

Supplementary Methods

Preliminary simulations

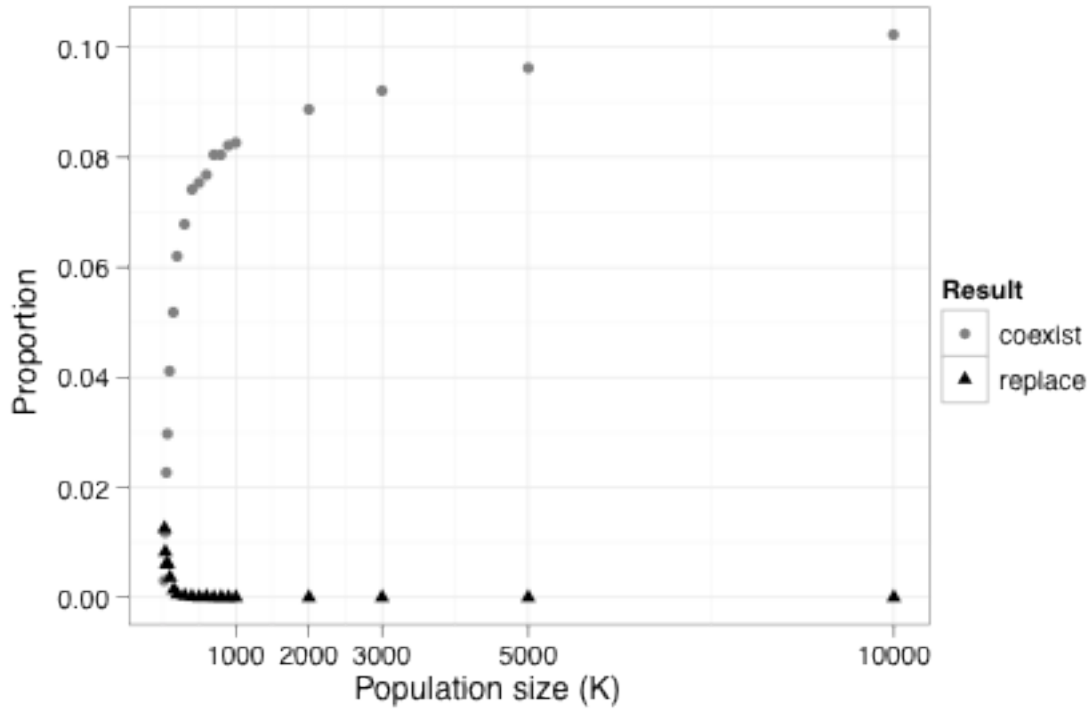
Due to the infinite size of parameter space, but finite computational power available, we performed preliminary simulations that allowed us to choose a subset of all the possible combinations of the non-focal parameters (population size, genetic architecture, h , M) without completely sacrificing generality. Each simulation began by assigning genotypes at random to K diploid individuals. Because we wanted to distinguish our results from the effects of genetic drift, we first tested for effects of population size. Our goal was to identify a population size above which stochastic establishment of novel polyploid populations became very rare (Rausch et al. 2005), but which still allowed for relatively efficient individual based computation. Preliminary simulations indicated that the probability of polyploid establishment and coexistence changed little above population sizes of 1000 individuals (Supplementary Figure S1). For this reason, we chose to focus on $K = 1000$. We also examined the effects of the genetic architecture on establishment and found that increasing the number of loci increases the probability of establishment for up to five loci, with decreasing probability of establishment beyond five loci (Supplementary figure S2). However, our preliminary simulations indicated that the number of alleles at each locus did not appreciably change the probability of establishment (Supplementary figure S3). We therefore performed the majority of our simulations using two loci and ten alleles in order to provide a conservative estimate of the rate of establishment. We tested multiple values for the number of ovules per individual (M), and found that increasing M beyond a minimum value necessary to

produce enough seeds to regenerate the population did not affect results. In order to decrease computational time, we therefore set M to be that minimum number, which was four. Similarly, as long as h was larger than approximately 8, results were unaffected. Therefore, we used $h=10$ for all simulations.

Source code for the simulations is available at: <http://www.benjaminoswald.org/apps.php>

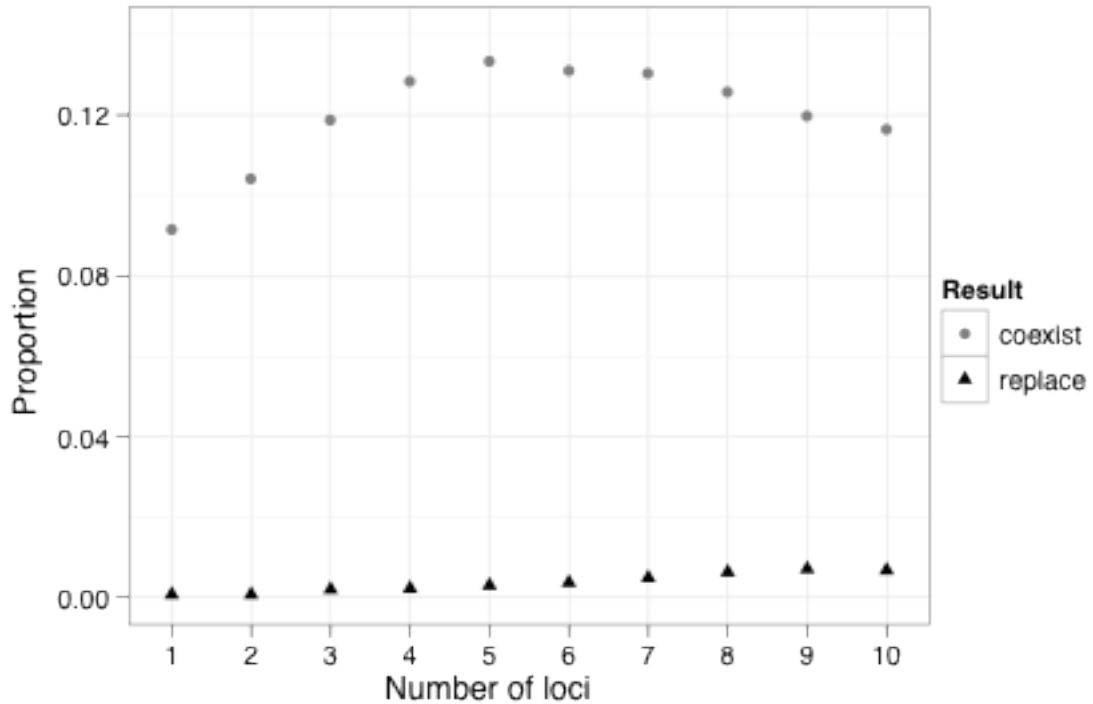
Supplementary Figures

Figure S1



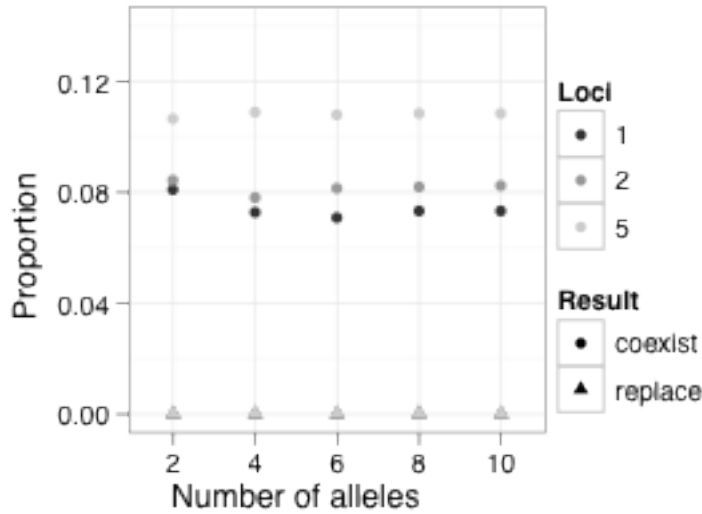
The proportion of simulations that resulted in either coexistence of both the diploid and tetraploid lineage (gray circles) or the replacement of the diploids by the tetraploids (black triangles) is shown for varying total population sizes. For each population size we ran a total of 1920 simulations, 20 simulations for each parameter combination. The parameters were: $loci = 2$, $alleles = 10$, $u = 0.005$, $t = 0.01$, $r = 0.9$, and all possible combinations of: $a = \{2, 4, 8, 50\}$, $c = \{2, 4, 8, 50\}$, $g = \{0, 0.2, 0.4\}$, $s = \{0, 0.05, 0.1, 0.2\}$, $d = \{1.1, 1.2, 1.3, 1.5, 1.7\}$.

Figure S2



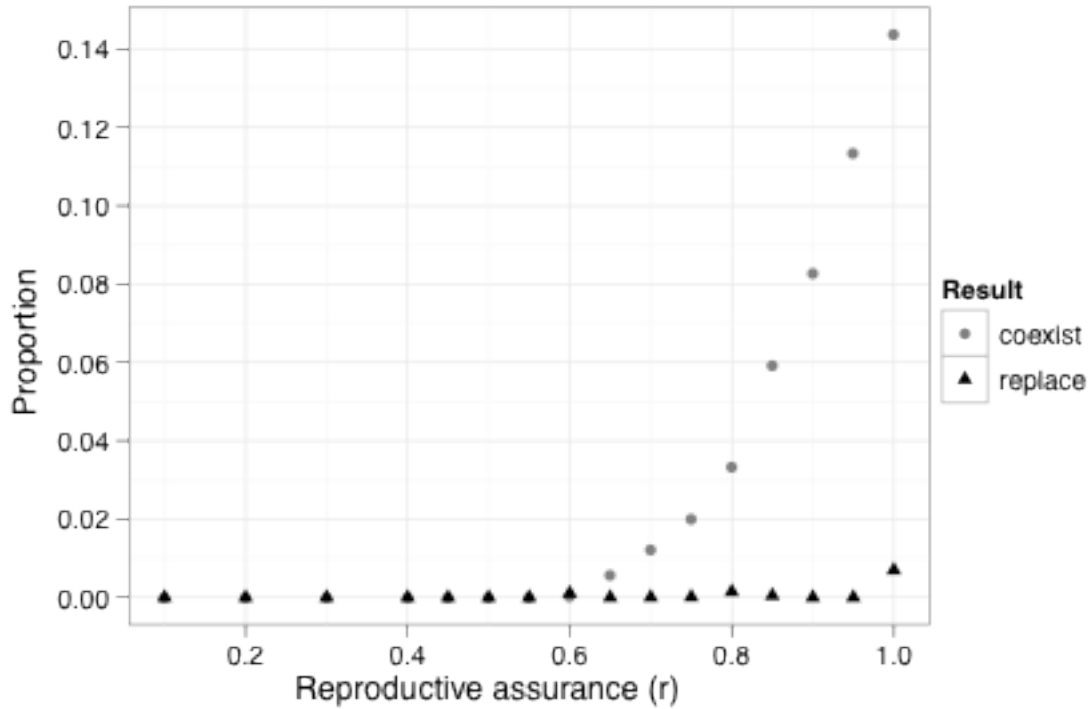
The proportion of simulations that resulted in either coexistence of both the diploid and tetraploid lineage (gray circles) or the replacement of the diploids by the tetraploids (black triangles) is shown for varying number of loci. For each number of loci we ran a total of 1920 simulations, 20 simulations for each parameter combination. The parameters were: $K=1000$, $alleles=10$, $u=0.005$, $t=0.01$, $r=0.9$, and all possible combinations of: $a=\{2, 4, 8, 50\}$, $c=\{2, 4, 8, 50\}$, $g=\{0, 0.2, 0.4\}$, $s=\{0, 0.05, 0.1, 0.2\}$, $d=\{1.1, 1.2, 1.3, 1.5, 1.7\}$.

Figure S3



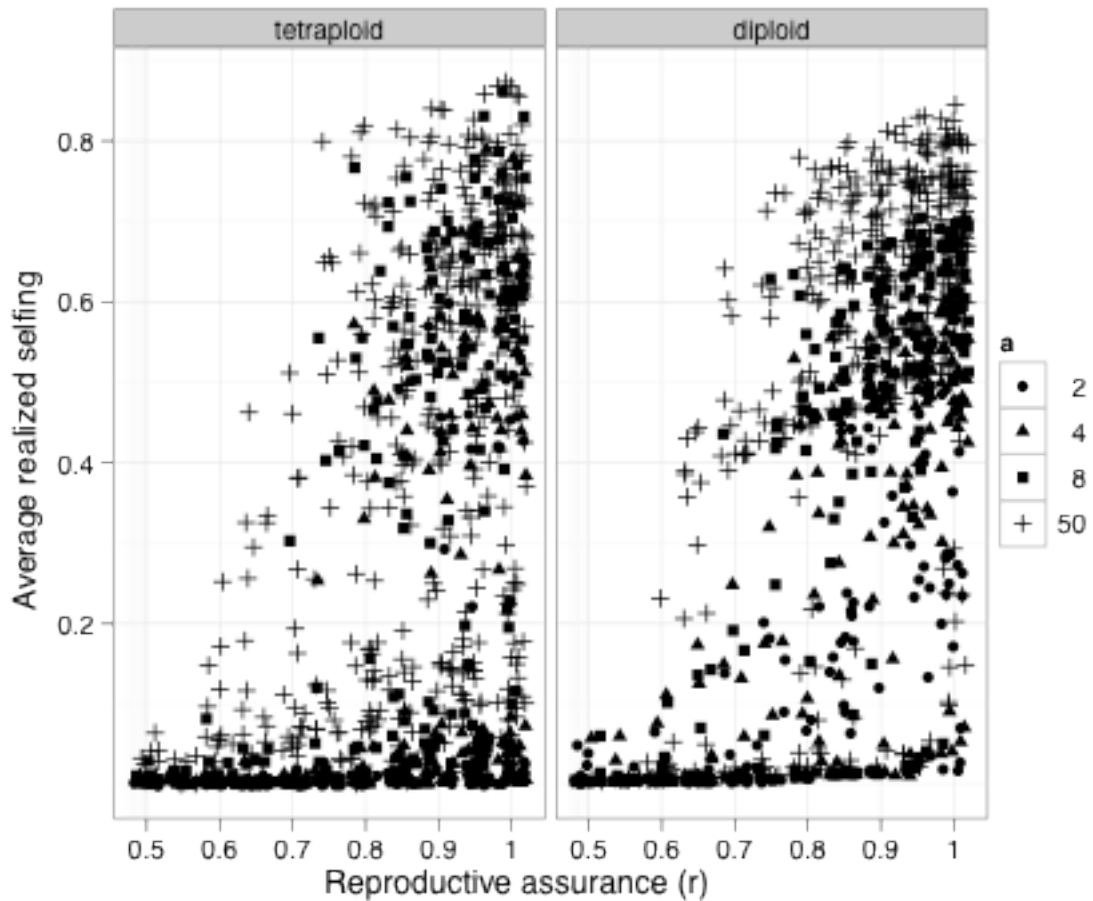
The proportion of simulations that resulted in either coexistence of both the diploid and tetraploid lineage (circles) or the replacement of the diploids by the tetraploids (triangles) is shown for varying number of loci (shades of grey) and alleles. For each number of alleles we ran a total of 57,600 simulations, 20 simulations for each of 2880 parameter combinations. The parameters were: $K=1000$, $u=0.005$, $t=0.01$, $r=0.9$, and all possible combinations of: $loci=\{1, 2, 5\}$, $a=\{2, 4, 8, 50\}$, $c=\{2, 4, 8, 50\}$, $g=\{0, 0.2, 0.4\}$, $s=\{0, 0.05, 0.1, 0.2\}$, $d=\{1.1, 1.2, 1.3, 1.5, 1.7\}$.

Figure S4



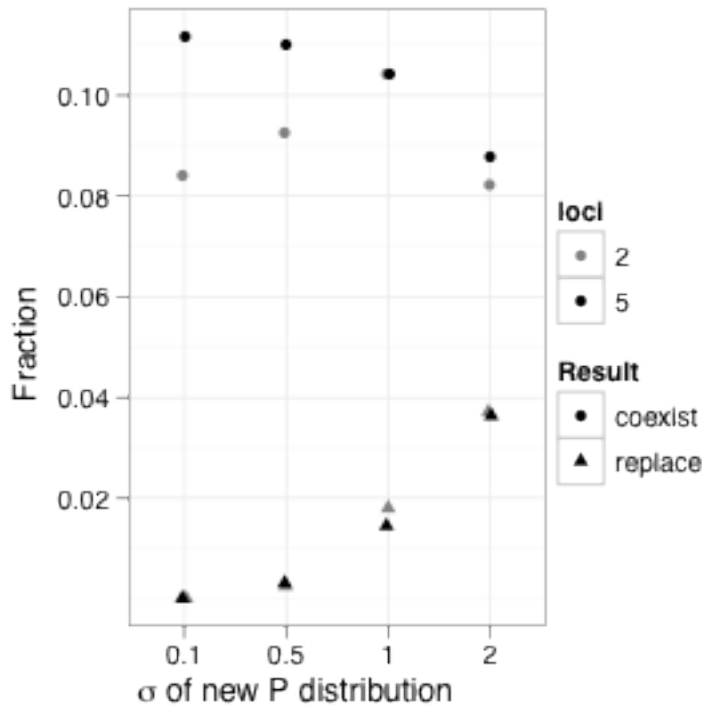
The proportion of simulations that resulted in either coexistence of both the diploid and tetraploid lineage (gray circles) or the replacement of the diploids by the tetraploids (black triangles) is shown for various values of r (reproductive assurance). For each value of r we ran a total of 19,200 simulations, 20 simulations for each of 960 parameter combinations. The parameters were: $K=1000$, $u=0.005$, $t=0.01$, $loci=2$, $alleles=10$ and all possible combinations of: $a=\{2, 4, 8, 50\}$, $c=\{2, 4, 8, 50\}$, $g=\{0, 0.2, 0.4\}$, $s=\{0, 0.05, 0.1, 0.2\}$, $d=\{1.1, 1.2, 1.3, 1.5, 1.7\}$.

Figure S5



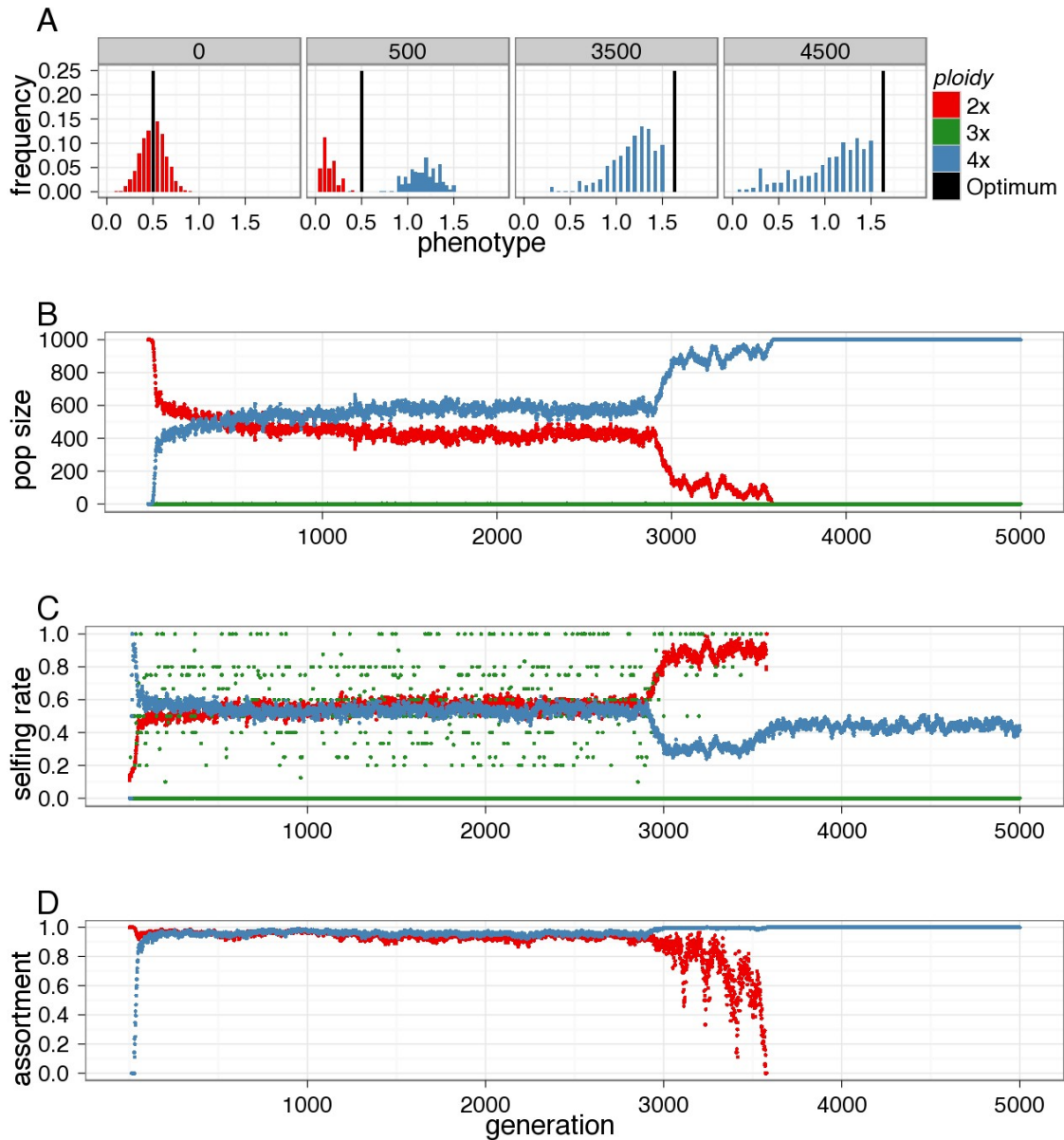
Realized selfing for the tetraploids and diploids is plotted versus the reproductive assurance parameter (r) for the various values of the assortative mating parameter (a) (shapes). Only simulations where the tetraploid population established are shown. Each point represents the rate of selfing for the either the tetraploid or diploid lineage averaged over all generations for one simulation. The average selfing rate varied widely, though there was some selfing necessary for coexistence or replacement. A total of 10560 simulations, one for each parameter combination, were used to produce this plot. The parameters were: $K=1000$, $u=0.005$, $t=0.0$, $loci=2$, $alleles=10$ and all possible combinations of: $a=\{2, 4, 8, 50\}$, $c=\{2, 4, 8, 50\}$, $g=\{0, 0.2, 0.4\}$, $s=\{0, 0.05, 0.1, 0.2\}$, $d=\{1.1, 1.2, 1.3, 1.5, 1.7\}$.

Figure S6



The proportion of simulations that resulted in either coexistence of both the diploid and tetraploid lineage (circles) or the replacement of the diploids by the tetraploids (triangles) is shown for varying number of loci (shades of grey) as a function of the standard deviation in the distribution of the shifting optimum. For each standard deviation we ran a total of 38,400 simulations, 20 simulations for each of 1920 parameter combinations. The parameters were: $K=1000$, $alleles=10$, $\mu=0.005$, $t=0.01$, $r=0.9$, and all possible combinations of: $loci=\{2, 5\}$, $a=\{2, 4, 8, 50\}$, $c=\{2, 4, 8, 50\}$, $g=\{0, 0.2, 0.4\}$, $s=\{0, 0.05, 0.1, 0.2\}$, $d=\{1.1, 1.2, 1.3, 1.5, 1.7\}$.

Figure S7



The results of one individual based simulation where the optimum shifts are shown here. In each panel, red represents diploids, blue the tetraploids, and green the triploids. Panels are as follows: A) distribution of phenotypes for each cytotype for the generation listed; B) population size of each cytotype over time; C) the realized rate of selfing over time; and D) rate of assortative mating within ploidy over time. The tetraploid subpopulation establishes early in the simulation, and coexists with the diploids until generation 3000, when the diploids are replaced by the tetraploids. Parameters for this run were: $K=1000$, $alleles=10$, $loci=5$, $r=1$, $u=0.01$, $a=4$, $c=4$, $g=0.4$, $s=0.1$, $d=1.5$, $t=0.01$.