Supplementary Text

S1. Materials and Methods

To derive a diffusion approximation we start with the standard Kolmogorov forward equation in two dimensions (Gardiner 2009),

$$\frac{\partial \phi}{\partial t} = \frac{1}{2}\left(\frac{\partial^2 V_{pp}\phi}{\partial p^2} + 2\frac{\partial^2 V_{ph}\phi}{\partial p \partial h} + \frac{\partial^2 V_{hh}\phi}{\partial h^2}\right) - \left(\frac{\partial M_p \phi}{\partial p} + \frac{\partial M_h \phi}{\partial h}\right). \tag{11}$$

Here, M_i and V_{ij} represent the instantaneous mean and variance of allele frequency change. Assuming only a fraction f of the population undergo mating according to Eq. 4, the expected frequencies in the next generation, p' and h', are given by replacing π and η with $f\pi + (1-f)p$ and $f\eta + (1-f)h$ in Eq. 5:

$$\begin{aligned}\mathrm{E}(p') &= \frac{(f\pi + (1-f)p) - s(f\eta + (1-f)h)}{1 - 2s(f\eta + (1-f)h)} \\ \mathrm{E}(h') &= \frac{(1-s)(f\eta + (1-f)h)}{1 - 2s(f\eta + (1-f)h)}\end{aligned}$$

The mean change per generation is then $M_p = E(p') - p$ and $M_h = E(h') - h$, which are rational functions in p and h of height $2n$. We take the limit $N \to \infty$, while holding both $Nf = \zeta$ and $Ns = \gamma$ constant, so that f and s are small parameters. Thus only first-order terms survive in the Taylor expansion of M_p and M_h around $(f, s) = (0, 0)$ even when Ns and Nf are large. We are left with

$$M_p = f(\pi - p) + sh\left(p - \frac{1}{2}\right), \quad M_h = f(\eta - h) - sh(1-h). \tag{12}$$

As f and s approach zero in this limit, so does the mean change in allele frequency, and $\mathrm{E}(p') \to p$ and $\mathrm{E}(h') \to h$. Thus the variance-covariance matrix of allele frequency change approaches the multinomial variance-covariance matrix of sampling from the current allele frequencies. Thus the V_{ij} are given simply by Eq. 6: $V_{pp}(p, h) = \mathrm{Var}(p)$, $V_{hh}(p, h) = \mathrm{Var}(h)$, and $V_{ph}(p, h) = \mathrm{Cov}(p, h)$, where $E(p) = p$.

We rescale time in Eq. 11, taking $\tau = t/N$:

$$\frac{\partial \phi}{\partial \tau} = \frac{N}{2}\left(\frac{\partial^2 V_{pp}\phi}{\partial p^2} + 2\frac{\partial^2 V_{ph}\phi}{\partial p \partial h} + \frac{\partial^2 V_{hh}\phi}{\partial h^2}\right) - N\left(\frac{\partial M_p \phi}{\partial p} + \frac{\partial M_h \phi}{\partial h}\right). \tag{13}$$

Writing Eq. 13 in terms of π, p, η and h and combining factors $Nf = \zeta$ and $Ns = \gamma$ gives Eq. 7.

We compute the integral in Eq. 10 and the manifold of equilibrium heterozygosity (Eq. 8) numerically using Mathematica (Wolfram Research, Inc, Mathematica, Version 10.0.2.0 (2015), Champaign, IL, USA). We also wrote software in OCaml using the GNU Scientific Library to estimate fixation probabilities of the discrete model by explicit Monte Carlo simulation. The software is open source and available on GitHub (https://github.com/mnewberry/nchoice).

We introduced the parameter f, describing the proportion of the population that undergoes mate choice as opposed to clonal reproduction. Although this parameter was introduced for technical reasons, in order to produce a well-defined diffusion limit, even in finite models Nf has a natural, physical interpretation as the rate of mating: the average number of matings per generation, or the relative strength in altering gene frequencies by the mating system versus by genetic drift. One might naively assume that f is always unity in natural populations, and yet many plants such as some grasses and aspen reproduce sexually on a background of clonal reproduction. Genetic drift due to accidents of sampling can be interpreted at many levels, including sampling induced by the outcomes of mating; or stochastically induced by persistence to the next generation through longevity.

Supplementary Figures (S1)

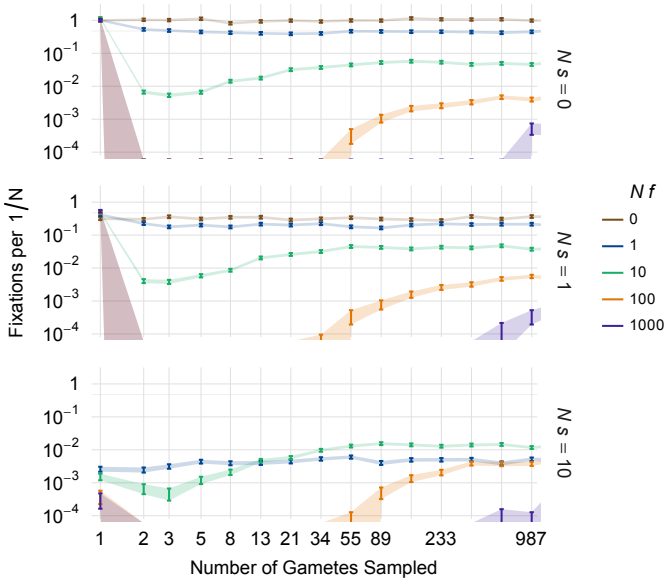

FIGURE S1. The fixation probability of one initial heterozygote in a model where females sample microgametes (sperm) attempting to raise homozygous offspring. This model is analogous to the n-choice model we study, but males are replaced by haplotypes. Females sample a limited number of gametes (n) and choose the first one that allows them to produce a homozygote, or, failing that, produce the heterozygote. The plot shows the fixation probability at different levels of viability selection against heterozygotes (Ns), and different rates of female participation in the mating system (Nf) on a background of clonal reproduction. Bands and error bars indicate the 95% confidence interval on the mean fixation rate in simulations with up to 100,000,000 runs in populations of size $N = 1,000$. For $Ns = 10$ and $Nf = 0$ (brown) the probabilities are below the range depicted. When females sample only one gamete ($n = 1$), the fixation probability is still roughly approximated by Eq. 1. At intermediate n, participation in the mating system induces strong fecundity selection against rare alleles. At large n, the fixation probability does not approach the neutral rate, because in order to form an initial mutant homozygote, an initial heterozygote must be chosen to reproduce, and it must also chose a mutant sperm instead of the more abundant wild-type. This depresses the fixation probability in the high-n limit relative to neutrality. Nonetheless, at large n and Ns the mating system can facilitate underdominant fixation.

Supplementary Figures (S2)

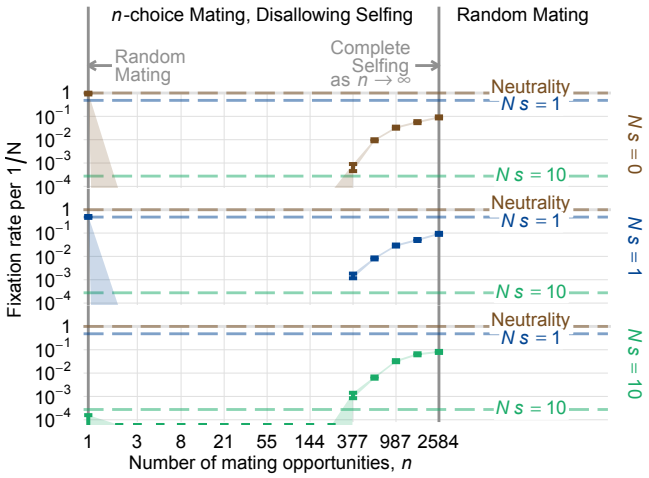

FIGURE S2. The effect of n-choice assortative mating on the fixation probability of an underdominant allele when self-mating is disallowed. The model and parameters are the same as those used in Figure 3, except that zygotes are drawn from a modified version of Eq. 2 which accounts for prohibition on self-mating. Vertical bars indicate the 95% confidence interval on the mean fixation rate observed in 100,000,000 replicate simulated populations of size $N = Nf = 1,000$ under no viability selection ($Ns = 0$, brown), weak viability selection ($Ns = 1$, blue), and strong viability selection ($Ns = 10$, green). Dashed horizontal lines indicate the corresponding fixation probabilities of the underdominant allele under random mating. The asymptotic fixation probabilities at high n are depressed relative to neutrality because an initial homozygote must first drift to copy number higher than 1 before its own genotype is available for mating.