. Survival of female flies following infection in (a) the Wolbachia-free and (b) the Wolbachia-infected populations. Frequency of the pastrel resistant allele in surviving flies 15 days after infection in (c) the Wolbachia-free and (d) the Wolbachia-infected populations. $p$-Values were obtained from a Dunnett’s test comparing all treatments to the non-stabbed control flies. n.s., non-significant differences. Error bars are standard errors.
Results from the evolutionary model showed that, in the absence of *Wolbachia*, the homozygote resistant genotype was clearly fitter than the heterozygote or homozygote susceptible genotypes (figure 3b). However, in the presence of *Wolbachia*, the maximum-likelihood fitness of the heterozygote genotype was increased (relative to the fitness of the susceptible genotype in the same environment), while the fitness of the homozygote-resistant genotype was decreased, such that the relative ordering of these fitnesses could not be firmly established. As a consequence, and in agreement with the observed data, the heterozygote genotype was inferred to exist in the population at significant frequencies in *Wolbachia*-infected populations at the end of the experiment (figure 3d).

In the control populations that were not infected with DCV there was no evidence of selection favouring either the resistant or susceptible allele of *pastrel*. The, resistant homozygotes, heterozygotes and susceptible homozygotes were all inferred to have similar fitnesses in both the *Wolbachia*-free and *Wolbachia*-infected populations (electronic supplementary material, figure S2bc).

(d) Changes in allele frequency correlate with *Drosophila* C virus resistance

The inferred evolutionary model suggests that flies evolved in the presence of *Wolbachia* would have a reduced inherent viral resistance, when *Wolbachia* was removed, than those flies that had been selected for without symbiont protection. The mean fitnesses of fly populations evolved with *Wolbachia* were inferred to be between 75% and 90% of the equivalent values for fly populations that had evolved without symbiont protection (figure 3c). To examine this experimentally, we treated all populations with tetracycline for two generations and examined the resistance to DCV after the removal of *Wolbachia*. Populations that had been selected for DCV resistance survived longer (figure 2b and table 2c). Although populations selected

![Figure 2. Survival of female flies upon DCV infection after selection. (a) Susceptibility to DCV at the end of the selection experiment and (b) after subsequent *Wolbachia* removal. Curves show for each replicate population the average proportion of live flies after infection.](dsb)
in the presence of Wolbachia tended to be more susceptible than those selected without the symbiont (figure 2b), this difference was not statistically significant (table 2c). This might be the result of a lack of statistical power due to the strong between-replicate variation, especially in the control populations. Alternatively, there could be other explanations such as the involvement of polymorphisms other than pastrel or the presence of transgenerational effects affecting DCV resistance. Mock-infected flies all showed high survival, and there was no effect of the selection treatment or Wolbachia (electronic supplementary material, figure S1b; table 2d).

As the presence of Wolbachia was associated with a lower frequency of the resistant allele of pastrel, we examined how the frequency of the allele correlated with changes in resistance. To do this, we compared the survival rates and allele frequency estimates described above. Before the populations were cured of Wolbachia, the frequency of pastrel resistant allele was negatively correlated with the DCV-induced mortality (linear model: $F_{1,8} = 16.87$, $p = 0.003$; figure 4a). Wolbachia greatly increased resistance also (linear model: $F_{1,8} = 136.2$, $p < 0.0001$; figure 4a), but there was no interaction between the effects of the symbiont and pastrel (linear model: $F_{1,8} = 0.05$, $p = 0.83$; figure 4a). The presence of Wolbachia can explain 85% of the variation in resistance among populations, while pastrel frequency explains only 10%. After removal of Wolbachia, the frequency of the pastrel resistant allele was also negatively correlated with virus-induced mortality ($r = -0.86$, d.f. = 10; $p = 0.0003$) and can explain 77% of the variation in resistance (figure 4b). Therefore, the frequency of the resistant allele of pastrel in a population affects its resistance to DCV.

(e) Selection for Drosophila C virus resistance did not affect Wolbachia density

As higher densities of Wolbachia are associated with higher protection against viruses, we tested whether we selected for higher symbiont densities in the populations exposed to DCV. We found no evidence that this had occurred, as selected and control populations had similar symbiont densities (linear mixed-effect model: d.f. = 1; $p = 0.69$; electronic supplementary material, figure S3).

4. Discussion

We have found that the presence of a protective symbiont in a population can affect how selection acts on host alleles that protect against infection. We, therefore, suggest that one long-term consequence of being associated with a defensive symbiont could be that conventional immune defences encoded by the host genome become less effective in individuals without the symbiont, such that losing the symbiont would leave the host
Antiviral immune genes would be a good model to test such a hypothesis as they often evolve exceptionally fast, which is thought to be due to an arms race with viruses [34–36]. We would predict that insect taxa in which Wolbachia is highly prevalent may show slower rates of evolution of these genes.

A key feature of our experimental design is that all individuals in the symbiont-infected populations carried Wolbachia, which reflects many natural populations where Wolbachia is near fixation. This is often thought to be because the symbiont is causing cytoplasmic incompatibility [24], and the prevalence of the symbiont is, therefore, independent of its defensive role. While this situation may be common for Wolbachia, other defensive symbions are present at an intermediate prevalence in the population [37–39]. Here the dynamics of host resistance alleles and defensive symbions may be more complex, as changes in population becoming dependent on its symbiont to ensure resistance against natural enemies—a form of evolutionary ‘addiction’ where the symbiont substitutes for host immune defences. If the selection exerted by pathogens is durable, then symbiont infection could become a state from which a host population cannot escape.

We investigated the interaction between D. melanogaster and its viral pathogen DCV, where the main factors that determine host susceptibility are the presence of the symbiont Wolbachia [4,8,20,21] and a polymorphism in the host-gene pastrel [27,28]. In populations where all the individuals were infected with Wolbachia, we found that exposure to DCV led to the resistant allele of pastrel reaching a lower frequency than in symbiont-free populations. The presence of Wolbachia substantially altered the relative fitnesses of both the homozygote- and heterozygote-resistant genotypes, suggesting that the symbiont may alter the fitness landscape of host resistance in complex ways. It is conceivable that the DCV-induced mortality may follow a nonlinear relationship with the amount of virus within the flies so that the lower virus titres reached in the presence of Wolbachia could blur the difference in fitness between heterozygotes and resistant homozygotes. Removing the symbiont alters the fitness landscape experienced by the host, reducing the fitness of virus-infected hosts compared with populations that evolved without the symbiont. While noting a clear difference between the observed populations, we note that the estimated selection and dominance coefficients should be treated with some caution as they may be affected by unknown complexities that are not accounted for in our model. For example, there may be multiple alleles of pastrel [27], infection itself may have transgenerational effects on resistance, or other loci may modify the effect of pastrel.

Wolbachia is thought to infect 52% of terrestrial arthropod species [33], and in the laboratory as many as half of the strains sampled confer resistance to viruses in a Drosophila host [21]. Although it is not clear yet the extent to which Wolbachia-mediated protection is at play in natural conditions, it clearly has the potential to have an important influence on the evolution of host-encoded antiviral resistance in many species. Antiviral immune genes would be a good model to test such population vulnerable to infection. This may result in the host population becoming dependent on its symbiont to ensure resistance against natural enemies—a form of evolutionary ‘addiction’ where the symbiont substitutes for host immune defences. If the selection exerted by pathogens is durable, then symbiont infection could become a state from which a host population cannot escape.

Figure 4. Correlation between DCV-induced mortality and the frequency of the pastrel resistant allele. Each dot represents the mean value of the trait for a given population that evolved without (blue) or with Wolbachia (red), (a) at the end of the selection experiment and (b) after subsequent Wolbachia removal. Squares: control populations; circles: selected populations. DCV-induced mortality is expressed as the ln of the hazard ratio estimated using a Cox’s mixed-effect model. The hazard ratio is the probability of mortality at a given time point relative to a control treatment. Here the control is the replicate population TIC that belongs to the control for the selection treatment (not selected for DCV resistance). Dashed lines indicate regressions inferred from a linear model.
suggesting the absence of strong costs associated with the pastrel resistant allele. Overall, it seems likely that symbiont-mediated protection is a more costly form of defence in this system.

Finally, a number of other factors may tip the balance in the favour of defensive symbions or host genes. If symbiont transmission between generations is imperfect, then the symbiont will spread more slowly. However, symbiont protection can spread in a population even if pathogens are rare if the symbiont is also able to manipulate its host reproduction [43]. Although Wolbachia shows a rather poor ability to manipulate reproduction in *D. melanogaster* [44,45], in other host species it induces strong sex-ratio distortion or cytoplasmic incompatibility that drives it through host populations independently of any beneficial effects [24,46].

Pathogens will also select for host and symbiont genes that increase the level of protection provided by the symbiont. In our experiments, this could be achieved by increasing the within-host density of Wolbachia, as antiviral protection is tightly linked to symbiont density and Wolbachia strains within *D. melanogaster* populations vary genetically in their density [19]. However, we did not observe such a change, suggesting that there was insufficient time, genetic variation or selection for this to occur. In particular, the symbiont strains that reach the highest density can reduce the lifespan of flies or other fitness-related traits [15,17–19], and this may have prevented them from spreading in the population.

Defensive symbions have been described in several associations, but their impact on the evolution of host defences has been poorly explored (but see [23]). We have shown that such symbionts have the potential to influence the short-term and possibly the long-term evolution of insect defences against viruses. Investigating how insect populations respond to the presence of symbions is a prerequisite to understand the evolution of symbioses. From an applied perspective, it is becoming more important to predict host evolutionary responses to the presence of defensive symbions, as Wolbachia is being introduced on a large scale into mosquito populations to block the transmission of arboviruses [47,48].

### References


