Sexual conflict and STDs: coevolution of sexually antagonistic host traits with a sexually transmitted disease

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Abstract

In many taxa, there is a conflict between the sexes over mating rate. The outcome of sexually antagonistic coevolution depends on the costs of mating and natural selection against sexually antagonistic traits. A sexually transmitted disease (STD) changes the relative strength of these costs. We study the three-way coevolutionary interaction between male persistence, female resistance, and STD virulence. By increasing the cost of mating, an STD escalates conflict between the sexes. The increased host mortality resulting from heightened sexual conflict, in turn, selects for increased STD virulence. Accelerating costs of the sexually antagonistic traits and diminishing benefits of virulence prevent unbounded escalation. Successful invasion by an STD becomes less likely if hosts are evolvable, especially if only the female trait can evolve. These results show that the evolution of both host and parasite traits operate differently in systems characterized by sexual conflict rather than by female mate choice.

Impact Summary

In nature, males tend to be more persistent than females when pursuing mates. Traits that increase male persistence (*e.g.* aggressiveness) can be harmful to females, selecting for resistance traits in females that dissuade male advances and reduce the mating rate. The conflict between the sexes over mating rate can give rise to a coevolutionary arms race between persistence and resistance traits; if female resistance increases to reduce the costs of mating, male persistence also increases to maintain high male mating rates. Sexually antagonistic traits that carry an accelerating energetic or ecological cost will not increase indefinitely but plateau at intermediate values defining the degree of conflict escalation. The degree of conflict escalation depends on the relative costs of expressing sexually antagonistic traits and the cost of mating to females. Sexually transmitted diseases (STDs), by definition transmitted via mating, have the potential to increase the costs of mating for both sexes and alter the outcome of the coevolutionary arms race. Moreover, an STD can itself evolve to become more or less virulent and disease dynamics and selection on virulence are affected by host traits. We model the coevolution of male persistence, female resistance, and STD

virulence. Our results show that coevolution with an STD drives an increase in costly sexually antagonistic host traits; female resistance increases to reduce mating rates and thereby the risk of contracting the STD, driving a corresponding increase in male persistence. Elevated host trait values are accompanied by increased host mortality, which subsequently drives the evolution of higher STD virulence. Our coevolutionary model predicts a higher degree of conflict escalation in populations infected with an STD. Overall, our results suggest that host-parasite interactions could play an important role in coevolutionary arms races.

Introduction

Sexual conflict over mating rate arises because male reproductive success increases with mating rate while female reproductive success is maximized at some intermediate rate (Bateman, 1948; Arnqvist & Rowe, 2005). Males evolve persistence traits to increase their mating or fertilization rate that often cause harm to females physically or physiologically. Females, in turn, evolve resistance traits that deter males or offset the physiological harm. This conflict gives rise to sexually antagonistic coevolution between male persistence traits and female resistance traits, the outcome of which determines the mating rate. Sexually transmitted diseases (STDs) are, by definition, transmitted during mating and thus may play an important role in the evolution of host mating strategies. Here, we explore the interplay between STD virulence evolution and host traits mediating the sexual conflict over mating rate.

Virulence of an STD evolves in much the same way as that of an ordinary infectious disease (OID), *i.e.* evolutionary stable virulence is proportional to the natural host mortality rate and depends on the shape of the tradeoff between transmission and virulence (Knell, 1999). Surprisingly, evolutionarily stable virulence (ESS virulence) of an STD does not depend on the mating rate, though its spread and infection prevalence does (Lipsitch & Nowak, 1995; Knell, 1999). In turn, STDs are known to affect the evolution of mating strategies. Theory has focused on STDs in hosts with conventional sexual selection. Traditionally, STDs were thought to select for monogamy (Immerman, 1986; Immerman & Mackey, 1997) but subsequent models showed that STDs can maintain both monogamy and promiscuity in a population, as well as select for risky female choice

(Thrall et al., 1997; Boots & Knell, 2002; Kokko et al., 2002). (Female choosiness based on attractiveness of males is considered a risky strategy because the most popular males have the highest mating rate and are most likely to be infected.)

By altering the mating system, the STD changes its own ecological landscape, possibly setting the stage for coevolution. The outcome of coevolution can be hard to intuit. Indeed, there are several examples in the host-parasite literature of coevolution leading to different or unexpected outcomes than when considering the evolution of either host or parasite in isolation (Gandon et al., 2002; Day & Burns, 2003; Best & White, 2009). Of particular interest is a coevolutionary model of host mate choosiness with STD virulence (Ashby & Boots, 2015). An investigation of STD virulence in the absence of host coevolution showed that a parasite that reduces the mating success of its host should evolve to be less virulent. Knell (1999) suggested that hosts would subsequently lose disease-avoidance behaviours such as mate choice based on the degree of parasitism of potential mates. However, when the level of host choosiness based on parasitism was allowed to coevolve with STD virulence, Ashby & Boots (2015) found that intermediate levels of disease-avoidance behaviour and virulence could evolve, and that coevolutionary cycling could occur between host choosiness and STD virulence. These unexpected results emphasize the importance of considering the coevolutionary feedbacks of an STD with host mating system.

Over the last 25 years, it has become clear that, in many systems, sexual conflict over mating rate plays at least as large a role in shaping the evolution of male-female interactions as conventional sexual selection processes (Rice & Holland, 1997; Arnqvist & Rowe, 2005). In the absence of an STD, there are several possible outcomes of sexually antagonistic coevolution depending on the biology of the system. If male persistence and female resistance carry no inherent cost, traits will continually escalate in an evolutionary arms race (Gavrilets & Hayashi, 2006). Incorporating natural selection prevents runaway evolution (Gavrilets et al., 2001) and allowing for the evolution of female sensitivity can lead to female indifference to male traits, halting the coevolutionary process (Rowe et al., 2005). In all of these cases, only females suffer the cost of mating. Given that a sexually transmitted disease increases the cost of mating to both males and females it is not obvious how an STD will affect sexually antagonistic host interactions. Though classic theory

indicates that the ESS virulence of an STD is unaffected by mating rates, there remains the potential for host-parasite coevolution. Because the traits mediating sexual conflict are themselves costly, evolutionary changes in these traits driven by the emergence of an STD can alter host demography and create epidemiological feedbacks that drive subsequent STD evolution.

We model coevolution of an STD in a host system with sexual conflict over mating rate. Using an analytical model and individual-based simulations, we allow the STD to coevolve with male persistence and female resistance (host traits). We show that the presence of an STD escalates sexual conflict primarily because females are selected to reduce mating rates to avoid becoming infected. Escalation of the host traits mediating sexual conflict results in increased host mortality, which feeds back to affect the evolution of STD virulence. While stable equilibria for hosts and parasites are typical when genetic variation is present in all three traits, a lack of genetic variation in the parasite allows hosts to evolve to drive the STD extinct. Our results suggest that the observed levels of sexual conflict in natural systems could be affected by an STD and that sexual conflict can mediate both the establishment of an STD and its equilibrium level of virulence via coevolutionary feedbacks.

Model Setup

Analytical Model

We use a system of differential equations to describe sexually antagonistic coevolution in a population of haploid hosts (parameter definitions summarized in Table 1). A male‘s mating effort is determined by a persistence trait whereas a female tries to deter mating with a resistance trait; these traits may be morphological or behavioural. The probability of mating during an encounter between a male with persistence y and a female with resistance x is an increasing function of the difference $u = y - x$ as given by $\phi[u] = 1/(1 + e^{-u})$. The mating rate plays several important roles in the model. First, it affects female fecundity. Females have a maximum birth rate b that can be decreased by density-dependence if population size exceeds the carry capacity K and by the probability of not mating, given by $\gamma[M] = (1 - \phi[u])^{\alpha M}$ (where α is the encounter rate and M is

the density of males). The mating rate also affects female mortality as females pay a viability cost d per mating. The total cost of mating depends on the number of males a female mates with, which is, on average, $\alpha M \phi[u]$. Males and females suffer baseline mortality rates, μ_m and μ_f, respectively, and face nonlinearly increasing costs of expressing their respective sexually antagonistic traits. A male pays a mortality cost for his persistence trait; the strength of this cost is ce^y where c is the "persistence cost" parameter. Likewise, a female pays a mortality cost for her resistance trait given by δe^y where δ is the "resistance cost" parameter. Natural selection against these constitutively expressed sexually antagonistic traits, together with the cost of mating experienced by females, results in three costs incurred by hosts (persistence costs to males and resistance and mating costs to females). The ecological dynamics are captured by the following system of equations:

$$\frac{dM}{dt} = \frac{1}{2}Fb(1 - \frac{M+F}{K})(1 - \gamma[M]) - (ce^y + \mu_m)M \tag{1a}$$

$$\frac{dF}{dt} = \frac{1}{2}Fb(1 - \frac{M+F}{K})(1 - \gamma[M]) - (d\alpha M\phi[u] + \delta e^x + \mu_f)F \tag{1b}$$

We find evolutionary stable (ESS) persistence and resistance, y^* and x^*, respectively, using sequential evolutionary invasion analyses for multiple traits (see Supplementary Material).

We introduce a sexually transmitted disease into the model by dividing the host population into susceptible and infected classes. Susceptible individuals may contract the disease by mating with infected individuals of the opposite sex. We model transmission of the STD as density-dependent because it is reasonable to assume that the number of matings per capita will increase with density in systems governed by sexual conflict (*i.e.*, at high density, females encounter more males and thus are likely to end up mating more total times holding x and y constant). To determine a female's full cost of mating, we must track the expected number of males a female mates with and not just the fraction of her mates that were infected (as would be done under frequency-dependent transmission). Density-dependent sexual disease transmission has been documented in nature (for example in two-spot ladybird beetles, *Adalia bipunctata*, Ryder et al. 2005).

STD virulence, v, results in higher mortality of disease carriers. We assume a tradeoff between

transmission and virulence such that the transmission rate during mating is a saturating function of virulence $\beta[v] = v/(w+v)$, where w determines the shape of the function (*i.e.*, low values of w cause the transmission benefits of increased virulence to saturate more quickly). The epidemiological dynamics are described by the following set of differential equations:

$$\frac{dS_m}{dt} = \frac{1}{2}\psi[S_m, S_f, I_m, I_f] - \alpha I_f \phi[u]\beta[v]S_m - (ce^y + \mu_m)S_m \tag{2a}$$

$$\frac{dS_f}{dt} = \frac{1}{2}\psi[S_m, S_f, I_m, I_f] - \alpha I_m \phi[u]\ \beta[v]S_f - (d\alpha(S_m + I_m)\phi[u] + \delta e^x + \mu_f)S_f \tag{2b}$$

$$\frac{dI_m}{dt} = \alpha I_f \phi[u]\beta[v]S_m - (ce^y + \mu_m + v)I_m \tag{2c}$$

$$\frac{dI_f}{dt} = \alpha I_m \phi[u]\ \beta[v]S_f - (d\alpha(S_m + I_m)\phi[u] + \delta e^x + \mu_f + v)I_f \tag{2d}$$

where

$$\psi[S_m, S_f, I_m, I_f] = b(S_f + I_f)\left(1 - \frac{S_m + S_f + I_m + I_f}{K}\right)(1 - \gamma[S_m, I_m]) \tag{3}$$

Similar to the STD-absent model, we find ESS persistence (y^*), resistance (x^*), and virulence (v^*) using evolutionary invasion analyses for multiple traits (see Supplementary Material).

Individual-Based Simulation

We also carried out individual-based simulations, relaxing some of the simplifying assumptions in the model. We allowed the hosts to be diploid instead of haploid and used discrete time steps (*i.e.*, breeding seasons). Variation in host and parasite traits were generated by random mutation such that many different alleles (of differing effect size) for each trait could be segregating in the population at a time. In comparison, the analytical model assumes a separation of ecological and evolutionary timescales (*i.e.* the population always reaches ecological equilibrium before a new mutant is introduced). Furthermore, the analytical model uses a sequential invasion analysis, meaning that a small-effect mutant of one trait fixes in the population before a mutant of another trait is introduced, thereby avoiding the complications that could arise from genetic correlations between

male and female traits; such correlations can develop in the simulation. In the individual-based simulation model, we change the assumption of density-dependent sexual disease transmission. We model a form of frequency-dependent transmission that assumes females always encounter a specified average number of males, with the actual number encountered by an individual female determined by a draw from a Poisson distribution with a mean that is independent of density. A female mates with each encountered male with probability $\phi[u]$ (as defined for the analytical model) . The probability of mating with an infected individual therefore depends on the fraction of infected males amongst all males. Individual-based simulations were carried out in Python for $50,000$ generations, well after the trait values appeared to reach evolutionary equilibrium. Values from the last 1000 generations were averaged and reported in Figs. 1 and 4. A detailed description of the simulation model is provided in the Supplementary Material.

Results

Evolution of Host Traits without STD

To understand how a coevolving sexually transmitted disease affects the outcome of sexually antagonistic coevolution we first consider how the host evolves in the absence of an STD (which has been previously studied, *e.g.* Gavrilets et al. 2001). In the main text we focus on the results of the individual-based simulations (numerical solutions to the analytical model, provided in the Supplementary Material, show similar patterns). To help us understand how the mating rate changes with various costs we plot the difference between male persistence and female resistance, $u = y - x$, in Fig. 1A. The average of the two trait values, $(y + x)/2$, is an indicator of the magnitude of the traits (thereby, the degree of escalation of conflict) and is plotted in Fig. 1C. Higher values (represented by lighter colours) correspond to higher mating rates (Fig. 1A) or a higher degree of conflict escalation (Fig. 1C). The evolutionary equilibrium trait values presented in Fig. 1 and all subsequent figures are stable to different initial values with the exception of very low initial virulence of the STD (which goes extinct due to lack of transmission).

For the range of parameters shown in Fig. 1, male persistence y always exceeds female resistance

x, so the difference u is positive and mating rates are not too low on average. Increasing persistence costs (to males) decreases the difference between male and female traits (u) (Fig. 1A). Mating rate also decreases with increasing mating costs (to females) because females are selected to increase resistance (Fig. 1A). As the cost of the female's resistant trait (resistance cost) increases, u increases as females with lower resistance better balance the tradeoff between sexually antagonistic selection and natural selection (data not shown). We observe negative differences between male persistence and female resistance ($u < 0$) when resistance costs are very small or zero; this results in very low mating rates. We do not explore this area of parameter space in depth because an STD cannot spread at low mating rates.

The extent of conflict escalation, as reflected by average trait values, increases substantially as the female mating cost increases (Fig. 1C). This is driven by the female trait increasing to reduce the mating rate, while the male trait increases slightly in response. Males with higher persistence have more mating success but must pay the nonlinearly increasing cost of natural selection against persistence. Average trait values do not change drastically with increasing persistence costs.

Evolution of Host Traits with Coevolving STD

We now consider evolution of the host traits in the presence of a coevolving sexually transmitted disease and then later discuss virulence of the STD. Introducing a coevolving STD escalates the conflict between the sexes. This increase is driven by females. If only the females are allowed to evolve (not shown), female resistance will evolve to be higher than male persistence to reduce the additional cost of mating arising from the risk of STD infection. In this case, $u = y - x$ is negative and the mating rate drops below 0.5. The STD cannot persist at low mating mates. In contrast, if only the males are allowed to evolve (not shown), male persistence increases from its STD-absent equilibrium, presumably because males are selected to more quickly obtain additional mates in the face of higher mortality rates due to infection (though the change is smaller compared to the case where females evolve). In this case the STD does not go extinct because mating rates remain high (as u increases). When females and males can both evolve, the increase in female resistance invokes a subsequent increase in male persistence so males ensure mating. Female values increase

more than male values thereby reducing the difference between them (Fig. 2). As such, the net effect of co-evolutionary feedback tends to be increased average trait values (*i.e.*, increased conflict escalation) and decreased differences between traits compared to when the STD is absent, in both the simulation (Fig. 1) and analytical (Fig. S1) models. It is worth emphasizing that the evolution of male persistence in response to the escalation in female resistance allows the STD to remain in the system. If a lack of genetic variation in the male trait prevented its coevolution, the STD would go extinct after female resistance increased and caused a decrease in mating rates.

Compared to the disease-absent model, we observe similar trends in average trait values and differences between traits with changing persistence and mating costs (Figs. 1 and S1). However, the difference between traits is less sensitive to the mating cost in the presence of a coevolving STD (Fig. 1B). This is likely because u is on average lower following the introduction of the STD. Consequently, females are mating less and female resistance evolution is driven more by trying to reduce the costs associated with acquiring an STD than by trying to reduce the cost of mating. Additionally, the degree of conflict escalation (as shown by the average trait values, Fig. 1D) is more sensitive to changes in persistence costs than in the absence of the STD because of coevolutionary feedbacks between STD virulence and sexually antagonistic host traits.

Establishment and Virulence of the Sexually Transmitted Disease

In the section above, we focused on cases where both hosts and parasites can evolve and the disease establishes itself within the host population. (We use the term disease "establishment" rather than the more typical term "persistence" to avoid confusion with the host male's "persistence" trait.) We now focus on understanding how a lack of genetic variation that prevents evolution of either host or parasite traits affects both the establishment and virulence of the STD. We discussed one important case above in which a lack of genetic variation in the male trait but not the female trait prevents the establishment of a coevolving STD. Here we focus on contrasts between hosts and parasites in their evolvability (rather than on differences in evolvability between male and female host traits).

When neither the host nor parasite can evolve, an STD near its equilibrium virulence always

persists when introduced into host populations at equilibrium except for rare stochastic extinctions (for the parameter values considered here). In comparison, a relatively avirulent STD will almost always go extinct and a highly virulent STD will only persist if mating rates are sufficiently high (requiring large positive values of u).

If the host but not the parasite can evolve, then females are selected to increase resistance in the presence of an STD, driving an increase in average host trait values and a decrease in the difference between the sexes. The accompanying decrease in mating rate can drive a highly virulent, non-evolving STD extinct if the difference between host trait values becomes small enough (*i.e.* at high persistence costs to males and high mating costs to females). In Fig. 3A we show the fraction of runs in which the parasite went extinct when hosts can evolve but parasites cannot. Extinction rates are higher over a wider range of parameter values when female resistance costs are low ($\delta = 0.001$, data not shown). As noted above, STD extinction is even more likely if the female trait can evolve but the male trait cannot. For any of the parameter values shown in Fig. 3 the STD is unable to invade if only the female host trait evolves (not shown).

If the STD can evolve but hosts cannot evolve, an initially virulent parasite does not go extinct for the parameters considered here (except rare stochastic extinctions) because virulence evolves down to a sustainable level. The evolutionary equilibrium virulence level, v', is typically lower than if hosts were coevolving (Fig. 4B) because average host trait values are lower in the absence of the STD (compare Fig.1C to D).

Finally we consider evolution in both the host and the STD. At negative ($u < 0$) or small positive ($u \sim 0$) differences between male persistence and female resistance, the mating rate is low enough that the STD goes extinct due to lack of transmission opportunity. Thus, when hosts and parasites coevolve, STD extinction occurs most often when the resistance cost to females is low (not shown). Even with higher resistance costs (*e.g.* $\delta = 0.0005$) STD extinction can occur if the persistence and high mating costs are high (Fig. 3B). At high mating costs, sexually antagonistic selection drives the female trait upwards and natural selection is not strong enough to keep female resistance far enough below male persistence to maintain sufficient STD transmission. Contrasting the findings without and with parasite evolution (Fig. 3A vs. B, respectively), we see that STD

coevolution with its hosts rescues the parasite from extinction.

Virulence of the Sexually Transmitted Disease

Conditional on establishment of the STD, the three-way coevolution of the STD with male and female traits gives rise to quantitatively different results than if the STD was introduced into a non-evolving host population (Fig. 4). In general, the STD becomes more virulent if hosts coevolve than if they do not. This is because the addition of the STD to the system causes evolutionary increases in female resistance and, consequently, male persistence, increasing the host mortality rate; optimal STD virulence is expected to increase with host mortality rate (Knell, 1999). The equilibrium virulence of the STD increases as the average host trait values increase and does not depend on the difference in trait values (*i.e.*, Figs. 4A and B mirror Figs. 1D and C, respectively). The difference in trait values only affects the spread and prevalence of the STD and not its evolutionary equilibrium virulence.

Discussion

We found that a sexually transmitted disease affects the outcome of sexual conflict. The introduction of an STD tends to result in hosts evolving a lower mating rate. Female resistance increases to reduce the additional cost of mating imposed by disease-induced mortality. As male persistence tries to stay above female resistance levels, average host trait values increase (*i.e.*, the conflict escalates). A co-evolving STD increases its virulence level in response to these changes in the host, not because of the change in host mating rate but rather because of the increased host death rate resulting from the escalated sexual conflict. The three traits reach a stable coevolutionary equilibrium. We find no evidence of cycling as has been observed under some conditions in a coevolution STD model involving conventional sexual selection Ashby & Boots (2015). Based on our understanding of why the observed changes occur, cycling is not expected.

Stabilizing selection maintains the coevolutionary equilibrium. Male persistence increases male reproductive success at the expense of increased mortality due to costs associated with persistence such as increased predation risk (Rowe, 1994) or reduced foraging time (Robinson & Doyle, 1985).

Females suffer costs of mating but must balance these with the direct cost of expressing the resistance trait and the risk of remaining unfertilized if resistance is too high. In the presence of an STD males experience stronger selection to obtain mates quickly in the face of higher total mortality and females experience stronger selection to reduce the additional cost of mating associated with a prevalent STD. The escalation of sexual conflict increases total host mortality, selecting for higher STD virulence, which in turn should drive further escalation of the sexual conflict traits. However, the "faster than linear" increasing costs to hosts of the escalating sexual conflict traits and the "slower than linear" increasing transmission benefits of increased STD virulence ensures that the system reaches an equilibrium rather than evolving to ever higher levels of all three traits.

One of the costs we did not explore in depth is the risk of females remaining unfertilized. In the simulation model, a female achieved her full fecundity provided that she mated with at least one male. However, if fertilization was not guaranteed by mating (*e.g.* we included a probability of fertilization given that a sexual encounter has occurred), the increased risk of being left unfertilized would affect the evolution of female resistance. Thrall et al. (1997) constructed a model investigating how male and female mating behaviour affected reproductive success in the presence of an STD. At high disease prevalence, females could achieve the same fitness by being monogamous and minimizing infection risk or by being promiscuous and minimizing the risk of being left unfertilized but increasing the risk of infection. It is possible that if there were higher probabilities of females being unfertilized in our model, divergent female strategies (low and high resistance) may be maintained.

We investigated the full three-way coevolutionary interaction over a range of mating costs to females. However, many empirical investigations of sexual conflict in natural systems have reported females suffer a cost of harassment instead of, or in addition to, the cost of mating (Alcock et al., 1977; Rowe, 1994; Stone, 1995; Jormalainen, 1998; Watson et al., 1998). At high male densities or male-biased sex ratios, the cost of rejecting harassing males can become so great that females are selected to decrease resistance, increasing overall mating activity in these systems (Rowe, 1992; Rowe et al., 1994; Lauer et al., 1996). However, the introduction of an STD would effectively increase the cost of mating, possibly tipping the balance in favour of high resistance for females.

The majority of models that have investigated the evolution of host mating strategies in the presence of an STD have assumed there is sexual selection, but no sexual conflict. The distinction between male attractiveness and female preference versus male persistence and female resistance has important consequences for the coevolution of an STD. Choosiness may help females gain indirect benefits from mating with a preferred male. Resistance on the other hand helps females avoid the direct costs of mating (Gavrilets et al., 2001). Unless indirect benefits are strong (Thrall et al., 1997; Boots & Knell, 2002), the presence of an STD will cause selection for non-choosy females because the most popular males have high infection prevalence (Thrall et al., 2000). In a system with sexual conflict, those males with the highest persistence traits would be more likely than average males to be infected, adding to the cost of mating for females. Females do not reduce their risk of mating with such males by having lower resistance (*i.e.*, lower resistance is not equivalent to being less choosy). A female with lower resistance may have a lower fraction of her matings with high persistence (probable STD-carrying) males but she will not have a fewer number of matings with such males. Moreover, she will have more total matings, increasing her infection risk. Consistent with this, we found that the presence of an STD resulted in increased female resistance, which might be construed as increased choosiness, opposite to what is observed in sexual selection models.

We have assumed that infection does not directly alter a male's persistence or a female's resistance. However, in some cases STDs manipulate host behaviour in ways that directly affect sexual conflict. An STD that influences male competitive ability could change the relative costs of mating. For example, parasitized males can be less competitive (Siva Jothy & Plaistow, 1999; Thomas et al., 1999), decreasing the risks of mating for females in a population with a highly prevalent STD. Conversely, as in the milkweed leaf beetle (Abbot & Dill, 2001), STD-infected males can be more aggressive than their uninfected counterparts, which could increase the number of matings and therefore the costs to females. Alternatively, the STD may manipulate host behaviour in such a way that its interests are aligned with one sex. It has been suggested that an STD that reduced female remating rate would be beneficial for males (Knell & Webberley, 2004) because a male that infects his mate would reduce her remating rate and ensure his own paternity. If the benefits

375 of reducing sperm competition outweigh the mortality costs of the STD, males may be selected
376 to increase persistence and consequently their likelihood of acquiring an STD. Similarly, there is
377 some evidence that infection by an STD increases oviposition rates in the fall army worm moth,
378 meaning that males could benefit from acquiring and transmitting an STD (Simmons & Rogers,
379 1994). There are numerous ways males and females could evolve in response to these changes in
380 host mating behaviour. However, all of these examples suggest that a change in the cost structure
381 in the presence of an STD could affect the outcome of sexual conflict, either increasing the differ-
382 ence between male persistence and female resistance such that males 'win', or further reducing the
383 difference between traits.

384 There are many well-known examples of STDs and sexual conflict but we are aware of no systems
385 where both are well studied. Evidence of sexual conflict and sexually transmitted diseases has
386 been reported in ungulates (conflict, Bro-Jørgensen 2010; STD, Lockhart et al. 1996), Drosophila
387 (conflict, *e.g.*, Rice et al. 2006; STD, Knell & Webberley 2004), and the two-spot ladybird *Adalia*
388 *bipuntata* (conflict, Haddrill et al. 2013; STD, Webberley et al. 2002; Ryder et al. 2005). Studies
389 of sexually antagonistic traits in populations infected with an STD should look for escalated trait
390 values compared to populations where the STD is absent. Research on STDs should compare
391 different populations or closely related host species that experience different costs of persistence to
392 males and costs of resistance and mating to females. Variation in the costs of sexually antagonistic
393 host traits could arise between populations if, for example, the persistence or resistance trait made
394 the bearer more vulnerable to predation in an open versus closed habitat (see Fricke et al., 2009, for a
395 discussion of the dependence of sexually antagonistic selection on environmental conditions). Higher
396 mortality rates in one habitat should select for higher virulence in an endemic STD. Additionally,
397 we expect lower disease prevalence (not shown) in populations where male persistence is strongly
398 selected against and there are high costs of mating for females.

399 We have shown that an STD has the potential to influence the outcome of sexually antagonistic
400 coevolution. Because STDs are ubiquitous in nature (Lockhart et al., 1996), they should co-occur
401 with sexual conflict often enough that it is worth considering how STDs change sexually antagonistic
402 selection. Furthermore, considering the full coevolutionary interaction has important implications

for both the susceptibility of a host population to invasion of a new STD and the level of virulence expected to evolve.

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Supplementary Material

Individual-Based Simulations

Below we describe the procedure for carrying out the individual-based simulations in Python (code available upon request).

Sexual Conflict

To initiate the population, diploid hosts are assigned trait values at the resistance and persistence loci by drawing random values from a normal distribution with mean $\bar{x}$ and $\bar{y}$, respectively, and variance 0.5. Each generation, females encounter a certain number of males, randomly drawn from a Poisson distribution with mean α, and mate with each encountered male with a probability that depends on the difference in their trait values, $u = y - x$, $\phi[u] = 1/(1 + e^{-u})$. Resistance (x) and persistence (y) levels expressed by a host are calculated as the average of the trait values from each chromosome (*e.g.*, $x = (x_1 + x_2)/2$ where x_1 is the resistance allele on chromosome one and x_2 is the resistance allele on chromosome two). Gametes are formed with free recombination between loci and alleles experience mutation with probability U_{hosts}. Effect size of a mutation is chosen from a normal distribution with a mean of zero. If the mutational step yields a negative trait value, the trait value is assumed to be zero. The number of offspring born to a mated female is drawn from a Poisson distribution with mean $b(1 - (M + F)/K)$. If a female has mated with multiple males (let m be the number of males she mated with), a given male sires an average of $1/m$ of her offspring, with the actual sire of each offspring chosen at random from the m males. After mating

(but before giving birth), adult females die with probability $(1 - e^{-(\mu_f + \delta e^x + d*m)})$ and adult males die with probability $(1 - e^{-(\mu_m + ce^y)})$. The surviving adults and newborn offspring make up the next generation, whose mean and variance in host trait values are recorded before undergoing another round of mutation, mating, and selection.

We explore a range of persistence and mating costs. The resistance cost presented in the text ($\delta = 0.0005$) was chosen because at very low resistance costs, female resistance evolves to be higher than male persistence and the host population cannot maintain itself. At moderately low resistance costs, female resistance is similar to male persistence and the mating rate is low enough that an STD cannot invade the host population. Beyond this, we did not investigate this area of parameter space because we were interested in the coevolution of host and STD when the STD had the potential to persist.

Sexual Conflict with an STD

In host populations infected with a sexually transmitted disease (STD), the STD is introduced into 5% of hosts with the virulence of each infection drawn from a normal distribution with mean $\bar{v}$ and variance 0.1. Given that mating has occurred, the STD is transmitted from an infected host to a susceptible host with probability $\beta[v]$. A newly infected host suffers additional mortality v but cannot infect other hosts unless it survives to the next generation (thus, the STD has a latent period before disease carriers are infectious). During this latent period the STD undergoes mutation with probability U_{STD}. Effect size of a mutation is chosen from a normal distribution with a mean of zero. If the mutational step yields negative virulence, virulence is assumed to be zero. At the start of each generation, the population mean and variance in virulence are recorded.

Analytical Model

Sexual Conflict

We conduct sequential evolutionary invasion analyses for multiple traits following Otto & Day (2007, Supplementary Material 12.1). To do so, we augment the system of equations presented in the text (eqn 1) by introducing a rare mutant for the persistence trait y, holding the resistance trait constant. It is important to note that the mutant persistence trait y_{Mut} is carried by both males and females but only expressed in males. The mutant will invade a population at ecological equilibrium if its invasion fitness $r_m[y, y_{Mut}, x]$ is greater than zero. Similarly, we can introduce a rare mutant for the resistance trait, x_{Mut}, holding the persistence trait fixed, and determine where its invasion fitness $r_f[y, x, x_{Mut}]$ is greater than zero. Individuals expressing a mutant trait will have a different mating rate than resident individuals, thus experiencing different reproductive success and imposing or suffering different naturally selected or sexually antagonistic costs.

A co-evolutionarily stable strategy can be found where the selection gradient for both traits equals zero,

$$\left.\frac{\partial r_m[y, \tilde{y}, x]}{\partial \tilde{y}}\right|_{\substack{\tilde{y}=y^* \\ y=y^* \\ x=x^*}} = 0 \qquad \text{and} \qquad \left.\frac{\partial r_f[y, x, \tilde{x}]}{\partial \tilde{x}}\right|_{\substack{\tilde{x}=x^* \\ x=x^* \\ y=y^*}} = 0, \tag{4}$$

and their second derivative is negative such that the co-ESS is a fitness maximum.

$$\left.\frac{\partial^2 r_m[y, \tilde{y}, x]}{\partial \tilde{y}^2}\right|_{\substack{\tilde{y}=y^* \\ y=y^* \\ x=x^*}} \leq 0 \qquad \text{and} \qquad \left.\frac{\partial^2 r_f[y, x, \tilde{x}]}{\partial \tilde{x}^2}\right|_{\substack{\tilde{x}=x^* \\ x=x^* \\ y=y^*}} \leq 0 \tag{5}$$

Sexual Conflict with an STD

Similar to eqn 4, there will be a three-way co-evolutionarily stable strategy when

$$\left.\frac{\partial r_m[y, \tilde{y}, x, v]}{\partial \tilde{y}}\right|_{\substack{\tilde{y}=y^*, y=y^* \\ x=x^*, v=v^*}} = 0 \quad \text{and} \quad \left.\frac{\partial r_f[y, x, \tilde{x}, v]}{\partial \tilde{x}}\right|_{\substack{\tilde{x}=x^*, x=x^* \\ y=y^*, v=v^*}} = 0 \quad \text{and} \quad \left.\frac{\partial r_v[y, x, v, \tilde{v}]}{\partial \tilde{v}}\right|_{\substack{\tilde{v}=v^*, v=v^* \\ y=y^*, x=x^*}} = 0, \tag{6}$$

and their second derivative is negative.

$$\left.\frac{\partial^2 r_m[y,\tilde{y},x,v]}{\partial \tilde{y}^2}\right|_{\substack{\tilde{y}=y^*,y=y^*\\ x=x^*,v=v^*}} \leq 0 \quad \text{and} \quad \left.\frac{\partial^2 r_f[y,x,\tilde{x},v]}{\partial \tilde{x}^2}\right|_{\substack{\tilde{x}=x^*,x=x^*\\ y=y^*,v=v^*}} \leq 0 \quad \text{and} \quad \left.\frac{\partial^2 r_v[y,x,v,\tilde{v}]}{\partial \tilde{v}^2}\right|_{\substack{\tilde{v}=v^*,v=v^*\\ y=y^*,x=x^*}} \leq 0 \tag{7}$$

We were unable to solve the system analytically; numerical solutions are provided in the supplementary figures.

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Table 1: Parameters

Parameter	Definition
y	male persistence trait
x	female resistance trait
$u = y - x$	difference between host traits
c	persistence cost to males
d	mating cost to females
δ	resistance cost to females
v	virulence of the STD

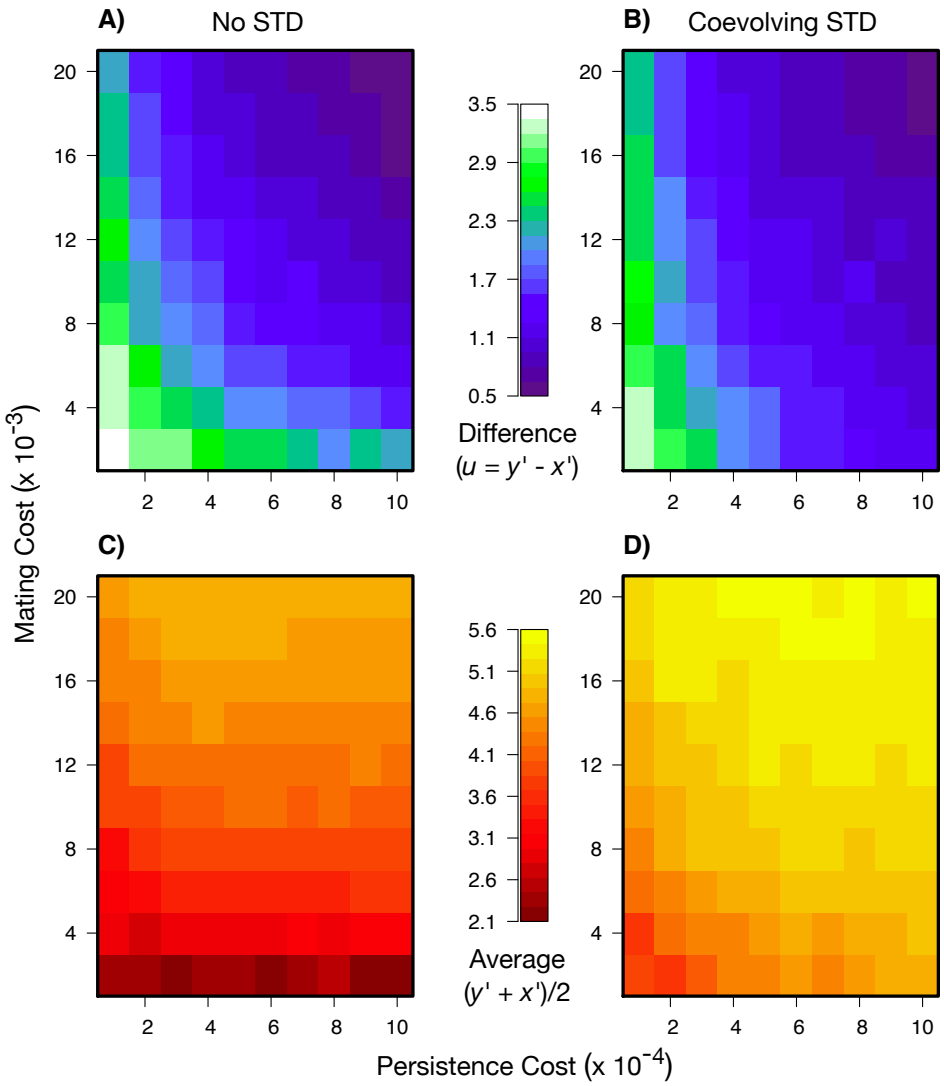

Figure 1: The outcome of coevolution between males and females in the absence of an STD (A and C) and in the presence of a coevolving STD (B and D) in individual-based simulations. Shown here are the difference between evolutionary equilibrium persistence, y', and evolutionary equilibrium resistance, x' (A and B), and the average of y' and x' (C and D). Simulations with a coevolving STD began at the STD-absent host trait values and the results (B and D) are a three-way coevolutionary equilibrium with an STD with evolutionary equilibrium virulence v' (see Fig. 4A). Parameter values: $\alpha = 10$, $\delta = 0.0005$, $\mu = 0.2$, $b = 4$, $K = 1000$, $w = 1$. Each cell represents the average of 20 independent simulations (a small number of simulations in which the disease went extinct are excluded from calculating the average). Similar patterns are observed in numerical solutions to the analytical model (see Supplementary Material Fig. S1).

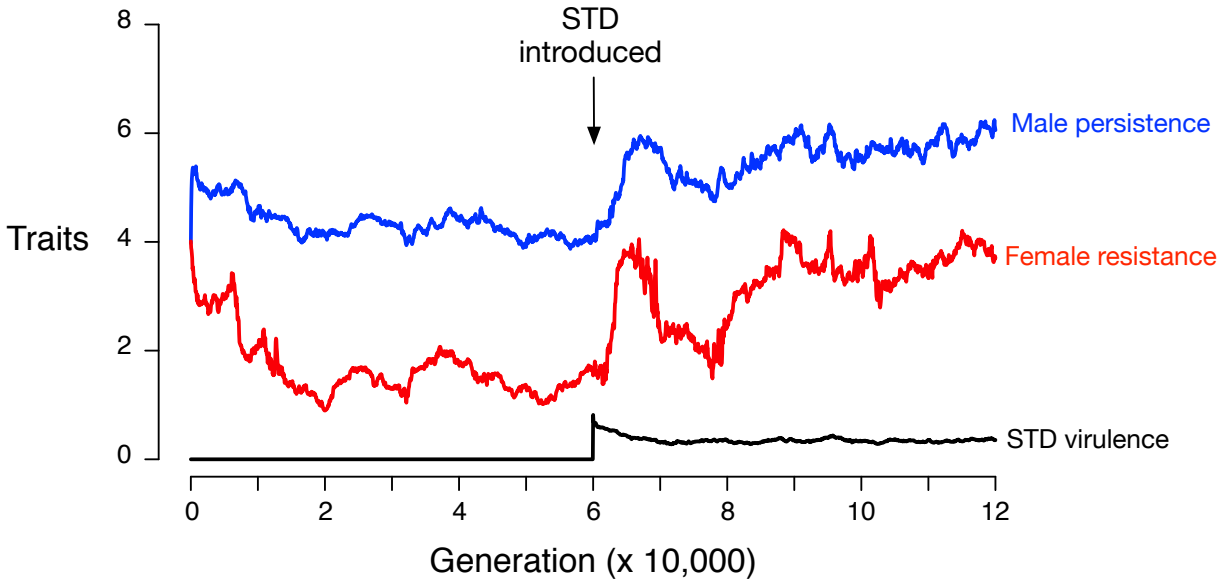

Figure 2: Sample run from an individual-based simulation where hosts evolve to their disease-absent equilibrium values before an STD is introduced. Male persistence is shown in blue, female resistance in red, and STD virulence in black. Parameter values: $\alpha = 10$, $\delta = 0.0005$, $\mu = 0.2$, $b = 4$, $K = 1000$, $w = 1$.

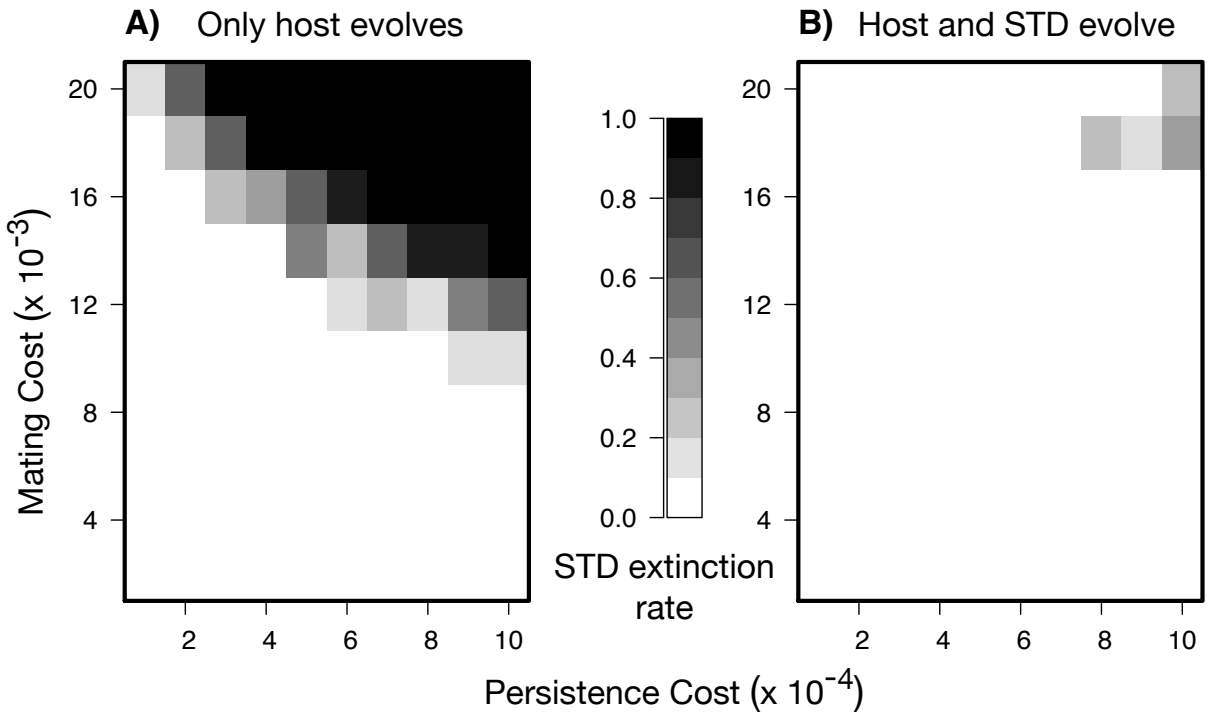

Figure 3: Fraction of simulation runs where an STD was driven extinct by sexually antagonistic host coevolution. The parasite was introduced at the STD-absent male persistence and female resistance host trait values but host traits evolved in the presence of the parasite. (A) Non-evolving STD with $v = 0.8$, (B) Coevolving STD initially introduced with $v = 0.8$. Parameter values: $\alpha = 10$, $\delta = 0.0005$, $\mu = 0.2$, $b = 4$, $K = 1000$, $w = 1$. The value for each cell was based on 20 independent simulations.

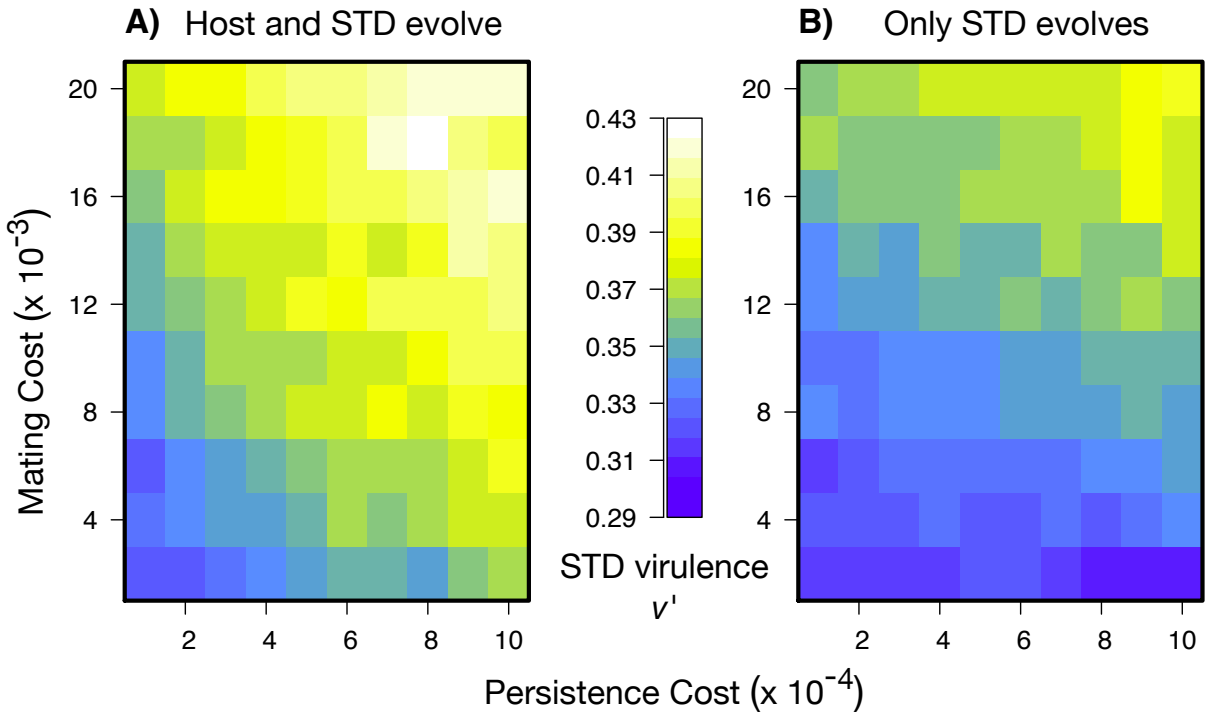

Figure 4: Evolutionary equilibrium virulence of an STD in a population where hosts (A) coevolve or (B) do not coevolve. The parasite was introduced with $v = 0.8$ at the STD-absent male persistence and female resistance host trait values. Parameter values: $\alpha = 10$, $\delta = 0.0005$, $\mu = 0.2$, $b = 4$, $K = 1000$, $w = 1$. Each cell represents the average of 20 independent simulations. A small number of simulations in which the disease went extinct are excluded from calculating the average. Similar patterns are observed in numerical solutions to the analytical model (see Supplementary Material Fig. S2).

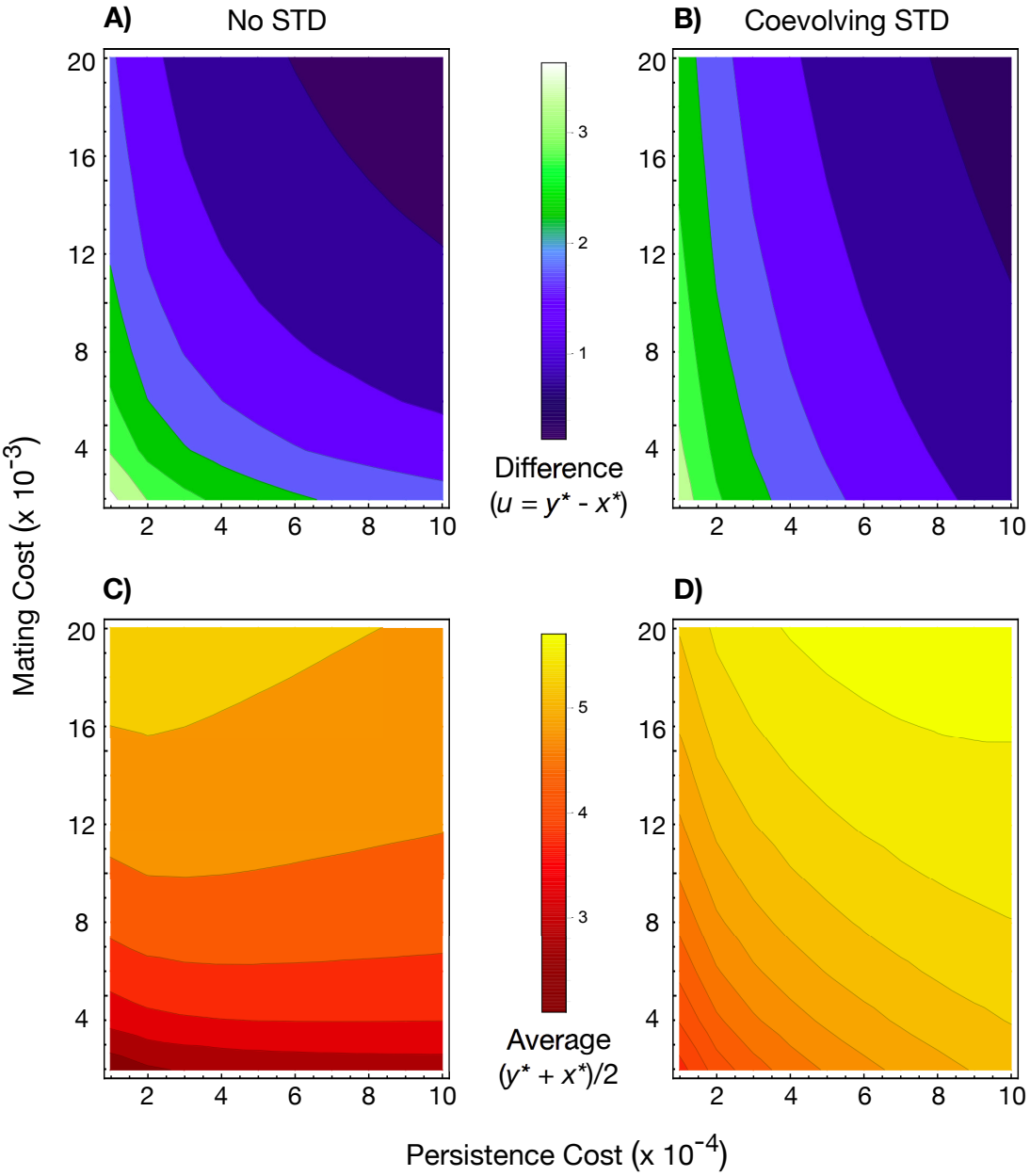

Figure S1: The outcome of coevolution between males and females in the absence of an STD (A and C) and in the presence of a coevolving STD (B and D) based on numerical solutions to the analytical model. Both scenarios yield evolutionary stable strategies (ESS). Shown here are the difference between ESS persistence, y^*, and ESS resistance, x^* (A and B), and the average of y^* and x^* (C and D). Panels B and D are a three-way co-ESS with an STD with ESS virulence v^* (see Fig. S2A). Parameter values: $\alpha = 0.03$, $\delta = 0.0005$, $\mu = 0.2$, $b = 4$, $K = 1000$, $w = 1$.

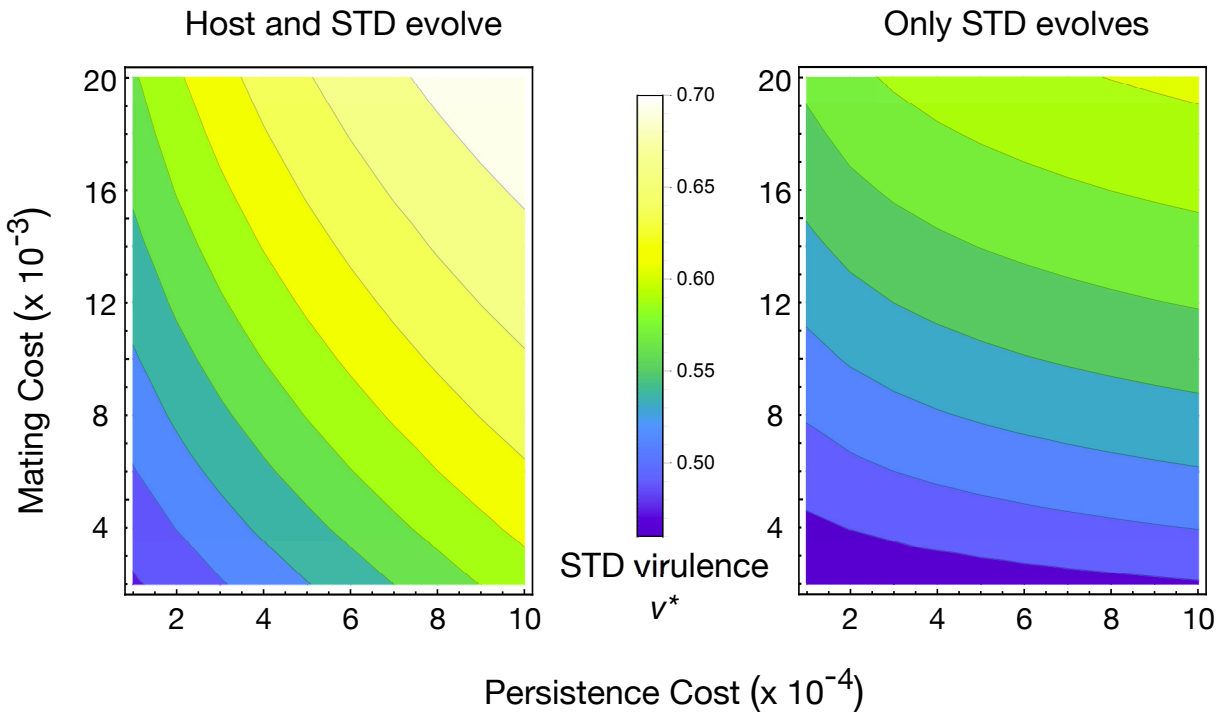

Figure S2: Evolutionary stable (ESS) virulence, v^* of an STD in a population where hosts (A) coevolve or (B) do not coevolve. Results are numerical solutions to the analytical model. In the absence of host coevolution (B), male persistence and female resistance were treated as constant parameters and set to their STD-absent ESS values. Parameter values: $\alpha = 0.03$, $\delta = 0.0005$, $\mu = 0.2$, $b = 4$, $K = 1000$, $w = 1$.