

## Appendix from A. F. Agrawal and S. P. Otto, ‘Host-Parasite Coevolution and Selection on Sex through the Effects of Segregation’ (Am. Nat., vol. 168, no. 5, p. 617)

### Results from Generalized Models of Infection

Here we generalize the MA, IMA, and GFG models of infection to allow more flexibility in describing the susceptibility of heterozygous hosts and the infectiousness of heterozygous parasites. To maintain generality, we use four parameters describing the gene expression of heterozygous hosts:  $d_{HA}$  is the probability that an  $Aa$  host expresses just the  $A$  allele (and has the same pattern of susceptibility as an  $AA$  host);  $d_{HAa}$  is the probability that an  $Aa$  host expresses both alleles;  $d_{Ha}$  is the probability that an  $Aa$  host expresses just the  $a$  allele (and has the same pattern of susceptibility as an  $aa$  host); and  $d_{H-}$  is the probability that an  $Aa$  host expresses neither allele. Note that  $d_{HA} + d_{HAa} + d_{Ha} + d_{H-} = 1$ . Similarly, we use the parameters  $d_{pA}$ ,  $d_{pAa}$ ,  $d_{pa}$ , and  $d_{p-}$  to describe the analogous properties for heterozygous parasites.

We also generalize the GFG model to allow heterozygotes to bear different costs. Specifically, we set the cost of resistance in heterozygous hosts to  $(d_{HA} + d_{HAa}h_c)c$ , where  $h_c c$  is the cost of expressing both alleles together, which might not be as great as the cost,  $c$ , of expressing only the resistant allele,  $A$ . Similarly, we set the cost of infectiousness in heterozygous parasites to  $(d_{pa} + d_{pAa}h_k)k$ , where  $h_k k$  is the cost of expressing both alleles together, which again might not be as great as the cost,  $k$ , of expressing only the infectious allele,  $a$ .

By using these parameters in conjunction with the logic underlying each model of infection, we can generate the interaction matrices given in tables A1–A3, describing a wide variety of biological scenarios. If we use these general interaction matrices in our analysis, we obtain the expressions for the selection coefficients and dominance measure,  $\Phi$ , given in table A4. These expressions can be directly substituted into the key equations (4)–(6) in the text to understand the evolution of sex for a wide range of interactions between hosts and parasites. In the simplest version of the MA model presented in the text, heterozygous hosts express both alleles and so are unable to identify any parasite as being nonself:  $d_{HAa} = d_{pAa} = 1$ , which reduces the fitness of heterozygotes relative to homozygotes ( $\Phi < 0$ ). Table A4 indicates that the opposite result ( $\Phi > 0$ ) is possible if, for example, expression in heterozygous hosts is such that neither  $A$  nor  $a$  alleles are recognized as self ( $d_{H-} = 1$ ). In the simplest version of the IMA model, heterozygous hosts express both alleles and so can successfully eradicate any parasite:  $d_{HAa} = d_{pAa} = 1$ , giving heterozygotes an advantage ( $\Phi > 0$ ). Again, the opposite result is possible if heterozygotes are unable to function effectively as either  $A$  or  $a$  carriers and cannot clear any parasite ( $d_{H-} = 1$ ). The version of the GFG model used in the text is motivated by the empirical literature showing that resistance alleles are typically dominant to susceptibility alleles and noninfectious alleles are typically dominant to infectious alleles:  $d_{HA} = d_{pA} = 1$ .

**Table A1**  
Matching alleles model

Host genotype	Parasite genotype		
	AA	Aa	aa
AA	$w_{HAApAA} = 1 - v$ $w_{PAAHAA} = 1$	$w_{HAApAa} = 1 - v(d_{pA} + d_{p-})$ $w_{PAAHAA} = 1 - u(d_{pA} + d_{pAa})$	$w_{HAApaa} = 1$ $w_{PaaHAA} = 1 - u$
Aa	$w_{HAaPAA} = 1 - v(d_{HA} + d_{HAa})$ $w_{PAAHAa} = 1 - u(d_{HA} + d_{H-})$	$w_{HAaPAa} = 1 - v(d_{HAa} + d_{p-} - d_{HAa}d_{p-} + d_{HA}d_{pA} + d_{HA}d_{pA})$ $w_{PAAHAa} = 1 - u[d_{pAa}(1 - d_{HAa}) + d_{pA}(d_{HA} + d_{H-}) + d_{pA}(d_{HA} + d_{H-})]$	$w_{HAaPaa} = 1 - v(d_{HA} + d_{HAa})$ $w_{PaaHAa} = 1$
aa	$w_{HaaPAA} = 1$ $w_{PAAHaa} = 1 - u$	$w_{HaaPAa} = 1 - v(d_{pA} + d_{p-})$ $w_{PAAHaa} = 1 - u(d_{pA} + d_{pAa})$	$w_{HaaPaa} = 1 - v$ $w_{PaaHaa} = 1$

**Note:** Fitness of host genotype  $ij$  when exposed to parasite genotype  $mn$  ( $w_{Hijpnm}$ ) and fitness of parasite genotype  $mn$  when exposed to host genotype  $ij$  ( $w_{PnmHij}$ ).

**Table A2**  
Inverse matching alleles model

Host genotype	Parasite genotype		
	AA	Aa	aa
AA	$w_{HAApAA} = 1$ $w_{PAAHAA} = 1 - u$	$w_{HAApAa} = 1 - v(d_{pA} + d_{p-})$ $w_{PAAHAA} = 1 - u(d_{pA} + d_{pAa})$	$w_{HAApaa} = 1 - v$ $w_{PaaHAA} = 1$
Aa	$w_{HAaPAA} = 1 - v(d_{HA} + d_{H-})$ $w_{PAAHAa} = 1 - u(d_{HA} + d_{HAa})$	$w_{HAaPAa} = 1 - v(d_{H-} + d_{p-} - d_{H-}d_{p-} + d_{HA}d_{pA} + d_{HA}d_{pA})$ $w_{PAAHAa} = 1 - u[d_{HAa}(1 - d_{p-}) + d_{HA}(d_{pA} + d_{pAa}) + d_{HA}(d_{pA} + d_{pAa})]$	$w_{HAaPaa} = 1 - v(d_{HA} + d_{H-})$ $w_{PaaHAa} = 1 - u(d_{HA} + d_{HAa})$
aa	$w_{HaaPAA} = 1 - v$ $w_{PAAHaa} = 1$	$w_{HaaPAa} = 1 - v(d_{pA} + d_{p-})$ $w_{PAAHaa} = 1 - u(d_{pA} + d_{pAa})$	$w_{HaaPaa} = 1$ $w_{PaaHaa} = 1 - u$

**Note:** Fitness of host genotype  $ij$  when exposed to parasite genotype  $mn$  ( $w_{Hijpnm}$ ) and fitness of parasite genotype  $mn$  when exposed to host genotype  $ij$  ( $w_{PnmHij}$ ).

**Table A3**  
Gene-for-gene model

Host genotype	Parasite genotype		
	AA	Aa	aa
AA	$w_{HAApAA} = 1 - c$ $w_{PAAHAA} = 1 - u$	$w_{HAApAa} = (1 - c) \times [1 - v(d_{pA} + d_{p-})]$ $w_{PAAHAA} = 1 - u(d_{pA} + d_{pAa}) - k[d_{pA} + d_{p-} + d_{pAa}h_k(1 - u)]$	$w_{HAApaa} = (1 - c)(1 - v)$ $w_{PaaHAA} = 1 - k$
Aa	$w_{HAaPAA} = 1 - c(d_{HA} + d_{HAa}h_c) - v(d_{HA} + d_{H-})$ $w_{PAAHAa} = 1 - u(d_{HA} + d_{HAa})$	$w_{HAaPAa} = 1 - c(d_{HA} + d_{HAa}h_c) - v(1 - d_{HA} - d_{HAa}) - v(d_{pA} + d_{p-})(1 - h_c)c d_{HAa} - v(d_{pA} + d_{p-})(1 - c)d_{HA}$ $w_{PAAHAa} = 1 - u(d_{HA} + d_{HAa})(d_{pA} + d_{pAa}) - k(d_{pA} + d_{p-} + d_{pAa}h_k) + k(d_{HA} + d_{HAa})d_{pAa}h_ku$	$w_{HAaPaa} = (1 - v) \times [1 - c(d_{HAa}h_c + d_{HA})]$ $w_{PaaHAa} = 1 - k$
aa	$w_{HaaPAA} = 1 - v$ $w_{PAAHaa} = 1$	$w_{HaaPAa} = 1 - v$ $w_{PAAHaa} = 1 - k(d_{pA} + d_{p-} + d_{pAa}h_k)$	$w_{HaaPaa} = 1 - v$ $w_{PaaHaa} = 1 - k$

**Note:** Fitness of host genotype  $ij$  when exposed to parasite genotype  $mn$  ( $w_{Hijpnm}$ ) and fitness of parasite genotype  $mn$  when exposed to host genotype  $ij$  ( $w_{PnmHij}$ ).

**Table A4**

Selection coefficients for different models of infection to leading order in the virulence,  $v$ , and cost of resistance,  $c$

Model	Parameter
Matching alleles	$s_{HAA}^{(MA)} \approx v[q_A^2 + 2q_A q_a(d_{PA} + d_{p-})];$ $s_{HAa}^{(MA)} \approx v\{q_A^2(d_{HA} + d_{Haa}) + q_a^2(d_{Ha} + d_{Haa}) + 2q_A q_a[d_{HA}(d_{PA} + d_{p-}) + d_{Ha}(d_{PA} + d_{p-}) + d_{Haa} + d_{H-}d_{p-}]\};$ $s_{Haa}^{(MA)} \approx v[2q_A q_a(d_{Pa} + d_{p-}) + q_a^2];$ $\Phi_{MA} \approx (s_{Haa}^{(MA)} + s_{Haa}^{(MA)}) - 2s_{HAA}^{(MA)}$
Inverse matching alleles	$s_{HAA}^{(IMA)} \approx v[2q_A q_a(d_{Pa} + d_{p-}) + q_a^2];$ $s_{HAa}^{(IMA)} \approx v\{q_A^2(d_{Ha} + d_{H-}) + q_a^2(d_{HA} + d_{H-}) + 2q_A q_a[d_{HA}(d_{Pa} + d_{p-}) + d_{Haa}d_{p-} + d_{Ha}(d_{PA} + d_{p-}) + d_{H-}]\};$ $s_{Haa}^{(IMA)} \approx v[q_A^2 + 2q_A q_a(d_{Pa} + d_{p-})];$ $\Phi_{IMA} \approx (s_{Haa}^{(IMA)} + s_{Haa}^{(IMA)}) - 2s_{HAA}^{(IMA)}$
Gene-for-gene	$s_{HAA}^{(GFG)} \approx c + v[q_a^2 + 2q_A q_a(d_{Pa} + d_{p-})];$ $s_{HAa}^{(GFG)} \approx c(d_{HA} + d_{Haa}h_c) + v\{q_A^2(d_{Ha} + d_{H-}) + q_a^2 + 2q_A q_a[d_{HA}(d_{Pa} + d_{p-}) + d_{Haa}(d_{Pa} + d_{p-}) + d_{Ha} + d_{H-}]\};$ $s_{Haa}^{(GFG)} \approx v;$ $\Phi_{GFG} \approx (s_{Haa}^{(GFG)} + s_{Haa}^{(GFG)}) - 2s_{HAA}^{(GFG)}$