Table 1. Model parameters and variables.

Variables and parameters	Definitions
v	Fitness cost in hosts of being infected.
X (**Y**)	

if it mimics host factors involved in self/nonself-recognition (e.g., Drayman et al. 2013).

The host has a second, biallelic, modifier locus (denoted here as the **M**-locus), which determines the strength of assortative or disassortative mating exhibited by females. Mating occurs according to one of three standard models: the animal model, plant model, or grouping model. For a full description of these mating models, see Otto et al. (2008). Briefly, the animal and plant models both assume that females choose their mates with relative preferences based on phenotype. In the animal model, all females have equal fecundities, whereas in the plant model, females suffer a fitness cost for being choosy. The animal model thus applies to cases where females are the limiting sex, such as in lekking

Table 5. Summary of evolutionary outcomes with two alleles at the interaction locus.

Case	Infection model	Mating model	Host ploidy	Parasite ploidy	Predominant result (%)
1	IMA, MA	Plant	1, 2	1, 2	Random mating (100)
2	IMA, MA	Animal	1	1, 2	Complete disassortative mating (100)
3 (MHC)	IMA	Animal	2	1, 2	Intermediate disassortative mating (99)
4	IMA, MA	Grouping	1	1, 2	Random mating (100)*
5	IMA	Grouping	2	1, 2	Random mating (100)*
6	MA	Animal	2	1	Complete assortative mating (93)
7	MA	Animal	2	2	Complete assortative mating (96)
8	MA	Grouping	2	1, 2	Complete assortative mating (100)*

We classify an ESS as "random mating," "intermediate," or "complete" if it lies, respectively, in the interval [0, 0.05], [0.05, 0.95], or [0.95, 1]. For each scenario, we only report the predominant outcome, with numbers in parentheses indicating the percentage of parameter combinations that led to that particular outcome. Because maternal transmission did not impact these results, we pooled our data across values of maternal transmission. As discussed in the main text, in cases under the grouping model (indicated with symbol "*"), only the evolution of assortative mating (and not disassortative mating) is applicable.

Table 6. Summary of evolutionary outcomes with five alleles at the interaction locus.

Case	Infection model	Mating model	Host ploidy	Parasite ploidy	Predominant result (%)
1	IMA, MA	Plant	1, 2	1, 2	Random mating (100)
2	IMA, MA	Animal	1	1, 2	Complete disassortative mating (100)
3 (MHC)	IMA	Animal	2	1, 2	Intermediate disassortative mating (25) Complete disassortative mating (75)
4	IMA, MA	Grouping	1	1, 2	Random mating (100)*
5	IMA	Grouping	2	1, 2	Random mating (100)*
6	MA	Animal	2	1	

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at equilibrium, there may be nonequilibrial cycles at the start of invasion when interaction locus allele frequencies are not exactly even (e.g., 50:50 for the two-allele case; see Fig. S1). This initial bout of frequency-dependent selection can be sufficient to promote the invasion of a modifier coding for a higher level of disassortative mating. Thus our analysis here applies to situations where allele frequencies are perturbed from equilibrium, such that transient cycles occur. It is also worth mentioning that, in contrast to Howard and Lively's stochastic model, we used a deterministic model that has a greater ability to detect slight changes at the modifier locus. Thus we might have reported an increase in frequency in a case when they would not have.

Although previous models focused only on single ploidy combinations (either both hosts and parasites haploid [Howard and Lively 2003, 2004], or both diploid [Nuismer et al. 2008]), here we examined all combinations of host and parasite ploidy. It is worth mentioning, however, that although we compared haploidy to diploidy, a comparison between one interaction locus haploids and two interaction locus haploids, would likely yield similar conclusions, provided an analogous infection scheme were implemented.