Electronic Supplementary Material, part A

Alternative Model in Which Recovereds Are Included and Birth Rate of Infecteds Is Decreased

In this section we generalize the model type by extending the categories to include, besides susceptible and infected individuals, also recovered and recovered/immune individuals. In addition, here we allow the birth rate of infected individuals to be an arbitrary value, a_{inf}, which can be less than the birth rate of resistant individuals, a_{RR}, so this corresponds to Case 4 in the text. This is done by using the following substitution to equation (2b):

$$gamX_r = \frac{a_{rr}X_{rr} + a_{inf}Y_{rr} + 0.5a_{Rr}X_{Rr}}{1+\rho N}. \quad \text{(A1)}$$

These generalizations do not affect our ability to analyze the system. The equations are generalized by allowing infecteds to recover and become immune at rate IY_{rr} or susceptible again at rate RY_{rr}. (Recovered/immunes are not expected in plants, so it is reasonable to set $I = 0$ in that case.) The differential equations for the system become:

$$dX_{RR}/dt = newX_{RR} - bX_{RR} \quad \text{(A2)}$$

$$dX_{Rr}/dt = newX_{Rr} - bX_{Rr} \quad \text{(A3)}$$

$$dX_{rr}/dt = newX_{rr} - (b + \beta Y_{rr})X_{rr} + RY_{rr} \quad \text{(A4)}$$

$$dY_{rr}/dt = \beta Y_{rr}X_{rr} - (b + \alpha + R + I)Y_{rr} \quad \text{(A5)}$$

$$dZ_{rr}/dt = IY_{rr} - bZ_{rr} \quad \text{(A6)}$$

where Z_{rr} is the number of recovered immune individuals in the population. The steady state solutions to this model are

$$X_{rr}^{*} = \frac{(b+\alpha+R+I)}{\beta} \tag{A7}$$

$$Y_{rr}^{*} = \frac{X_{rr}^{*} b\left(\frac{a_{rr}}{a_{RR}} - 1\right)}{\left(\beta X_{rr}^{*} - R - \frac{a_{\inf}}{a_{RR}} b - \frac{a_{rr}}{a_{RR}} bI\right)} \tag{A8}$$

$$Z_{rr}^{*} = IY_{rr}^{*}/b \tag{A9}$$

$$X_{RR}^{*} + X_{Rr}^{*} = (a_{RR} - b)/(\rho b) - X_{rr}^{*} - Y_{rr}^{*} - Z_{rr}^{*} \tag{A10}$$

Note that this solution, as in Case 2, is independent of the inbreeding coefficient *F*. We can examine the effects of a_{inf} alone (Case 4), by setting $R = I = 0$. Then it is easy to see that reduction of the birth rate of infecteds from a_{rr} to a lower value, say $a_{inf} < a_{RR}$, causes Y_{rr}^{*} to decrease.

Electronic Supplementary Material, part B

General Expression for Infection Rate

For simplicity in the text we used a basic Lotka-Volterra function for the rate of infections, $\beta Y_{rr} X_{rr}$. However, this can be generalized to any function of the form $f(X_{rr}) Y_{rr}$ without affecting our ability to analyze the model. For example, suppose $f(X_{rr})$ takes the form of a Holling Type II functional response,

$$f(X_{rr}) = \frac{\beta_1 X_{rr}}{1 + \beta_2 X_{rr}} \quad . \tag{B1}$$

Then Equation (6a) in the text becomes

$$X_{rr}^{*} = \frac{b+\alpha}{\beta_1 - \beta_2 (b+\alpha)} \tag{B2}$$

and (6b) takes the form

$$Y_{rr}^{*} = \frac{X_{rr}^{*} \times b[(a_{rr} / a_{RR}) - 1]}{f(X_{rr}^{*}) - b(a_{rr} / a_{RR})} \qquad \text{(B3)}$$

Other steady state values are modified through the above changes in X_{rr}^{*} and Y_{rr}^{*}. Note that for the Holling Type II response, the value of X_{rr}^{*} is likely to be higher than in the case of the Lotka-Volterra interaction. This would tend to have a negative effect on the value of X_{RR}^{*} and X_{Rr}^{*}, due to limited carrying capacity.

The above solutions are independent of *F*. But we can also consider the case where the infection rate itself depends on *F*. The reason for such an assumption is that greater inbreeding would increase the probability of susceptibles coming in contact with infecteds, both being homozygous in *r*. That effect could easily be incorporated into our model by generalizing the interaction function to $f(X_{r}, F)$. For interaction rates of this form, analytic solutions of the same form as Equations (B2) and (B3) are possible. One situation might be for β_1 to be an increasing function of *F*, $\beta_1(F)$. In this case, X_{rr}^{*} would decrease with increasing *F*, but Y_{rr}^{*} could increase as the denominator of Equation (B3) decreases. The results of Cases 2 and 3 could change substantially. We have not tried to explore this possibility numerically, but will in future work. More complex interaction functions that involve not only *F* and X_{rr}, but also X_{Rr}, and X_{RR}, can also be imagined, and these might be beyond the possibility of analytic solution.

Electronic Supplementary Material, part C

Calculation of X_{Rr}^* and X_{RR}^*

It is possible, using the right hand side of equation (1b) set to zero, to solve for X_{Rr}^*, given $X_{Rr}^* + X_{RR}^*$ from equation (6b). Let's put the previously calculated sum of the resistant homozygote and heterozygote in parentheses to be treated as a known unit, as follows:

$$\{X_{Rr}^* + X_{RR}^*\} \equiv X_{Rr}^* + X_{RR}^* \ .$$

Then we can show, using (1b), that

$$X_{Rr}^* = -0.5(B/A) - 0.5\sqrt{(B/A)^2 - 4(C/A)} \qquad \text{(C1)}$$

where

$$A = b(1 + \rho N^*)(a_{RR} - a_{Rr}) - (1-F)(a_{RR} - 0.5a_{Rr})a_{Rr}$$

$$B = (1-F)a_{RR}\{X_{RR}^* + X_{Rr}^*\}a_{Rr} - 2(1-F)(a_{RR} - 0.5a_{Rr})(a_{rr}X_{rr}^* + a_{rr}Y_{rr}^*)$$
$$-b(1+\rho N^*)[a_{RR}\{X_{RR}^* + X_{Rr}^*\} + a_{rr}X_{rr}^* + a_{rr}Y_{rr}^*]$$

$$C = 2(1-F)a_{RR}\{X_{RR}^* + X_{Rr}^*\}(a_{rr}X_{rr}^* + a_{rr}Y_{rr}^*)$$

From X_{Rr}^*, it is next possible to solve for X_{RR}^*, using the known value of $\{X_{Rr}^* + X_{RR}^*\}$ from equation (6b); that is,

$$X_{RR}^* = \{X_{Rr}^* + X_{RR}^*\} - X_{Rr}^* \qquad \text{(C2)}$$

In some cases, the cost of resistance may be so high that the *R*-allele goes to extinction (Figure E1). However, if $a_{RR} < a_{Rr}$, then when F is small (high outcrossing), the presence of the heterozygote may be able to maintain the *R*-allele in the population, as occurs in Figure E1. An additional feature of the behaviour of the variables for Case 3

($a_{RR} < a_{Rr} < a_{rr}$), not mentioned in the main text, is the possibility of unimodal behaviour of X_{RR}^* as a function of F (electronic Figure E2). This intermediate peak can occur when there is a high cost of disease resistance (i.e., the value of a_{RR} is significantly smaller than a_{rr}), and the heterozygote reproduction rate is intermediate between the two homozygotes. Because the *RR*- homozygote is a poor competitor against the *rr*-homozygote, X_{RR} has a small value for high rates of selfing. For intermediate selfing rates, the presence of the heterozygote, which has higher fitness than the *RR*-homozygote, can help X_{RR} maintain higher values.

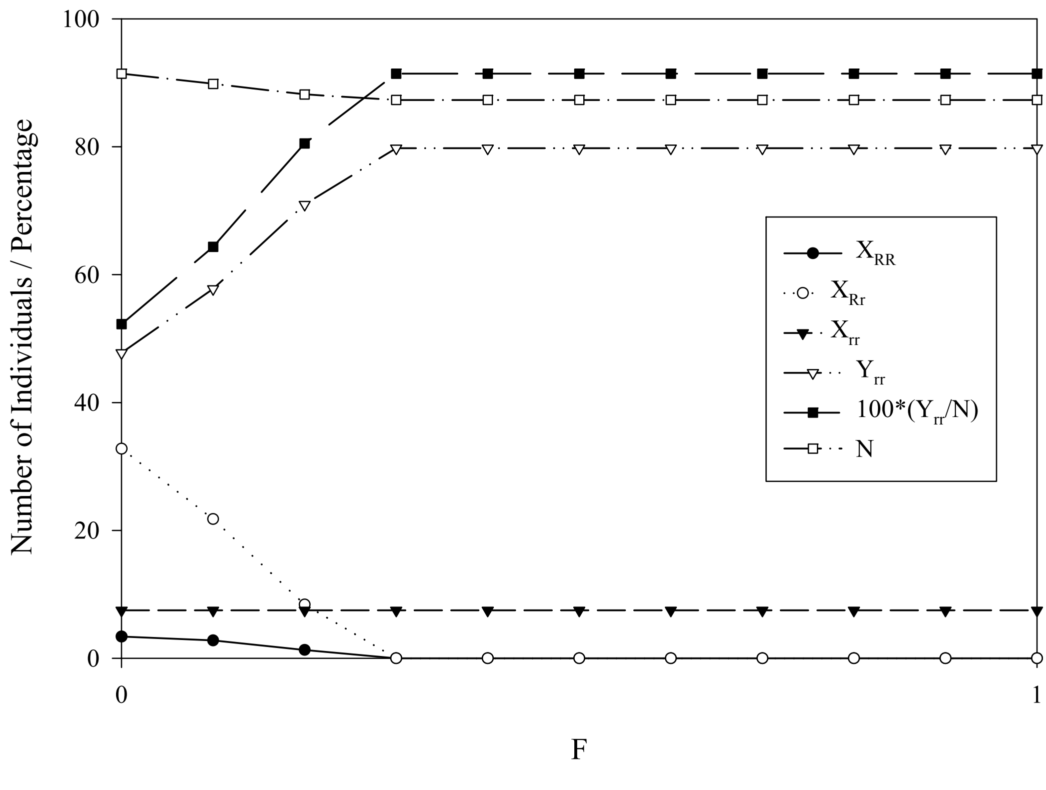

Figure E1: The number of homozygous resistant, heterozygous resistant, susceptible, and infected individuals, percentage infected in the population, and total number of individuals at equilibrium for the range of complete selfing through complete outcrossing. Parameters: $a_{RR} = 0.4$, $a_{Rr} = 0.6$, $a_{rr} = 0.8$, $b = 0.2$, $\alpha = 0.1$, $\beta = 0.04$, $\rho = 0.02$. (Case 3, $a_{RR} < a_{Rr} < a_{rr}$)

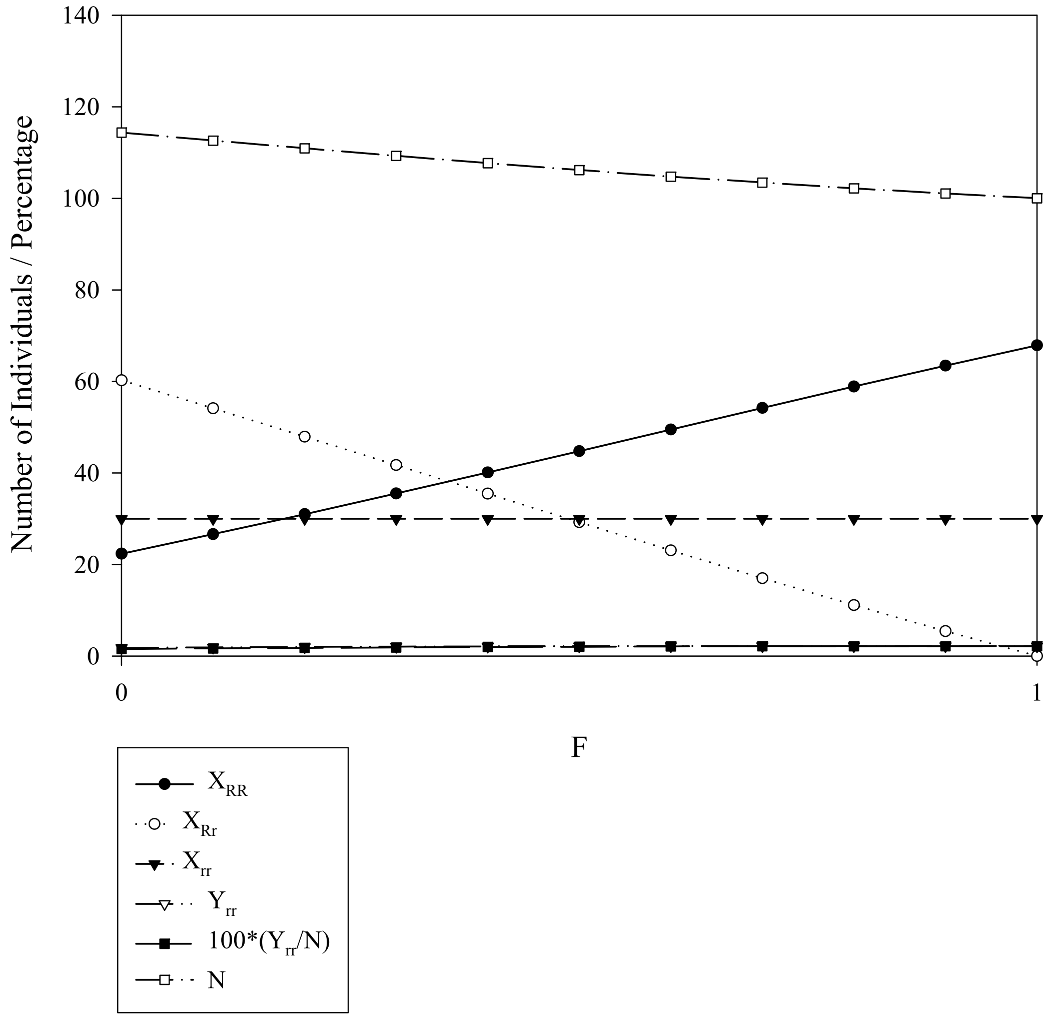

Figure E2: The number of homozygous resistant, heterozygous resistant, susceptible, and infected individuals, percentage infected in the population, and total number of individuals at equilibrium for the range of complete selfing through complete outcrossing. Parameters: $a_{RR} = 0.6$, $a_{Rr} = 0.7$, $a_{rr} = 0.8$, $b = 0.2$, $\alpha = 1.0$, $\beta = 0.04$, $\rho = 0.02$. (Case 3, $a_{RR} < a_{Rr} < a_{rr}$)

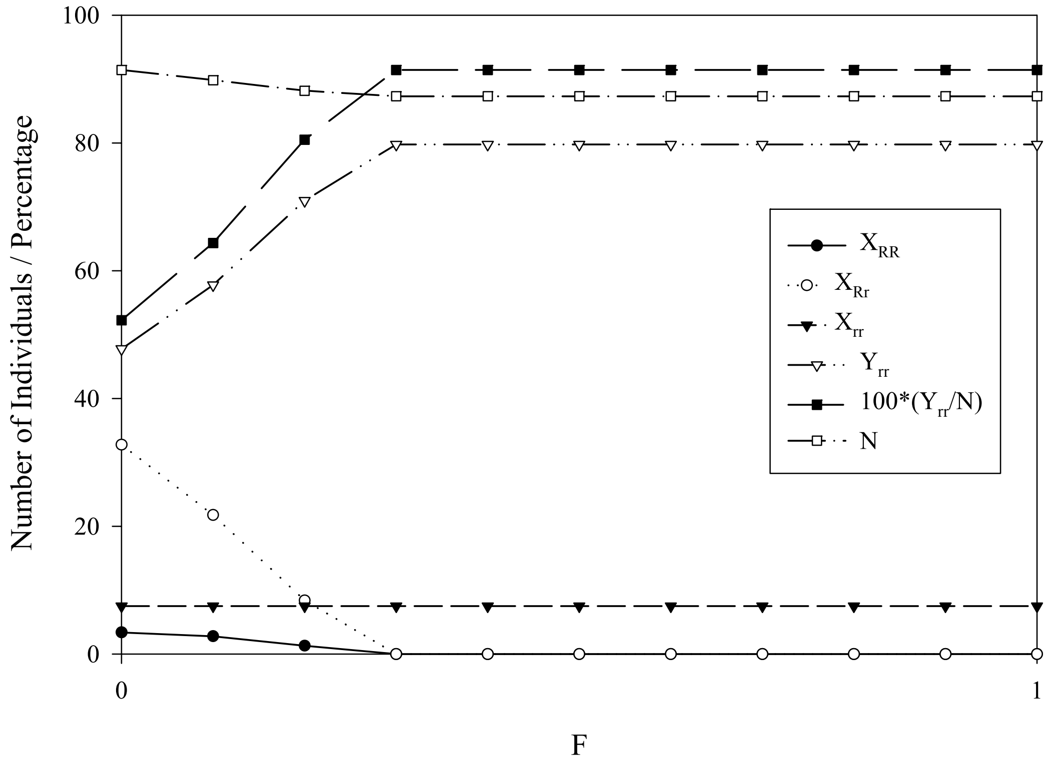

Figure E3: The number of homozygous resistant, heterozygous resistant, susceptible, and infected individuals, percentage infected in the population, and total number of individuals at equilibrium for the range of complete selfing through complete outcrossing. Parameters: $a_{RR} = 0.4$, $a_{Rr} = 0.6$, $a_{rr} = 0.8$, $b = 0.2$, $\alpha = 1.0$, $\beta = 0.04$, $\rho = 0.02$. (Case 3, $a_{RR} < a_{Rr} < a_{rr}$)