

Supplementary material for “Understanding the drivers of dispersal evolution in range expansions and their ecological consequences”

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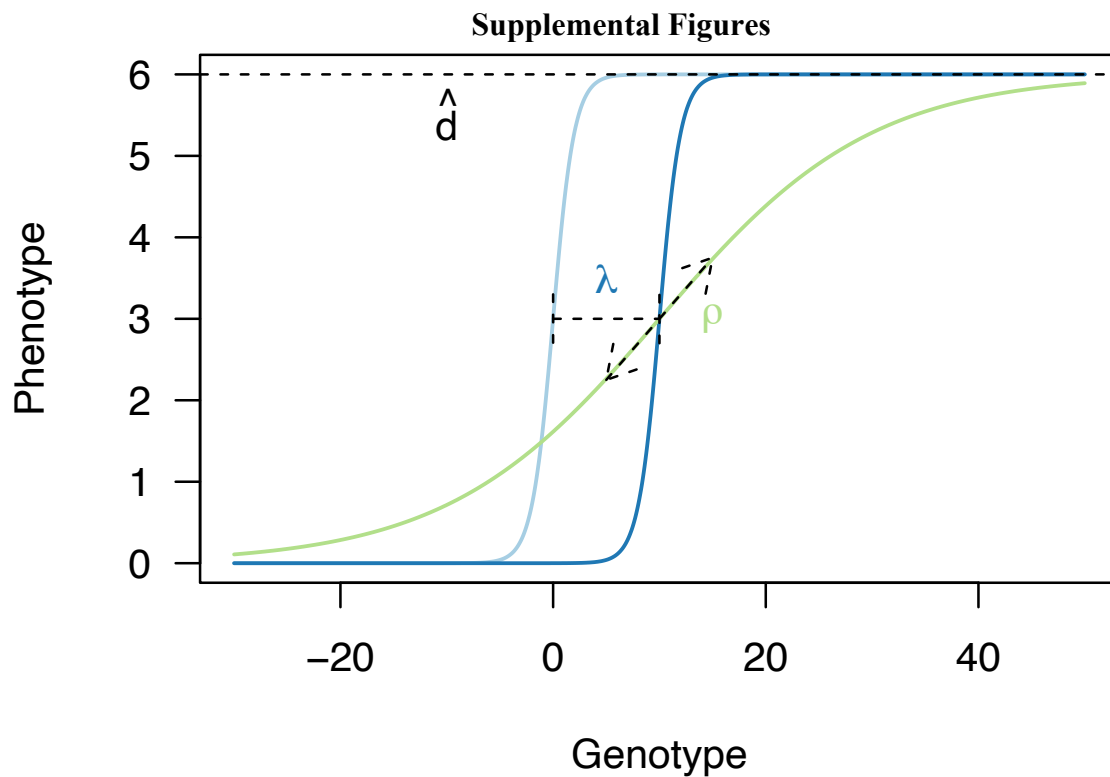
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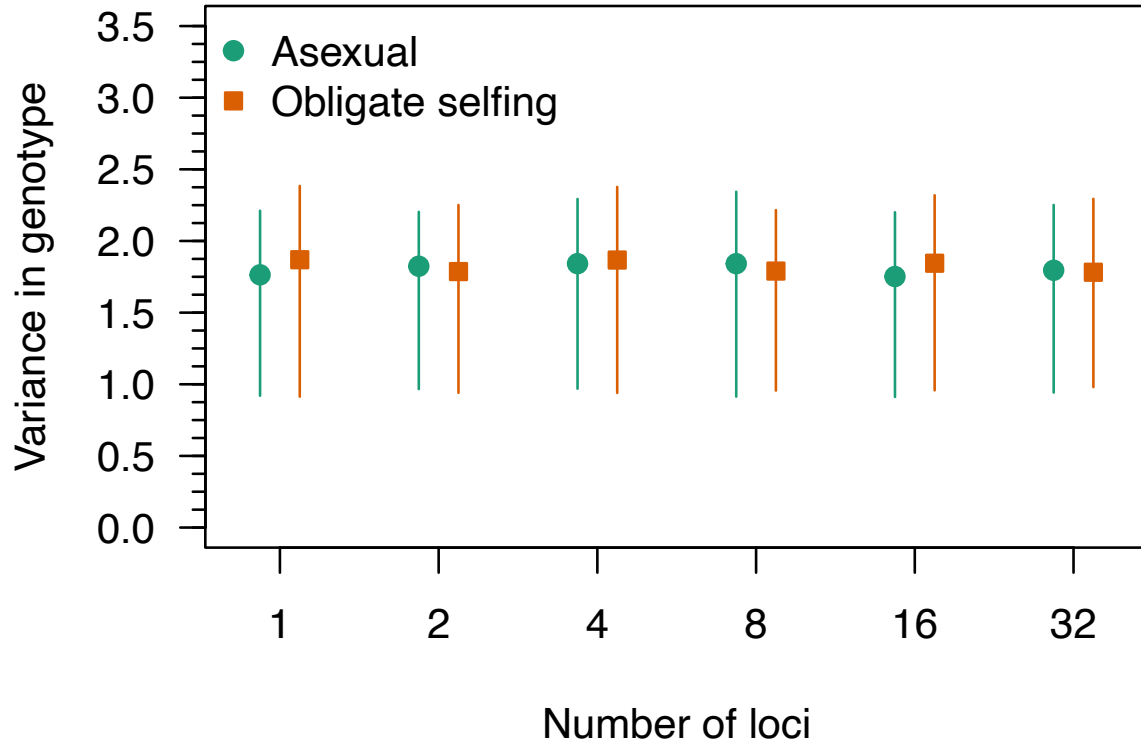
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**Figure S1:** Visual description of the function transforming individuals’ allele sums (“genotype”) to their expected dispersal distance (“phenotype”). The maximum expected dispersal distance,  $\hat{d}$ , is illustrated by the horizontal dashed line at the top of the graph. The comparison of the function with  $\lambda = 0$  and  $\rho = 1$  (light blue line) to other parameterizations illustrates the impact of these parameters. During the burn-in phase of the simulations, there is no selection on dispersal, so allele values in the population stay centered on 0. Given that, with  $\lambda = 0$ , populations would start the main simulations with average phenotypes being half of  $\hat{d}$ . By increasing  $\lambda$  to 10 as an offset (dark blue line), the simulations begin with populations at a lower dispersal phenotype, providing room for dispersal evolution. Finally, by using a lower value of  $\rho$  (green line), the slope of the transition between 0 and  $\hat{d}$  is decreased to better approximate a linear transition between these values for a larger range of possible genotypes.



**Figure S2:** Comparison of the variance in genotype (summed alleles) values for populations with no genetic mixing before range expansions or shifts (i.e. calculated at the end of the 50,000 generation burn-in period). In asexual and obligately self-fertilizing populations, alleles do not mix among individuals during reproduction, meaning that selection acts primarily on the sum of alleles contributing to dispersal. This could lead to inflated genetic variance in these scenarios since an individual with alleles -10 and 10 would have the same phenotype as an individual with alleles -1 and 1 and both combinations of alleles would be inherited together and selected for or against to the same degree. To ensure this possibility did not skew the results of our additive genetic variance calculations presented in the main text, we compared the variance in the sum of allele values across haploid and obligately self-fertilizing populations. While investigating the variance in this way emphasizes the similarities among these scenarios, the scale of variance in the summed allele values matches the additive genetic variance values presented in the main text, meaning those values can be used confidently in making comparisons among different scenarios.

### **Sensitivity analyses**

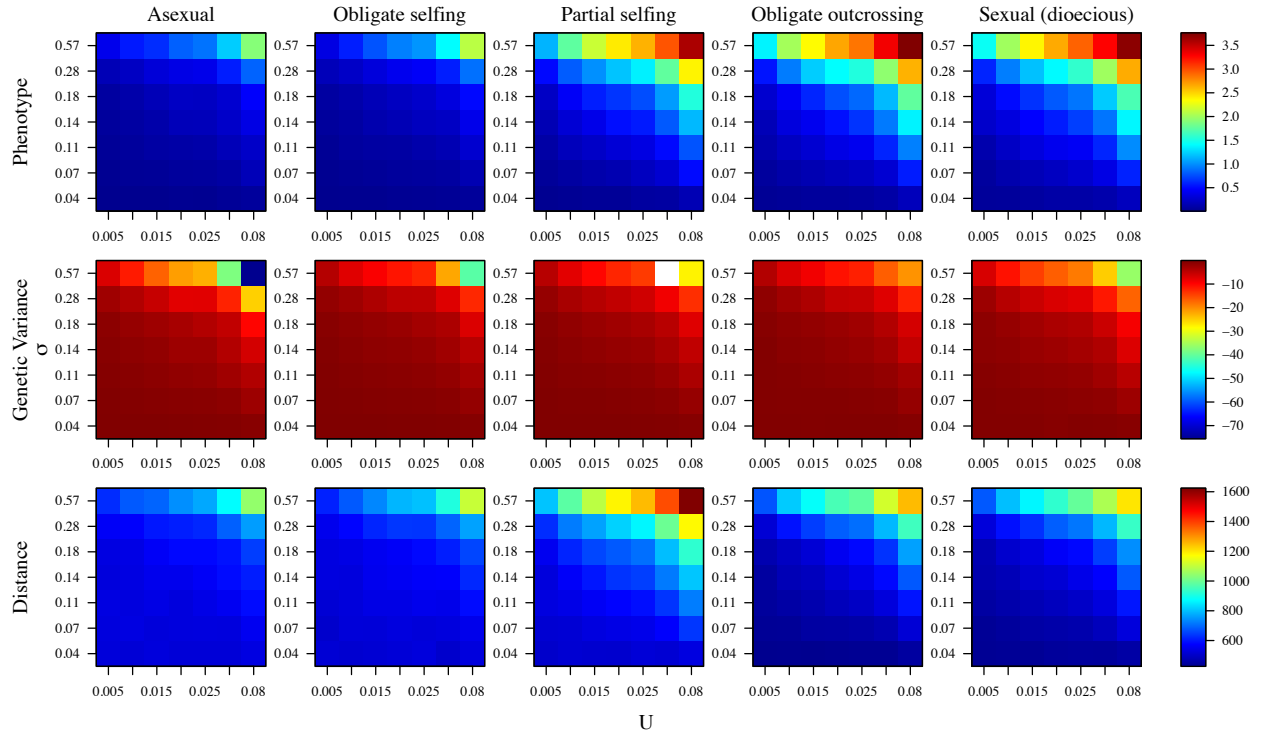
To explore the role of parameters governing mutation, population growth, and dispersal in our results, we performed three sensitivity analyses varying (1) the values of the genome-wide probability of mutation ( $U$ ) and the standard deviation of mutation effect size ( $\sigma$ ), (2) the intrinsic growth rate ( $R$ ) and maximum carrying capacity ( $K_{max}$ ), and (3) the maximum dispersal phenotype ( $\hat{d}$ ) and the slope of the transition of phenotypes from 0 to  $\hat{d}$  ( $\rho$ ). In each of the three sensitivity analyses, we simultaneously explored 49 parameter combinations (7 values of each of the two parameters explored in each analysis). In all sensitivity analyses presented here, if a parameter was not directly under investigation, it was held constant at the value used for the simulations in the main text (Table 1).

For each of these parameter combinations, we restricted loci number to 4 and explored population dynamics in all five population types from the main text (asexual, monoecious with obligate selfing, monoecious with partial selfing, monoecious with obligate outcrossing, and dioecious) for a total of 735 scenarios (5 population types x 49 parameter combinations x 3 sensitivity analyses). For each scenario, we performed 100 full simulations, consisting of a 50,000 generation burn-in period, 200 generations of unbounded range expansion, and 200 generations of range shift as described in the main text.

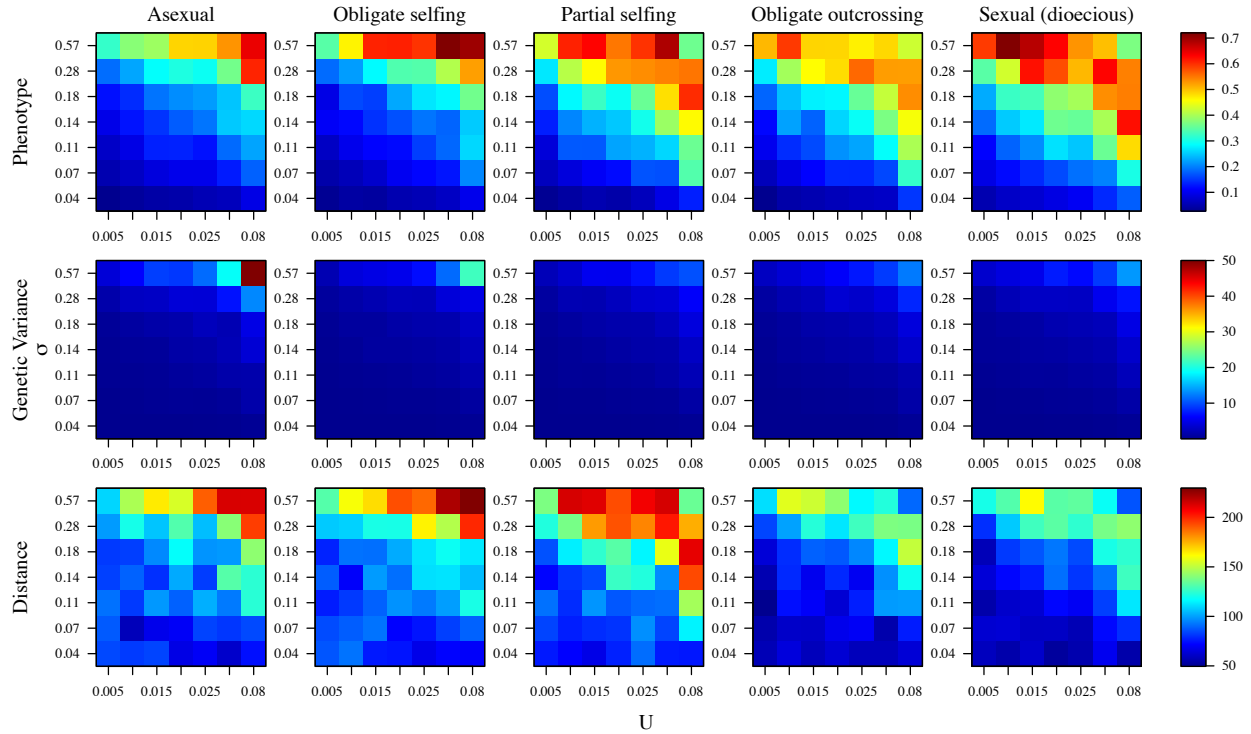
### **Model sensitivity to mutation parameters**

To explore the effects of the mutation parameters, we altered the values of each from the main text by 25%, 50%, 75%, 100%, 125%, and 200% so that half the range was below and half above the values used for the results presented in the main text.

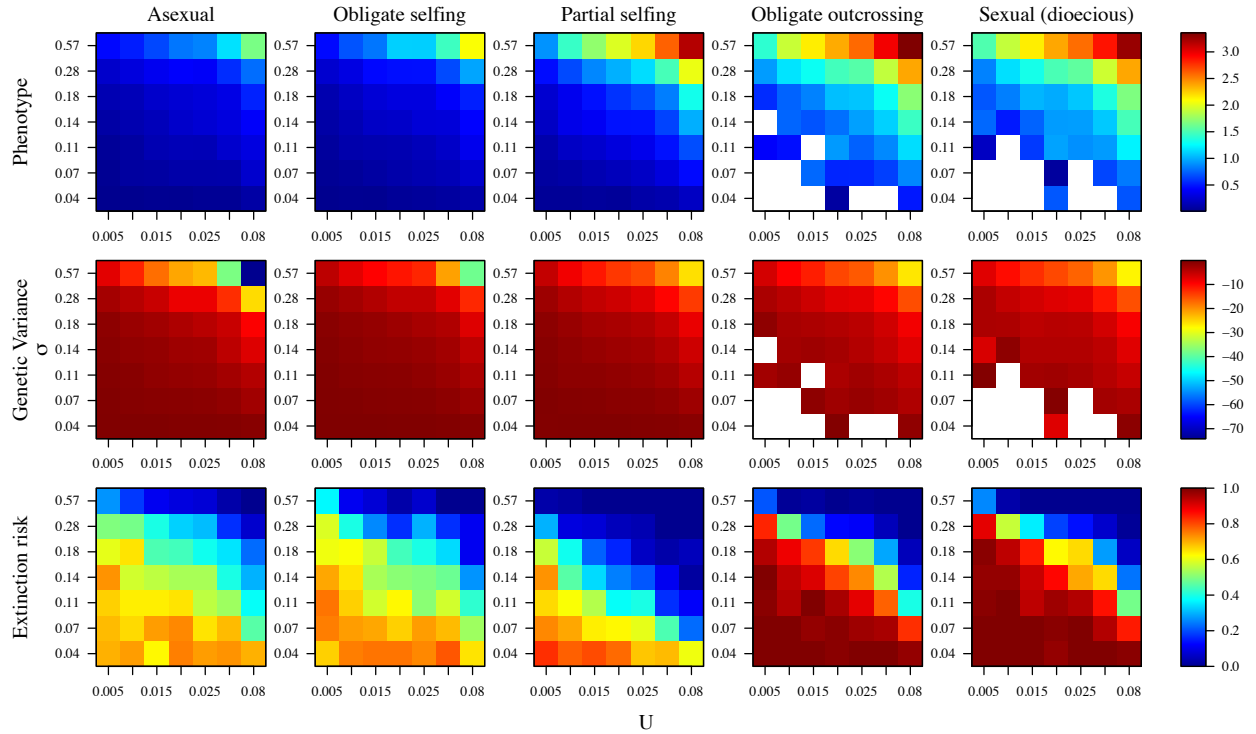
As demonstrated in Figures S3-S6, higher mutation rates and higher mutation effect sizes led to the evolution of larger dispersal phenotypes and correspondingly greater distances spread (in expansions) and lower extinction risk (in shifts). However, the values used for the main simulations show similar dynamics to much of the explored parameter space and, importantly, the qualitative relationships among the different population types do not change under different combinations of mutation parameters.



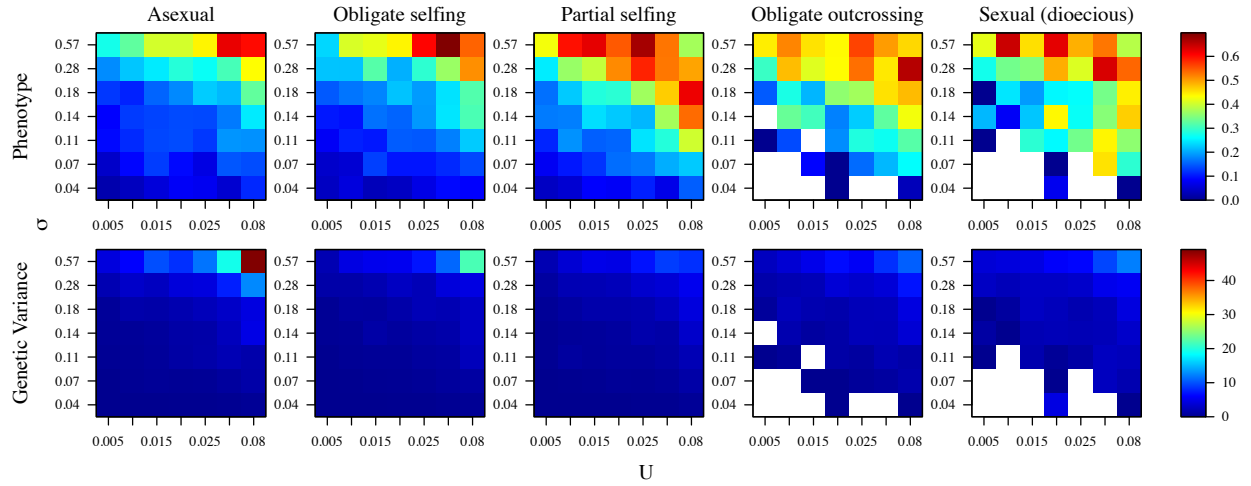
**Figure S3:** Effect of mutation parameters on dispersal phenotype, additive genetic variance, and distance spread in unbounded range expansions. Color indicates the mean change (compared to initial conditions) after 200 generations of unbounded range expansion for dispersal phenotype (row 1), additive genetic variance (row 2), and distance spread (row 3). The values explored for  $U$  are on the x axis and the  $\sigma$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.



**Figure S4:** Effect of mutation parameters on the among-simulation variation in dispersal phenotype, additive genetic variance, and distance spread in unbounded range expansions. Color indicates the width of interquartile ranges across simulations, with the first row showing the width of the interquartile range for changes to dispersal phenotype (compared to initial conditions) after 200 generations of unbounded range expansion. The second row shows the width of the interquartile range for changes to additive genetic variance and the third row shows the width of the interquartile range of distance spread by expanding populations. The values explored for U are on the x axis and the  $\sigma$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.



**Figure S5:** Effect of mutation parameters on dispersal phenotype, additive genetic variance, and distance spread in range shifts. Color indicates the mean change (compared to initial conditions) after 200 generations of range shift for dispersal phenotype (row 1), additive genetic variance (row 2), and extinction risk (row 3). The scenarios in which all simulations went extinct correspond to white boxes in the first and second rows as those scenarios have no values for the changes in dispersal phenotype or genetic variance. The values explored for  $U$  are on the x axis and the  $\sigma$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.

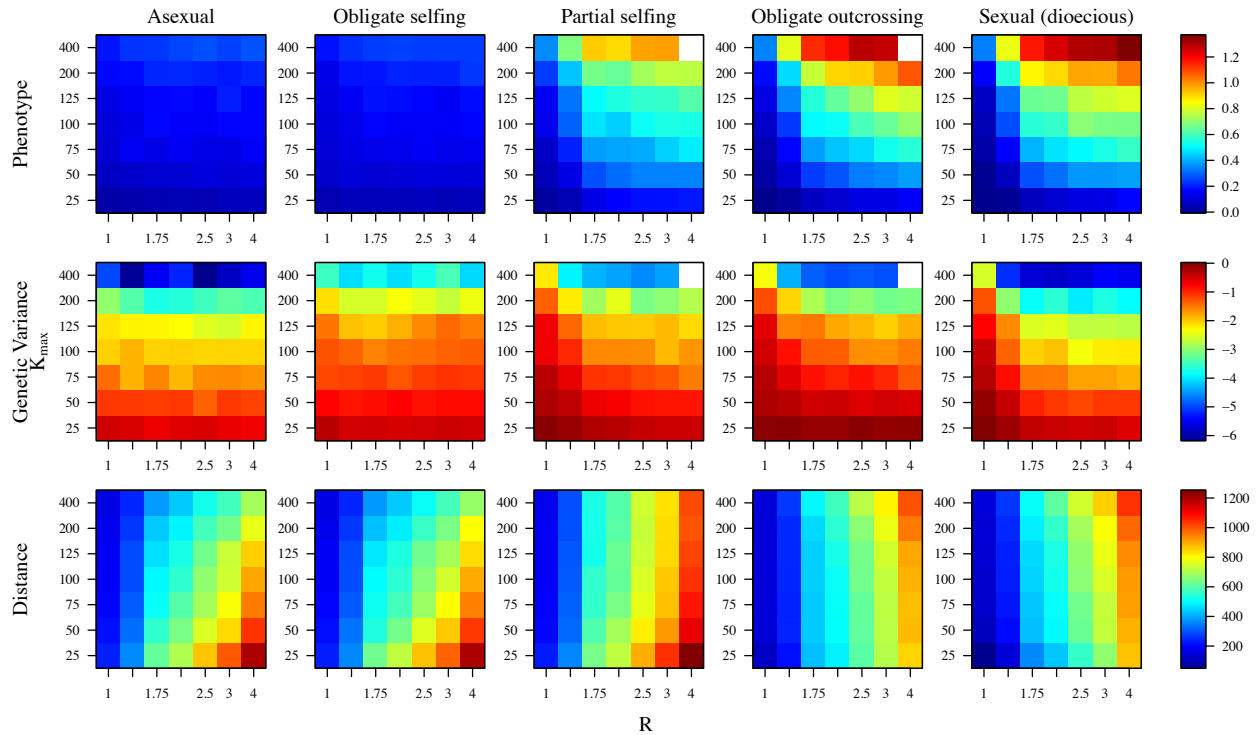


**Figure S6:** Effect of mutation parameters on the among-simulation variation in dispersal phenotype and additive genetic variance in range shifts. Color indicates the width of interquartile ranges across simulations, with the first row showing the width of the interquartile range for changes to dispersal phenotype (compared to initial conditions) after 200 generations of range shift. The second row shows the width of the interquartile range for changes to additive genetic variance. White squares indicate scenarios in which all populations went extinct during the range shift. The values explored for  $U$  are on the x axis and the  $\sigma$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.

### Model sensitivity to demographic parameters

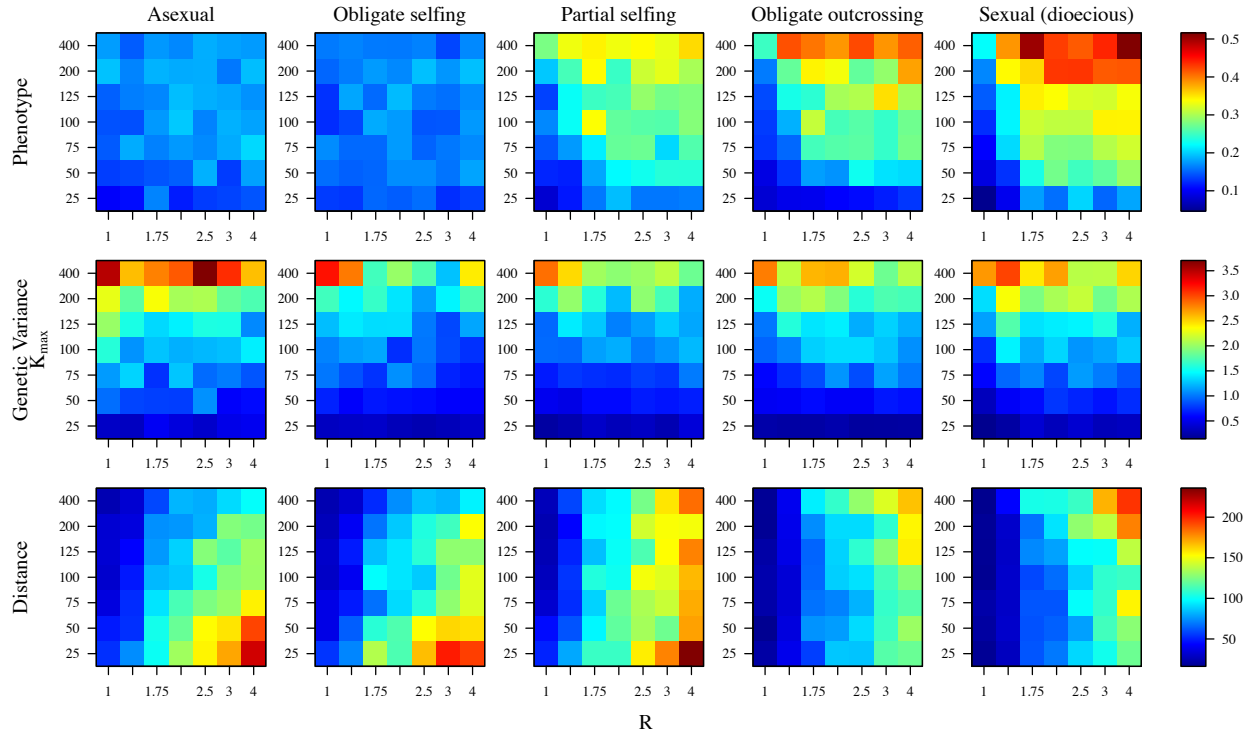
To explore the effects of the demographic parameters, we set  $R$  to 1.1, 1.25, 1.75, 2, 2.5, 3, and 4 (the results in the main text use  $R = 2$ ). Similarly, we set  $K_{max}$  to 25, 50, 75, 100, 125, 200, and 400 (the results in the main text use  $K_{max} = 100$ ).

As demonstrated in Figures S7-S10, higher values of both  $R$  and  $K_{max}$  lead to greater distance spread and lower extinction risk. However, similarly to the results from the mutation sensitivity analysis, no parameter combination resulted in patterns that are qualitatively different from those presented in the main text in terms of the relative comparisons among population types.

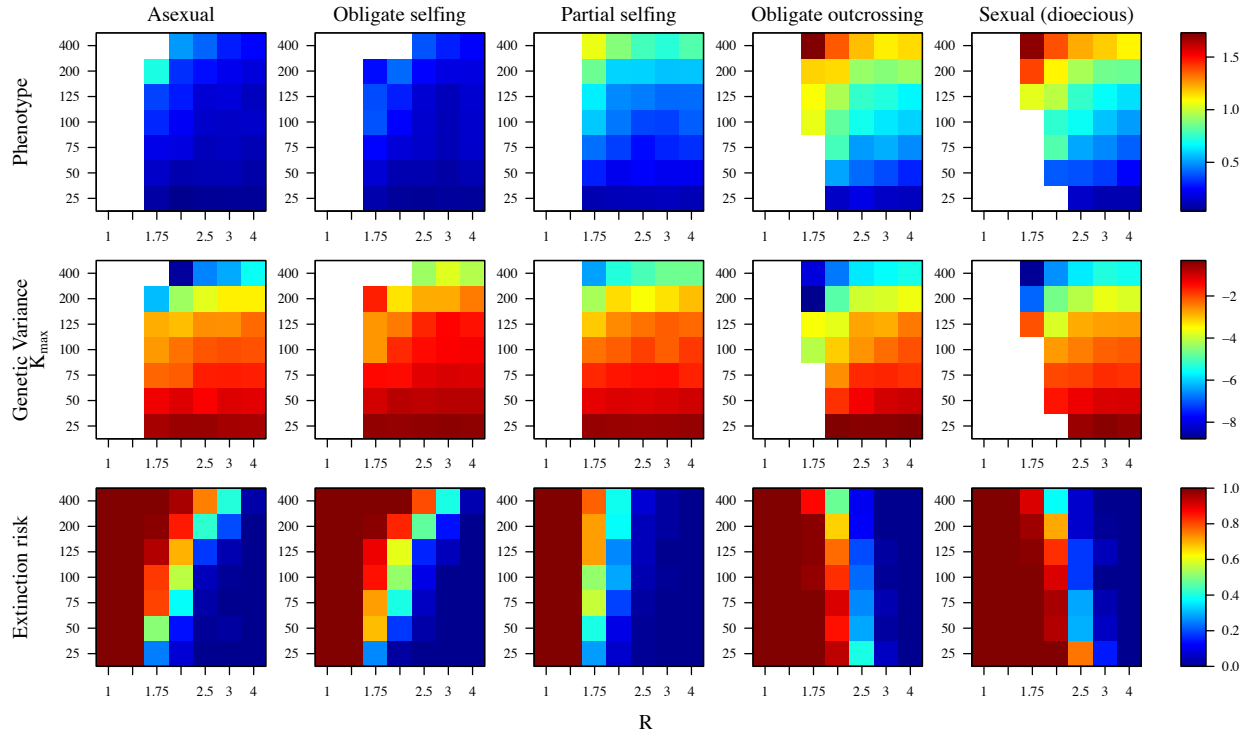


**Figure S7:** Effect of demographic parameters on dispersal phenotype, additive genetic variance, and distance spread in unbounded range expansions. Color indicates the mean change (compared to initial conditions) after 200 generations of unbounded range expansion for dispersal phenotype (row 1), genetic variance (row 2), and distance spread (row 3). The values explored for  $R$  are on the x axis and the  $K_{max}$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.

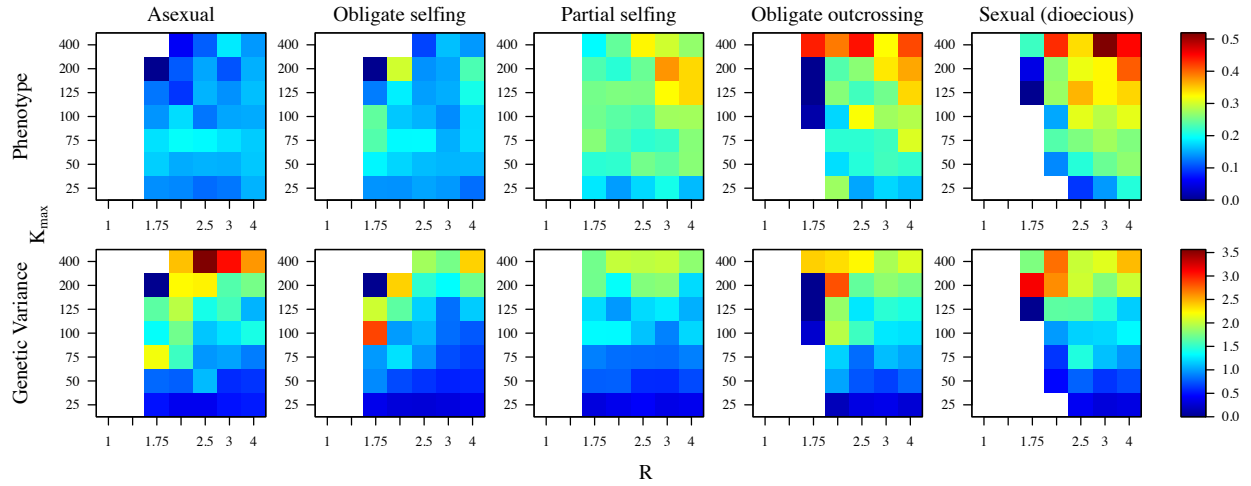




**Figure S8:** Effect of demographic parameters on the among-simulation variation in dispersal phenotype, additive genetic variance, and distance spread in unbounded range expansions. Color indicates the width of interquartile ranges across simulations, with the first row showing the width of the interquartile range for changes to dispersal phenotype (compared to initial conditions) after 200 generations of unbounded range expansion. The second row shows the width of the interquartile range for changes to additive genetic variance and the third row shows the width of the interquartile range of distance spread by expanding populations. The values explored for  $R$  are on the x axis and the  $K_{max}$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.



**Figure S9:** Effect of demographic parameters on dispersal phenotype, additive genetic variance, and distance spread in range shifts. Color indicates the mean change (compared to initial conditions) after 200 generations of range shift for dispersal phenotype (row 1), genetic variance (row 2), and extinction risk (row 3). The scenarios in which all simulations went extinct correspond to white boxes in the first and second rows as those scenarios have no values for the changes in dispersal phenotype or genetic variance. The values explored for  $R$  are on the x axis and the  $K_{max}$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.

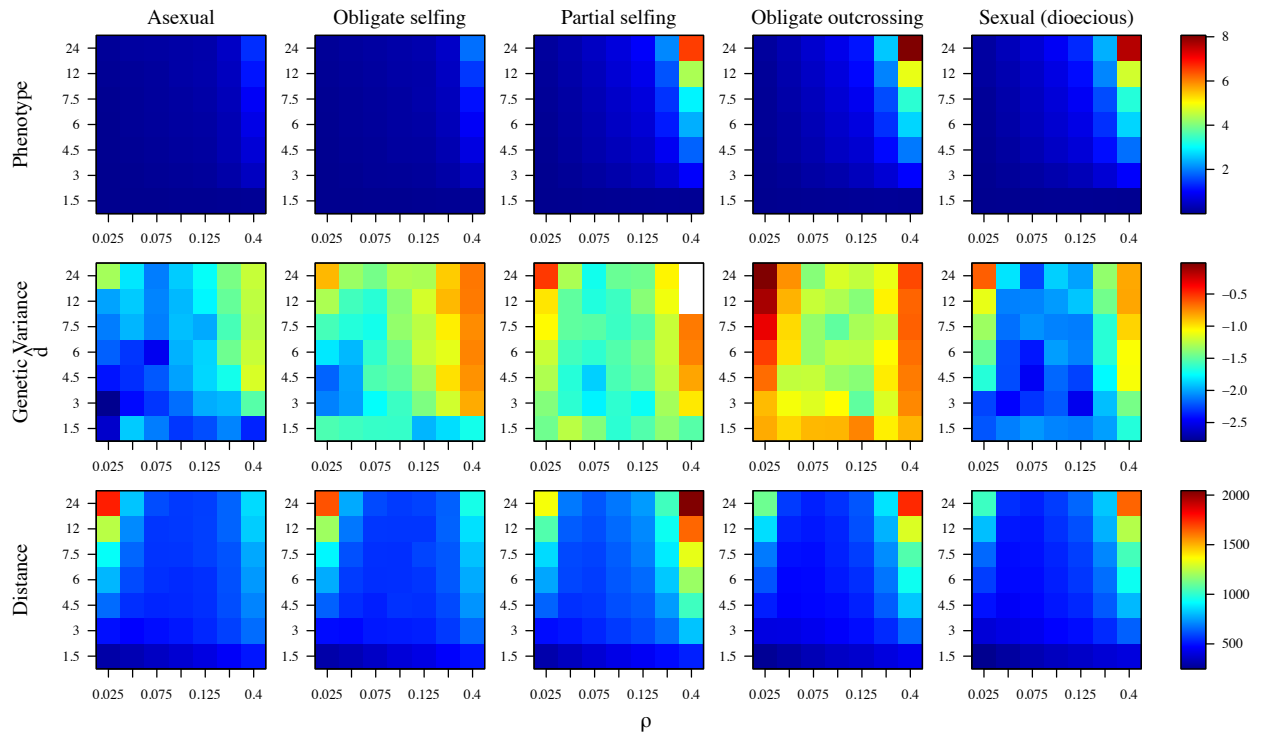


**Figure S10:** Effect of demographic parameters on the among-simulation variation in dispersal phenotype and additive genetic variance in range shifts. Color indicates the width of interquartile ranges across simulations, with the first row showing the width of the interquartile range for changes to dispersal phenotype (compared to initial conditions) after 200 generations of range shift. The second row shows the width of the interquartile range for changes to additive genetic variance. White squares indicate scenarios in which all populations went extinct during the range shift. The values explored for  $R$  are on the x axis and the  $K_{max}$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.

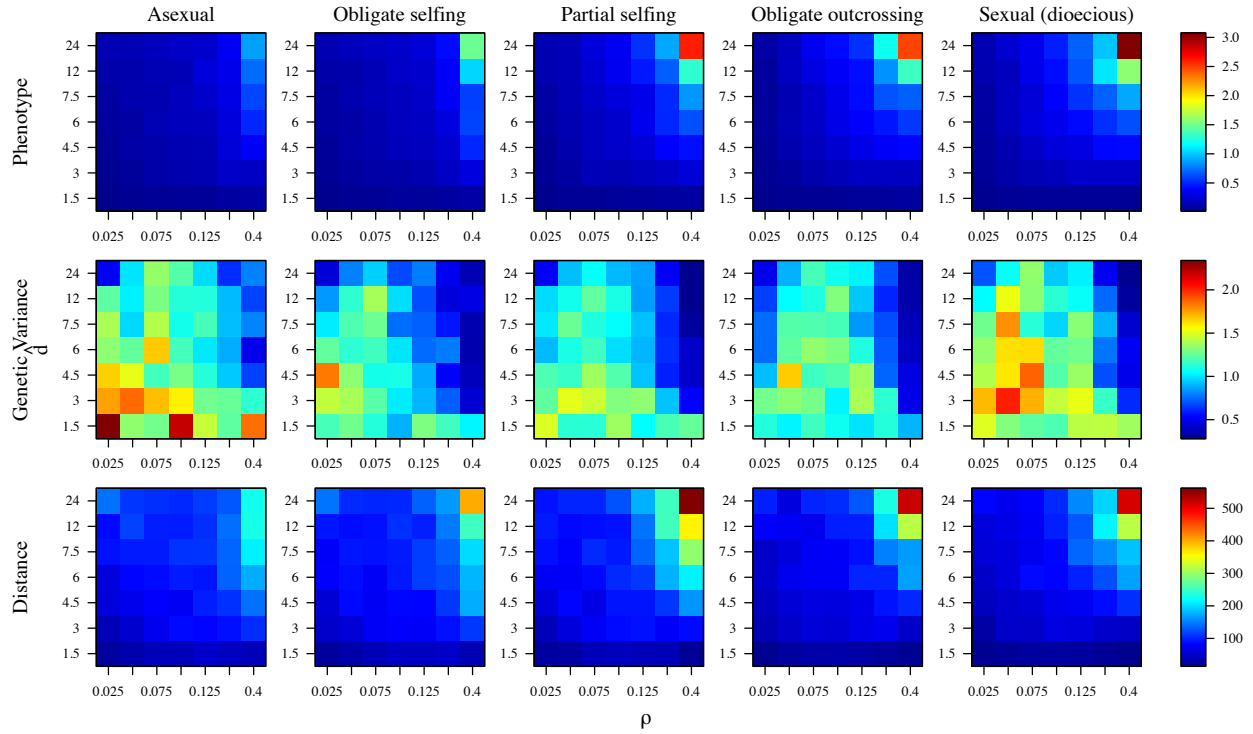
### Model sensitivity to dispersal parameters

To explore the effects of the dispersal parameters, we set  $\hat{d}$  and  $\rho$  to 25%, 50%, 75%, 100%, 125%, 200%, and 300% of the values used for the results presented in the main text ( $\hat{d} = 6$  and  $\rho = 0.1$ ).

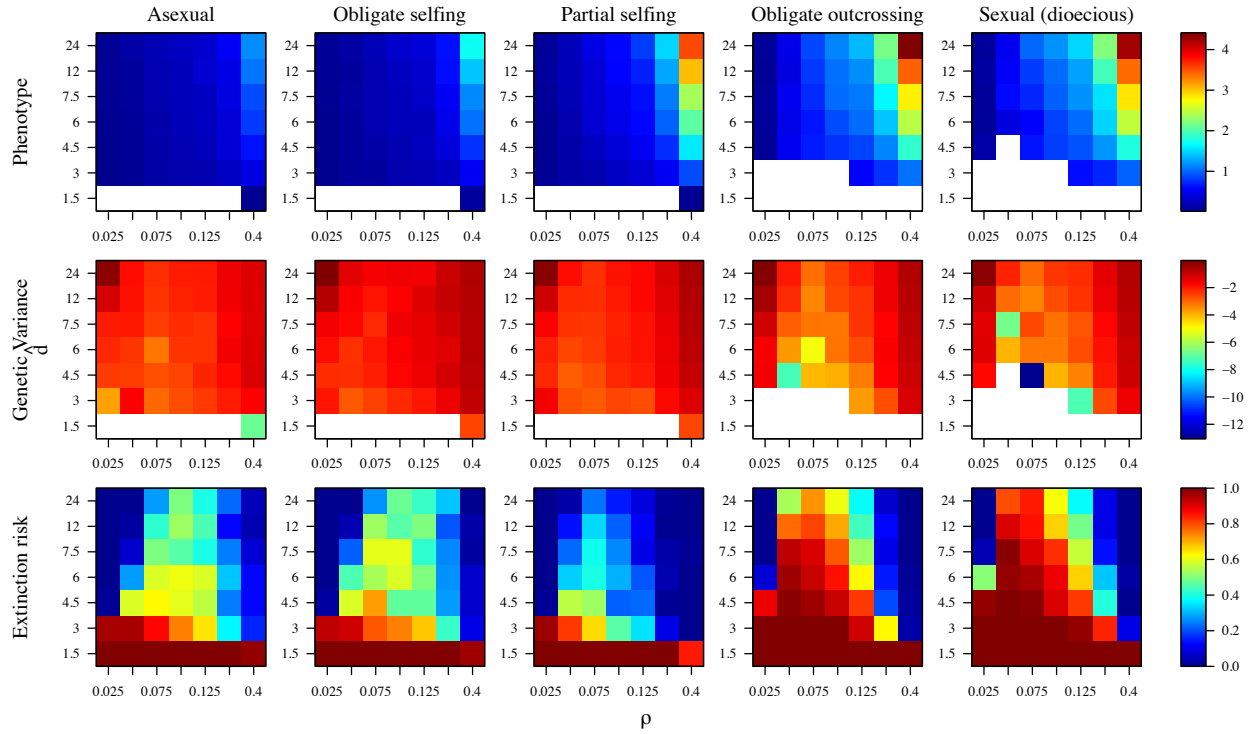
As demonstrated in Figures S11-S14, higher values of  $\hat{d}$  and extreme (either low or high) values of  $\rho$  can lead to increased distance spread in range expansions and reduced extinction risk in range shifts. However, similarly to the results from the previous sensitivity analyses, no parameter combination resulted in patterns that are qualitatively different from those presented in the main text in terms of the relative comparisons among population types.



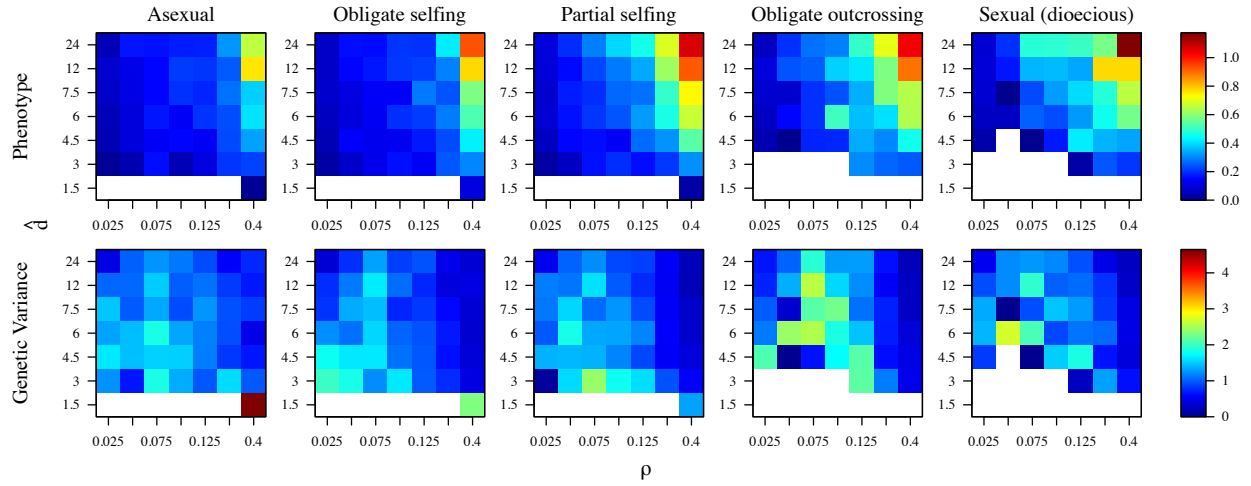
**Figure S11:** Effect of dispersal parameters on dispersal phenotype, additive genetic variance, and distance spread in unbounded range expansions. Color indicates the mean change (compared to initial conditions) after 200 generations of unbounded range expansion for dispersal phenotype (row 1), genetic variance (row 2), and distance spread (row 3). The values explored for  $\rho$  are on the x axis and the  $\hat{d}$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.



**Figure S12:** Effect of dispersal parameters on the among-simulation variation in dispersal phenotype, additive genetic variance, and distance spread in unbounded range expansions. Color indicates the width of interquartile ranges across simulations, with the first row showing the width of the interquartile range for changes to dispersal phenotype (compared to initial conditions) after 200 generations of unbounded range expansion. The second row shows the width of the interquartile range for changes to additive genetic variance and the third row shows the width of the interquartile range of distance spread by expanding populations. The values explored for  $\rho$  are on the x axis and the  $\hat{d}$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.



**Figure S13:** Effect of dispersal parameters on dispersal phenotype, additive genetic variance, and distance spread in range shifts. Color indicates the mean change (compared to initial conditions) after 200 generations of range shift for dispersal phenotype (row 1), genetic variance (row 2), and extinction risk (row 3). The scenarios in which all simulations went extinct correspond to white boxes in the first and second rows as those scenarios have no values for the changes in dispersal phenotype or genetic variance. The values explored for  $\rho$  are on the x axis and the  $\hat{d}$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.



**Figure S14:** Effect of dispersal parameters on the among-simulation variation in dispersal phenotype and additive genetic variance in range shifts. Color indicates the width of interquartile ranges across simulations, with the first row showing the width of the interquartile range for changes to dispersal phenotype (compared to initial conditions) after 200 generations of range shift. The second row shows the width of the interquartile range for changes to additive genetic variance. White squares indicate scenarios in which all populations went extinct during the range shift. The values explored for  $\rho$  are on the x axis and the  $\hat{d}$  values are on the y axis. The parameter combination used in the main simulations are at the center of each plot.