

INTROGRESSIVE HYBRIDIZATION AS A MECHANISM FOR SPECIES RESCUE
ONLINE SUPPLEMENTAL APPENDICES
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A Mathematical details of the deterministic model

Here we describe the mathematical details of the deterministic model. The model follows the number of individuals $N_{\frac{ik}{jl},t}$ at time t with each genotype $\frac{ik}{jl}$, where $i, j \in \{A, a\}$ and $k, l \in \{B, b\}$. From this the total number of individuals is $N_t = \sum_{i,j \in \{A,a\}, k,l \in \{B,b\}} N_{\frac{ik}{jl},t}$, and the proportion of individuals with each genotype is $p_{\frac{ik}{jl},t} = N_{\frac{ik}{jl},t}/N_t$. First we find the number of offspring with each genotype $N'_{\frac{ik}{jl},t}$ as a product of the proportion of each mating pairing and the proportion of the given genotype from those pairings, summed over all possible mating pairs and multiplied by the number of offspring per successful mating. Then we multiply by both the density-dependent and density-independent survivorships to determine the number of individuals with each genotype in the next generation.

The proportion of each mating pairing between parental genotypes $\frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4}$ occurring is the normalized product of the probability of encounter (the product of their frequencies)

$$Pr_E \left(\frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4} \right) = p_{\frac{x_1y_1}{x_2y_2},t} p_{\frac{x_3y_3}{x_4y_4},t} \quad (1)$$

and the probability that they mate given an encounter as it depends on the probability of two individuals of different species mating n

$$Pr_M \left(\frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4} \right) = \begin{cases} 1 & x_1x_2 = x_3x_4 \text{ or } x_1x_2 = x_4x_3 \\ n & x_1 \neq x_3, x_4 \text{ and } x_2 \neq x_3, x_4 \\ (1+n)/2 & \text{otherwise} \end{cases} \quad (2)$$

The proportion of offspring inheriting each genotype $\frac{ik}{jl}$ from the mating pair $\frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4}$ depends on the recombination probability R according to

$$Pr_I \left(\frac{ik}{jl} \mid \frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4} \right) = \begin{cases} (1-R)^2/4 & \forall \frac{ik}{jl} \in \left\{ \frac{x_1y_1}{x_3y_3}, \frac{x_1y_1}{x_4y_4}, \frac{x_2y_2}{x_3y_3}, \frac{x_2y_2}{x_4y_4} \right\} \\ R^2/4 & \forall \frac{ik}{jl} \in \left\{ \frac{x_1y_2}{x_3y_4}, \frac{x_1y_2}{x_4y_3}, \frac{x_2y_1}{x_3y_4}, \frac{x_2y_1}{x_4y_3} \right\} \\ (1-R)R/4 & \forall \frac{ik}{jl} \in \left\{ \frac{x_1y_2}{x_3y_3}, \frac{x_1y_2}{x_4y_4}, \frac{x_2y_1}{x_3y_3}, \frac{x_2y_1}{x_4y_4}, \frac{x_1y_1}{x_3y_4}, \frac{x_1y_1}{x_4y_3}, \frac{x_2y_2}{x_3y_4}, \frac{x_2y_2}{x_4y_3} \right\} \end{cases} \quad (3)$$

(summing the proportions in cases of multiple matches for $\frac{ik}{jl}$). Given these proportions and the number of offspring per mating pair ρ , the number of offspring with genotype $\frac{ik}{jl}$ is

$$N'_{\frac{ik}{jl},t} = \frac{N_t \rho}{2} \sum_{\{x_1, x_2, x_3, x_4\} \in \{A, a\}, \{y_1, y_2, y_3, y_4\} \in \{B, b\}} \frac{Pr_E \left(\frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4} \right) Pr_M \left(\frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4} \right) Pr_I \left(\frac{ik}{jl} \mid \frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4} \right)}{Pr_E \left(\frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4} \right) Pr_M \left(\frac{x_1y_1}{x_2y_2} \times \frac{x_3y_3}{x_4y_4} \right)} \quad (4)$$

Of these offspring, the proportion that survive density-dependent mortality depends on the carrying capacity K , the number of offspring of each species $N'_{ij,t} = \sum_{kl \in \{B,b\}} N'_{\frac{ik}{jl},t}$, strength of interspecific competition s , and the per-pair offspring production of each species $\rho_{ij,t} = 2 \cdot \max(N'_{ij,t}/N_{ij,t}, 1.000001)$ according to

$$m_{ij,t} = \begin{cases} \left(1 + \frac{\rho_{AA,t}/2-1}{(1+s)K\rho_{AA,t}/2} \left(N'_{AA,t} + \frac{1+s}{2} N'_{Aa,t} + s N'_{aa,t} \right) \right)^{-1} & ij = AA \\ \left(1 + \frac{\rho_{aa,t}/2-1}{(1+s)K\rho_{aa,t}/2} \left(N'_{aa,t} + \frac{1+s}{2} N'_{Aa,t} + s N'_{AA,t} \right) \right)^{-1} & ij = aa \\ \left(1 + \frac{\rho_{Aa,t}/2-1}{(1+s)K\rho_{Aa,t}/2} \left(N'_{Aa,t} + \frac{1+s}{2} (N'_{AA,t} + N'_{aa,t}) \right) \right)^{-1} & \text{otherwise} \end{cases} \quad (5)$$

Then the proportion that survive density-independent mortality is $w_{ij}v_{kl}$, where the fitness at the first locus depends on hybrid inferiority h

$$w_{ij} = \begin{cases} 1 & ij \in \{aa, AA\} \\ h & \text{otherwise} \end{cases}, \quad (6)$$

and the fitness at the second locus depends on the relative fitness of the b allele g

$$v_{kl} = \begin{cases} 1 & kl = BB \\ g & kl = bb \\ (1+g)/2 & \text{otherwise} \end{cases}. \quad (7)$$

Given these survivorship functions, the number of individuals in the next generation with each genotype is

$$N_{\frac{ik}{jl},t+1} = w_{ij}v_{kl}m_{ij,t}N'_{\frac{ik}{jl},t}. \quad (8)$$

B Results without environmental change

For introgressive hybridization to play a role in the response to environmental change, distinct species must persist before the environmental change, otherwise any hybridization would not occur as introgression. The maintenance of separate species without environmental change ($g = 1$) requires low hybrid fitness (h ; figs. B.1a, B.2a) and high assortative mating (low probability of mating the other species given an encounter n ; figs. B.1b, B.2b). The prevalence of rare hybrids increases slightly with increasing recombination (R ; figs. B.1c, B.2c). The increased stochasticity with increasing strength of interspecific competition (s ; figs. B.1d, B.2d) and decreasing carrying capacity (K , figs. B.1e, B.2e) leads to greater variation in population size but has little effect on the maintenance of separate species.

In the deterministic version of the model, the parameter space with coexistence (fig. B.3) is analogous to that in the stochastic model with the promiscuous mating function (fig. B.1; as expected because the deterministic model employs the dynamics of the promiscuous mating function). For the deterministic results in fig. B.3, the initial conditions are the number of individuals with genotypes aabb and AABB both at their carrying capacities with all other genotypes at zero density, and we census the population sizes at 150 generations. Runs of the deterministic model with variable initial conditions (results not shown) indicated that coexistence requires both species to have initial densities above a threshold ($\sim 0.3K$); otherwise, if one species starts at its carrying capacity and the other at low density, then the species at low density will go extinct. For further discussion of initial-condition dependencies in the deterministic model and longer-term outcomes, see Appendix C.

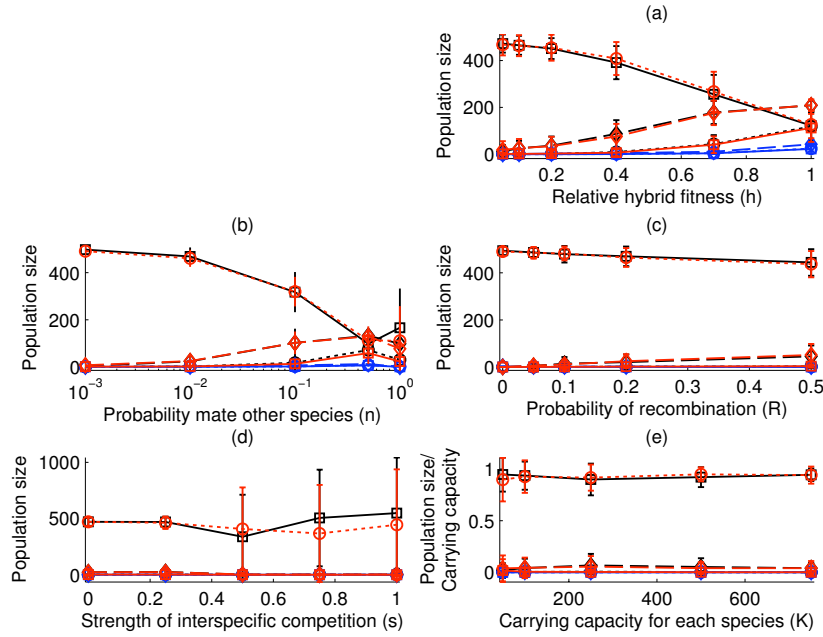


Fig. B.1 Equivalent to fig. 3 without any change in fitness ($g = 1$; all other parameters are as in table 1 when not otherwise specified in the x-axis) given the promiscuous mating function: (a) the relative hybrid fitness $w_{Aa} = h$, (b) the probability of interspecific mating given an encounter n (stronger assortative mating occurs with lower probability; note the log scale on the x-axis), (c) the probability of recombination R , (d) the strength of interspecific competition s , and (e) the carrying capacity K (note the y-axis scaled to K). All colors, lines, and symbols are as in fig. 3, where solid black lines with squares (AABB) and dotted red lines with circles (aabb) at their carrying capacities indicate the maintenance of separate species.

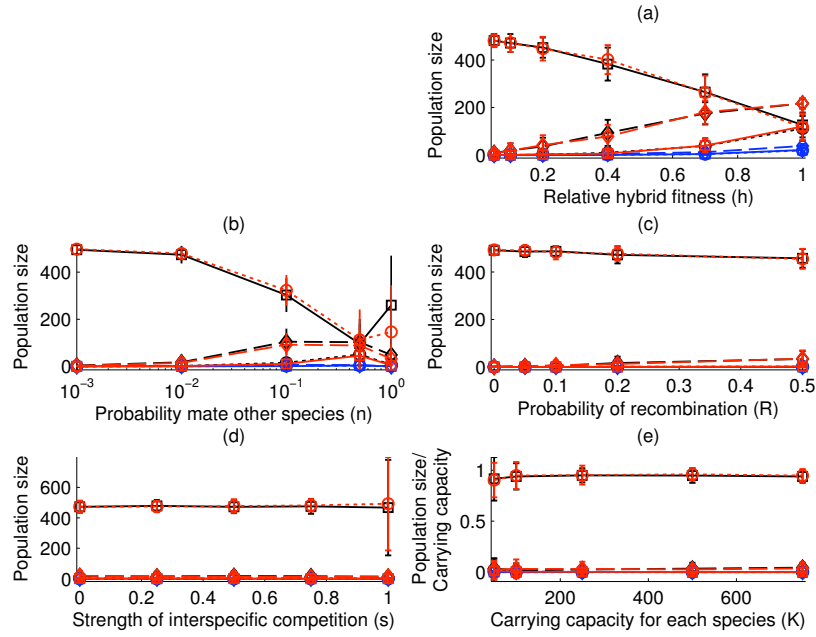


Fig. B.2 Equivalent to fig. 4 without any change in fitness ($g = 1$; all other parameters are as in table 1 when not otherwise specified in the x-axis) given the monogamous mating function: (a) the relative hybrid fitness $w_{Aa} = h$, (b) the probability of interspecific mating given an encounter n (stronger assortative mating occurs with lower probability; note the log scale on the x-axis), (c) the probability of recombination R , (d) the strength of interspecific competition s , and (e) the carrying capacity K (note the y-axis scaled to K). All colors, lines, and symbols are as in fig. 3, where solid black lines with squares (AABb) and dotted red lines with circles (aabb) at their carrying capacities indicate the maintenance of separate species.

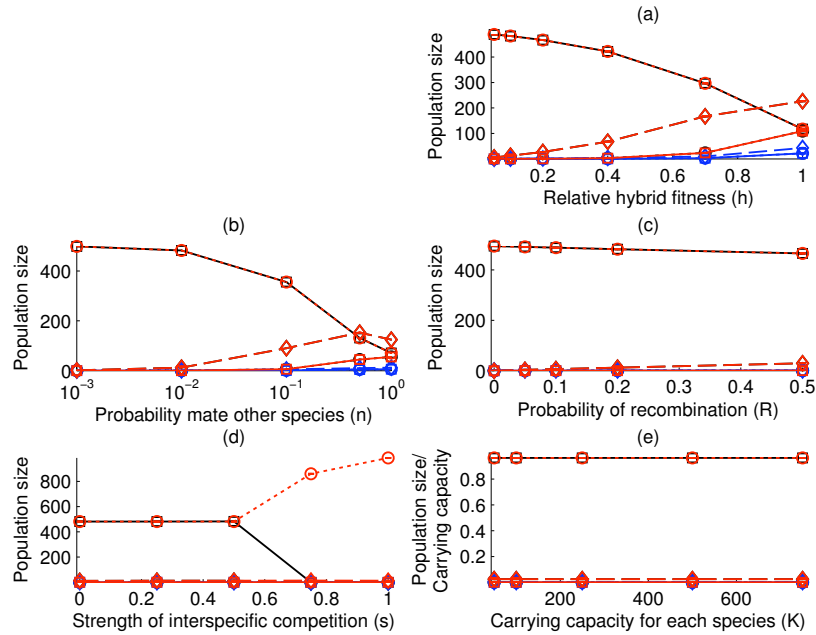


Fig. B.3 Equivalent to fig. 5 without any change in fitness ($g = 1$; all other parameters are as in table 1 when not otherwise specified in the x-axis) given the deterministic model (which employs the promiscuous mating function): (a) the relative hybrid fitness $w_{Aa} = h$, (b) the probability of interspecific mating given an encounter n (stronger assortative mating occurs with lower probability; note the log scale on the x-axis), (c) the probability of recombination R , (d) the strength of interspecific competition s , and (e) the carrying capacity K (note the y-axis scaled to K). All colors, lines, and symbols are as in fig. 3, where solid black lines with squares (AABb) and dotted red lines with circles (aabb) at their carrying capacities indicate the maintenance of separate species.

C Additional results from the deterministic model

In the main text, we present the equilibrium results from the deterministic version of the model, which show that successful introgression does not occur (fig. 5) throughout much of the range where it is observed when accounting for demographic stochasticity (figs. 3-4). In other words, in the deterministic version, a population comprised of AABB and aabb genotypes will not transition to a population comprised of AABB and aaBB genotypes after environmental change reduces fitness of individuals carrying the b allele unless the environmental change is minimal ($g \geq 0.8$, fig. 5a). Coexistence of AABB and aaBB genotypes is possible with greater environmental change (e.g., the default parameter values in table 1 where $g = 0.7$) in the deterministic version but depends on the initial conditions: the initial proportion of aaBB or aaBb phenotypes must be above a given threshold in order for the species 2 (aa) individuals to persist (example results in figs. C.1-C.2; i.e., which of the alternative states of coexistence or extinction of one species is the outcome depends on the initial conditions). In the case where the initial population consists entirely of AABB and aabb genotype (the initial conditions for fig. 5), the proportion of aaBB genotypes does not rise above this threshold, and therefore species 2 collapses and only species 1 remains.

When no environmental change occurs, or $g = 1$, the short-term outcome given an initial population of entirely AABB and aabb individuals is the continued coexistence of the homozygotes for each type near their carrying capacities (fig. 5a). However, extending the run time beyond 150 generations reveals that, over longer time scales, the populations approach an equilibrium with heterozygosity in the second locus (i.e., both the AA and aa populations contain a combination of BB, Bb, and bb genotypes; fig. C.3a). The analogous time series with environmental change ($g = 0.7$, fig. C.3b) leads to the rapid loss of the species carrying the b allele given the initial conditions, as described above.

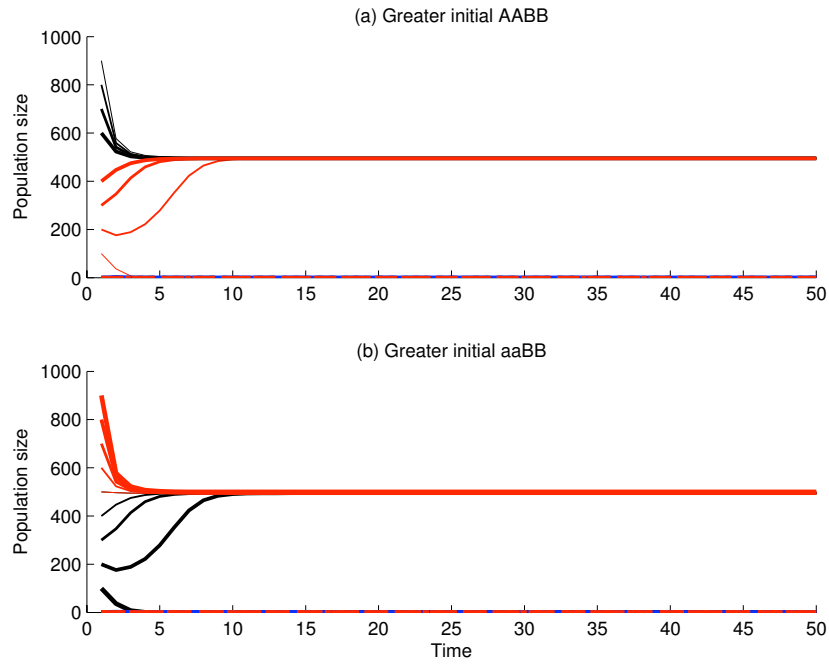


Fig. C.1 Time series of the deterministic model with varying initial conditions for both species and default parameter values (table 1). All populations start with a combination of AABB (red solid lines) and aaBB (black solid lines) individuals. In panel (a), the initial proportion of AABB individuals is greater, and in panel (b) the initial proportion of aaBB individuals is greater or the two are equivalent. Different line thicknesses indicate different runs (i.e., red and black lines of the same thickness are from the same run) within each plot.

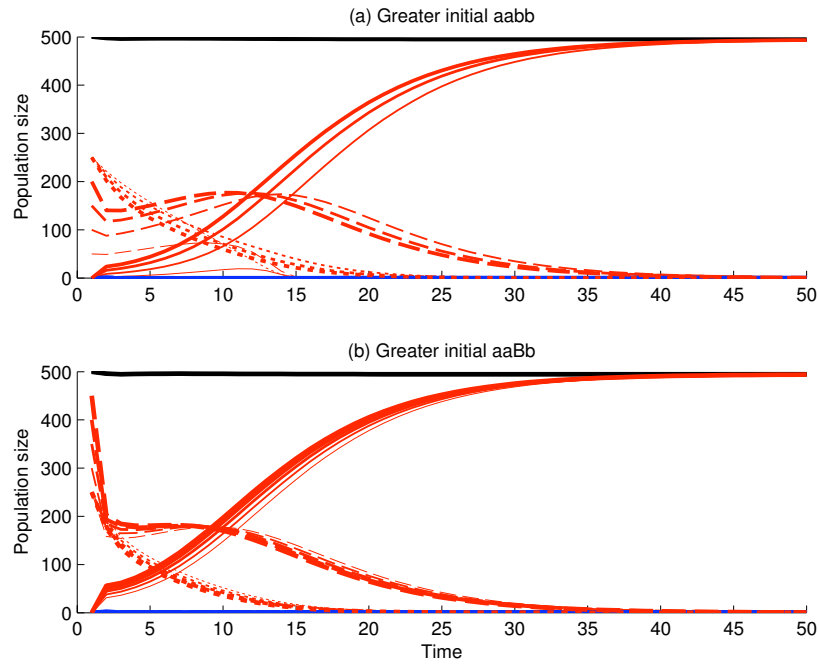


Fig. C.2 Time series of the deterministic model with varying initial conditions for the second (aa) species and default parameter values (table 1). All populations start with half AABB individuals (black solid lines, first species) and the other half (second species) a combination of aabb (red dotted lines) and aaBb (red dashed lines) individuals. In panel (a), the proportion of aabb individuals is greater, and in panel (b) the proportion of aaBb individuals is greater or the two are equivalent. Different line thicknesses indicate different runs within each plot.

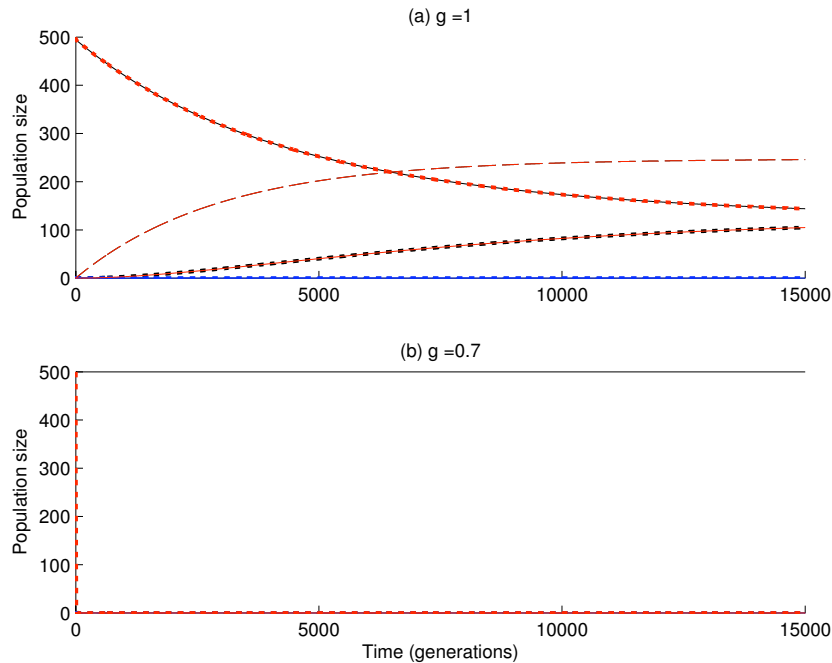


Fig. C.3 Deterministic equivalent to fig. 2a,b (with a longer run time): time series simulations runs for the default parameter values (table 1), starting with entirely AABB (solid black lines) or aabb (dotted red lines) individuals. Without environmental change ($g = 1$, panel a), the population approaches a heterozygous equilibrium in terms of the second locus over very long time scales (solid lines indicate BB, dotted lines indicate bb, and dashed lines indicate Bb genotypes associated with each species, indicated by color). With environmental change leading to a decrease in fitness in individuals carrying the b allele ($g = 0.7$, panel b), species 2 rapidly collapses (no successful introgression).