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**The genetic consequences of fluctuating inbreeding depression and the evolution of plant  
selfing rates**

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**Running title:** Genetics of fluctuating inbreeding depression

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1           **Abstract**

2           The magnitude of inbreeding depression, a central parameter in the evolution of plant  
3 mating systems, can vary depending on environmental conditions. However, the underlying  
4 genetic mechanisms causing environmental fluctuations in inbreeding depression, and the  
5 consequences of this variation for the evolution of self-fertilization, have been little studied.  
6 Here, we consider temporal fluctuations of the selection coefficient in an explicit genetic  
7 model of inbreeding depression. We show that substantial variance in inbreeding depression  
8 can be generated at equilibrium by fluctuating selection, although the simulated variance  
9 tends to be lower than has been measured in experimental studies. Our simulations also reveal  
10 that purging of deleterious mutations does not depend on the variance in their selection  
11 coefficient. Finally, an evolutionary analysis shows that, in contrast to previous theoretical  
12 approaches, intermediate selfing rates are never evolutionarily stable when the variation in  
13 inbreeding depression is due to fluctuations in the selection coefficient on deleterious  
14 mutations.

15

16           **Keywords:** Mixed mating / genetic load / purging / environmental variation.

17

18

## 1           **Introduction**

2           Over the last thirty years, theoretical studies of plant mating systems have considered  
3           the role of inbreeding depression as central for the evolution of self-fertilization (Lloyd, 1979;  
4           Lande & Schemske, 1985; Charlesworth & Charlesworth, 1990). Inbreeding depression is the  
5           main evolutionary force that opposes the automatic 50% advantage of selfing (Fisher, 1941),  
6           it dictates the cost of seed discounting and determines the extent to which selfing causes  
7           reproductive assurance (Lloyd, 1992), so that the predicted outcome of mating system  
8           evolution critically depends on inbreeding depression values. Simple evolutionary models  
9           with a constant inbreeding depression,  $\delta$ , predict a dichotomous outcome of evolution:  
10          complete selfing when  $\delta < 0.5$  and complete outcrossing when  $\delta > 0.5$ . Importantly,  
11          incorporating purging, *i.e.* a decrease in inbreeding depression with increasing population  
12          selfing rate due to the elimination of recessive deleterious mutations by selection, does not  
13          change these conclusions (Lande & Schemske, 1985; Charlesworth & Charlesworth, 1990;  
14          but see Uyenoyama & Waller, 1991a). Yet, the existence of natural populations with  
15          intermediate stable selfing rates is now widely acknowledged and a variety of theoretical  
16          models have been proposed to account for the maintenance of such mixed mating systems  
17          (reviewed in Goodwillie et al., 2005). Although several models rely on ecology (e.g.  
18          pollination biology, Holsinger, 1991; Johnston, 1998; Vallejo-Marin & Uyenoyama, 2004;  
19          Porcher & Lande, 2005; Johnston et al., 2009 or population dynamics, Morgan et al., 2005) to  
20          explain mixed mating systems, numerous studies have elaborated on the prominent role of  
21          inbreeding depression by examining various genetic mechanisms (including overdominance,  
22          biparental inbreeding in isolated or structured populations, or decline in fitness with  
23          generations of selfing, Lloyd, 1979; Uyenoyama, 1986; Holsinger, 1988; Uyenoyama &  
24          Waller, 1991b; Latta & Ritland, 1993; Ronfort & Couvet, 1995; Rausher & Chang, 1999).

1           Recently studies have demonstrated that the magnitude of inbreeding depression is  
2 sensitive to environmental factors (reviewed in Armbruster & Reed, 2005; Cheptou, 2006;  
3 Willi et al., 2007). Some theoretical models have shown that environmentally-induced  
4 variation in inbreeding depression is likely to influence the evolution of mating systems,  
5 particularly to favour mixed mating systems (Cheptou & Mathias, 2001; Cheptou & Schoen,  
6 2002). However, these models do not incorporate a genetic basis of inbreeding depression and  
7 hence do not include the purging process that destabilizes mixed mating systems in most  
8 explicitly genetic models (e.g. Lande et al., 1994; Husband & Schemske, 1996; Kelly, 2007).  
9 In addition, the effectiveness of purging itself may depend on environmental fluctuations, as a  
10 result of environment-dependent inbreeding depression (e.g. Bijlsma et al., 1999), a  
11 phenomenon that has received little theoretical attention so far. To properly assess the actual  
12 role of environmental fluctuations in inbreeding depression on the evolution of plant mating  
13 systems, we therefore need to (1) determine the genetic mechanisms underlying fluctuations  
14 in inbreeding depression and (2) examine the combined effects of fluctuating inbreeding  
15 depression and purging on the evolution of selfing.

16           Here, we use a common genetic model of inbreeding depression to examine one  
17 possible genetic mechanism of fluctuating inbreeding depression and to test whether such  
18 fluctuations can maintain mixed mating systems when purging occurs. Consistent with the  
19 bulk of experimental data (Charlesworth & Charlesworth, 1999), we assume that inbreeding  
20 depression is caused by partly recessive, deleterious mutations. Such a mutation can be  
21 characterized by its selection coefficient ( $S$ ) and its dominance coefficient ( $h$ ). From this  
22 genetic perspective, environmental variation in inbreeding depression could result from  
23 fluctuations in either  $S$  or  $h$  or both (Bijlsma et al., 1999; Armbruster & Reed, 2005), but little  
24 is known so far regarding the most likely source(s) of variation in inbreeding depression  
25 (Cheptou, 2006). Numerous experimental observations of larger inbreeding depression in

1 stressful environments (e.g. Bijlsma et al., 1999; and reviews in Armbruster & Reed, 2005;  
2 Willi et al., 2007) suggest that environmental conditions may influence the selection  
3 coefficient of deleterious alleles, although other experiments comparing the mean fitness of  
4 *Arabidopsis thaliana* mutation accumulation lines across light and nutrient gradients failed to  
5 demonstrate any environment-specific effects of spontaneous mutations (Chang & Shaw,  
6 2003; Kavanaugh & Shaw, 2005). In the present study, we assume that fluctuations in  
7 inbreeding depression are caused by temporal changes in the selection coefficient of  
8 deleterious mutations. We apply an analytical approach assuming an infinite population size.  
9 We address (1) the effect of temporal fluctuations of selection coefficients on the temporal  
10 variation in inbreeding depression, and compare this predicted variation to that observed in  
11 natural populations, (2) the effectiveness of purging under fluctuating selection, and (3) the  
12 evolution of mating systems. We specifically investigate whether intermediate selfing rates  
13 are evolutionarily stable when inbreeding depression is subjected to fluctuating selection and  
14 is allowed to co-evolve with the mating system.

15

## 1 **The model**

2 In the following theoretical approach, we define mixed mating systems as mating  
3 systems with a selfing rate  $r > 0$  and  $r < 1$ , which is broader than the definition used in  
4 empirical studies (generally  $0.2 < r < 0.8$ ; reviewed in Goodwillie et al., 2005), because we  
5 focus on genetically determined selfing rates, with no environmental effects and no  
6 measurement errors.

7

### 8 *Inbreeding depression with a fluctuating selection environment*

9 Inbreeding depression, the relative decrease in mean fitness of selfed vs. outcrossed  
10 individuals, is described by the model of Kondrashov (1985), which models the evolution of  
11 the distribution of the number of homozygous and heterozygous deleterious mutations per  
12 individual in an infinite population with selfing rate  $r$ . Mutation occurs at an infinite number  
13 of loci, following a Poisson process with rate  $U$  per diploid zygote per generation. Each  
14 generation, the selection coefficient of mutations,  $S$ , is randomly sampled from a normal  
15 distribution truncated to the interval  $[0,1]$ , with mean  $\mu_S$  and variance  $\sigma_S^2$  before truncation.  
16 This selection coefficient is applied to all mutations, which also have the same dominance  
17 coefficient,  $h$ . Mutations have multiplicative effects on fitness, so that the fitness of an  
18 individual carrying  $x$  homozygous mutations and  $y$  heterozygous mutations is given by  $(1 -$   
19  $S)^x(1 - hS)^y$ .

20 Each generation, the modelled population undergoes mating, followed by mutation to  
21 deleterious alleles and selection. Recursion equations describing the distribution of number of  
22 homozygous and heterozygous mutations per individual are detailed in an online appendix  
23 and can also be found in Kondrashov (1985) or Charlesworth et al. (1990). These equations  
24 were iterated for 1000 generations (C++ code for numerical iterations available upon request  
25 from E.P.), by which time the population had reached steady-state for all parameter



1 combinations. To identify steady state, we considered the growth rate in the number of  
2 mutations across generations,  $N_{t+1}/N_t$ : the population was considered at steady state when the  
3 average growth rate over 50 generations did not differ significantly from 1 (one sample  
4 Student's t-test). Equations were subsequently iterated for another 1000 generations, to record  
5 fluctuations in inbreeding depression at (statistical) steady state. For each set of parameter  
6 values, we recorded (1) the mean and variance of the number of homozygous and  
7 heterozygous deleterious mutations per individual and (2) the mean and variance of  
8 inbreeding depression, measured over the last 1000 generations. Because inbreeding  
9 depression is constrained between 0 (in the present study) and 1, the variance in inbreeding  
10 depression depends on the mean (e.g. the variance must be 0 if the mean is 0 or 1). To account  
11 for this dependence on the mean, we compared the simulated variance in inbreeding  
12 depression to the maximum possible variance:

$$13 \quad \sigma_{max}^2 = \mu_{ID} (1 - \mu_{ID}) \quad [1]$$

14 where  $\mu_{ID}$  is the mean inbreeding depression.

15 The predicted mean and variance in inbreeding depression were compared to empirical  
16 means and variances in inbreeding depression, estimated in contrasting environments  
17 (compiled by Armbruster & Reed, 2005). Most of these studies measured inbreeding  
18 depression in only two environments, which were obviously not chosen at random, but  
19 instead likely represent extremes of a distribution (e.g. stressful vs. benign environments).  
20 Therefore, it was not appropriate to estimate variance using the classical estimator

$$21 \quad s^2 = \frac{1}{n-1} \sum (x_i - \bar{x})^2 . \text{ We thus chose to calculate the sample variance, } \sigma_{ID}^2 = \frac{1}{n} \sum (x_i - \bar{x}_{ID})^2 :$$

22 due to small sample sizes and non-random sampling, this crude procedure provides an order  
23 of magnitude estimate for the actual variance in inbreeding depression.

24

1 *Evolutionarily stable mating systems*

2 We analyzed the joint evolution of selfing rate and inbreeding depression using an  
3 adaptive dynamics framework (Dieckmann, 1997). The fitness of a rare mutant with selfing  
4 rate  $r'$  is compared to that of the resident genotype, with selfing rate  $r$ . We assumed that the  
5 selfing rate is controlled by a single locus, with two alleles. Once the population with selfing  
6 rate  $r$  reached steady-state (after 1000 generations), a mutant allele with a selfing rate  $r'$   
7 different from the resident was introduced at a low frequency in linkage and identity  
8 equilibrium with deleterious mutations, and the recursion equations were numerically iterated  
9 for 1000 generations to detect invasion (or not) by the mutant.

10 We deduce stable selfing rates using Pairwise Invasibility Plots (PIP), in which regions  
11 of invasion (in grey) and non-invasion (in white) of a rare mutant are plotted against the  
12 selfing rate of the resident genotype,  $r$  and the selfing rate of the mutant,  $r'$  (see Fig. 3).  
13 Hence, regions located below the  $r = r'$  line correspond to emergence of a mutant with a  
14 smaller selfing rate than the resident, and vice versa. If a mutant with selfing rate  $r' > r$  can  
15 invade (i.e. the point with coordinates  $(r, r')$  is located in a region of invasion), then evolution  
16 favours increased selfing rates and vice versa. Evolutionary equilibria occur at the intersection  
17 of the  $r = r'$  line and a line separating regions of invasion and non-invasion. Details regarding  
18 the criteria to infer stability of equilibria can be found in Dieckmann (1997). The equilibrium  
19 selfing rates discussed here, denoted by white circles on the figures, are evolutionarily stable  
20 (they cannot be invaded by neighbouring mutant selfing rates) and are evolutionary attractors  
21 or convergence stable (evolution by a series of small steps proceeds towards the equilibrium).  
22 We refer to these equilibria as stable selfing rates.

23

24 *Parameter values*

1 We either chose parameter values according to experimental values or we used a wide  
2 range of biologically plausible values. The genomic mutation rate to deleterious mutations  
3 was  $U = 0.02, 0.2$  or  $1$ , which encompasses the range of experimental estimates among  
4 multicellular organisms (reviewed in García-Dorado et al., 2004). The dominance coefficient  
5 of mutations was either  $h = 0.02$ , as in the only available experimental data for highly  
6 deleterious mutations (Simmons & Crow, 1977) or  $h = 0.3$ , a more reasonable value for  
7 mildly deleterious mutations (García-Dorado et al., 2004). Exploratory analyses showed that  
8 the mean selection coefficient of deleterious mutations had little effect on the results  
9 presented here, which is consistent with previous theory showing that equilibrium inbreeding  
10 depression in a population depends little on the selection coefficient of deleterious mutations,  
11 and is much more influenced by their dominance coefficient (e.g. Charlesworth et al., 1990).  
12 Hence, we considered a single, intermediate value for the average selection coefficient of  
13 deleterious mutations,  $\mu_S = 0.5$ , so that this coefficient, which is constrained between 0 and 1,  
14 could be submitted to significant environmental variation. The initial variances were set to  
15  $\sigma_S^2 = 0.01$  and  $0.09$ , but the latter was actually smaller ( $\sigma_S^2 = 0.06$ ) due to truncation of  $S$   
16 values below 0 or above 1. Note that truncation did not bias the mean selection coefficient.  
17 For comparative purposes, we also considered constant selection ( $\sigma_S^2 = 0$ ), with  $S = 0.5$ .  
18 Finally, we considered different values of the selfing rate, across the range of  $r = 0$  to  $1$ .

19

### 20 *Analytical approximation*

21 To characterize the effect of purging on the selection of self-fertilization in a fluctuating  
22 environment, we compared the results of the Kondrashov model with stochastic variation in  
23 selection coefficients to Cheptou and Schoen's (2002) analytical phenotypic approach.  
24 Following Lande and Schemske (1985), an approximate measure of the strength of selection  
25 on a rare genotype with selfing rate  $r'$  is given by the expected fitness of such genotypes:

1 
$$w = r'(1 - \delta) + \frac{1}{2}(1 - r') + \frac{1}{2}(1 - r) \quad [2]$$

2 where  $r$  is the mean selfing rate in the population and  $\delta$  is the inbreeding depression.

3 If  $\delta$  varies in time and if evolution of the selfing rate occurs much slower than the fluctuations  
 4 in inbreeding depression, the conditions for invasion of a rare genotype with selfing rate  $r'$  are  
 5 given by its long-run growth rate (Lande, 2007, 2008), i.e. the geometric mean of fitness over  
 6 time or similarly by the expectation of the logarithm of the annual fitness,  $E[\text{Log}(w)]$  (Kisdi &  
 7 Meszina, 1995). Without any specific information on the distribution of  $\delta$ , this quantity can  
 8 be approximated using a second order approximation (Jensen approximation: Bulmer, 1994)  
 9 by:

10 
$$s = E[\log(w)] \approx \log[E(w)] - \frac{1}{2E(w)^2} \text{var}(w) \quad [3]$$

11 Assuming small effects of mutation on the selfing rate, the evolution of self-fertilization can  
 12 be analysed by modelling the invasion of a rare genotype with selfing  $r'$  in a population with  
 13 selfing rate  $r$ . The success of invasion can be evaluated via  $D(r)$ , the selection gradient  
 14  $\partial s / \partial r'$  at  $r$ : if the latter is positive (negative) mutants with slightly higher (lower) selfing rate  
 15 may successfully invade. The selection gradient  $D(r)$  for an inbreeding depression  
 16 distribution with mean  $\mu_\delta$  and variance  $\sigma_\delta^2$  is given by:

17 
$$D(r) = \frac{0.5 - \mu_\delta}{1 - \mu_\delta r} - \frac{\left(1 - \frac{r}{2}\right)r}{(1 - \mu r)^3} \sigma^2 \quad [4]$$

18 (see Cheptou & Schoen, 2002 for details). A necessary condition for mixed selfing rates to be  
 19 stable is thus that  $D(r) = 0$  (no mutant can invade) for intermediate values of the selfing rate  
 20 ( $0 < r < 1$ ). Moreover, a sufficient and more stringent condition for mixed selfing rates to  
 21 evolve is that boundaries ( $r = 0$  and  $r = 1$ ) are unstable, i.e.:

22  $(1) D(0) > 0$                       (Increased selfing is favoured in a fully outcrossing population)



## 1 **Results**

### 2 *Effectiveness of purging under fluctuating inbreeding depression*

3 Temporal variation in the selection coefficient of deleterious mutations appeared to  
4 have little effect on the extent of purging (Fig. 1). Regardless of the mean (not shown) and  
5 variance of selection coefficients, the relationship between the average inbreeding depression  
6 at equilibrium and the population selfing rate differed little between variable vs. constant  
7 selection, i.e. the occurrence of purging was unchanged as the variance in selection  
8 coefficients was increased. As expected, inbreeding depression was large in predominantly  
9 outcrossing populations, and decreased with increasing selfing rate. The decrease was  
10 progressive under moderate mutation rate ( $U = 0.02$  or  $0.2$ , Fig. 1) or large dominance  
11 coefficient ( $h = 0.3$ , Fig. 1), but sharper under higher mutation rates and with nearly recessive  
12 mutations ( $U = 1$  and  $h = 0.02$ , Fig. 1). This pattern was unaffected by fluctuations in the  
13 selection coefficient of deleterious mutations, although the average inbreeding depression in a  
14 predominantly outcrossing population tended to be slightly lower under large fluctuations of  
15 selection than in a constant environment (Fig. 1,  $\sigma_s = 0.3$  and  $h = 0.02$ ).

16

### 17 *Magnitude of variation in inbreeding depression*

18 As expected, temporal fluctuations in the selection coefficient of deleterious mutations  
19 generated variation in inbreeding depression across generations. Variation in inbreeding  
20 depression increased with the selection coefficient,  $\sigma_s^2$  up to ca. 0.05. It was also affected by  
21 the population selfing rate and the purging process, with a peak in variance when the average  
22 inbreeding depression was closest to 0.5. Because mean and variance of inbreeding  
23 depression are not independent (equation [1]), the changes in variance under different  
24 population selfing rates were in great part attributable to changes in mean inbreeding  
25 depression. Depending on the mutation rate and dominance coefficient of deleterious

1 mutations, variation in mean inbreeding depression explained 51-97% of the variance of  
2 inbreeding depression (these values were obtained by examining the correlation between the  
3 variance in the simulations and the maximum variance in inbreeding depression calculated  
4 from equation [1]).

5

#### 6 *Comparison of simulated vs. observed variation in inbreeding depression*

7 Overall, the empirical data generally exhibited more variation in inbreeding depression  
8 than simulations (Fig. 2,  $\sigma_{ID}^2$  up to 0.18 and 0.046, respectively). The parameter space of  $\mu\delta$   
9 (mean inbreeding depression) and  $\sigma_{\delta}^2$  (variance in inbreeding depression) where the  
10 analytical model of Cheptou and Schoen (2002) predicts stable mixed mating systems  
11 (equation [4],  $D(r) = 0$ ) are plotted on Figure 2 (shaded area). Interestingly, none of the  
12 empirical points fall within this parameter space. Despite relatively low variance in  
13 inbreeding depression generated by our theoretical approach, the simulations nonetheless  
14 generated some situations for which Cheptou and Schoen's (2002) model predicts stable  
15 mixed mating: this was the case with  $U = 0.2, h = 0.02, \sigma_S = 0.3$  and  $U = 1, h = 0.02, \sigma_S = 0.3$   
16 (combination of  $\mu\delta$  and  $\sigma_{\delta}^2$  within the shaded area, Fig. 2).

17

#### 18 *Evolution of self-fertilization under fluctuating inbreeding depression.*

19 Evolutionarily stable selfing rates can be deduced from Pairwise Invasibility Plots  
20 (PIP, Fig. 3), where regions of invasion (in grey) and non-invasion (in white) of a rare mutant  
21 are plotted against the selfing rate of the resident genotype,  $r$  and that of the mutant,  $r'$ .  
22 Evolutionarily stable selfing rates are located at the intersection of the  $r = r'$  line and a line  
23 separating regions of invasion and non-invasion, and are characterized by the fact that no  
24 mutant can invade (i.e. the areas just above and below are white on the PIP). The main result  
25 of our study is that intermediate selfing rates were never evolutionarily stable (Fig. 3), even

1 though large variances in the selection coefficient of deleterious mutations generated  
2 fluctuations in the magnitude of inbreeding depression. This was true regardless of the  
3 mutation rate, the dominance coefficient of deleterious mutation, as well as the mean and  
4 variance of the selection coefficient of mutations (and hence variance in inbreeding  
5 depression). The only stable mating systems were complete outcrossing with nearly  
6 codominant deleterious mutations ( $h = 0.3$ , Fig. 3) and complete outcrossing or complete  
7 selfing (depending on the initial conditions) with nearly recessive mutations ( $h = 0.02$ , Fig. 3).  
8 In addition, the threshold for the selection of pure selfing or pure outcrossing did not depend  
9 on the variance in inbreeding depression. Thus, in our genetic model, fluctuations in  
10 inbreeding depression do not favour the maintenance of mixed mating.

11 This was confirmed by considering the modified version of Cheptou and Schoen  
12 (2002) analytical approach, accounting for purging via selfing rate dependent inbreeding  
13 depression. Under this model, condition (2) for the maintenance of stable mixed mating  
14 (namely  $D(1) < 0$ , invasion of a mutant with selfing rate  $< 1$  in a completely selfing  
15 population) requires substantial variance in inbreeding depression in a completely selfing  
16 population where average inbreeding depression is generally low. Under the Kondrashov  
17 model, high variance is generated by a high mutation rate (e.g.  $U = 1$ , Fig. 1). However, this  
18 set of parameters also generates high average inbreeding depression ( $\mu_\delta$  close to 1) at  $r = 0$ ,  
19 which invalidates condition (1) for the maintenance of mixed mating (namely  $D(0) > 0$ ,  
20 invasion of a mutant with the selfing rate  $> 0$  in a completely outcrossing population,  $\Leftrightarrow$   
21  $\mu_\delta < 0.5$ ). Hence, although some combinations of  $\mu_\delta$  and  $\sigma_\delta$  fell within the ‘mixed mating’  
22 window of Fig. 2, sufficient conditions for stable mixed mating (1) and (2) were never met.  
23 Mixed mating can therefore never be maintained when inbreeding depression is modelled  
24 with partly recessive deleterious mutations in an infinite population (as in Kondrashov, 1985).

25

26



## 1 **Discussion**

2        In this study, we generated fluctuating inbreeding depression using a genetic model  
3 where environmental variation affects the selection coefficient. This allowed us to  
4 characterize purging under a fluctuating environment and analyse the evolution of plant  
5 mating systems in this context, specifically testing for conditions that allow the maintenance  
6 of mixed mating.

7

### 8 *Fluctuations in selection coefficients have little effect on purging*

9        Temporal variation in the selection coefficient of the deleterious mutations has very  
10 little effect on the average equilibrium inbreeding depression. This is consistent with single  
11 locus theory in randomly mating populations: Crow and Kimura (1970) showed that with  
12 incompletely recessive ( $h > 0$ ), mildly deleterious mutations ( $S \gg u$ ) mutant homozygotes are  
13 kept sufficiently rare by selection so that most selection occurs against mutant heterozygotes.  
14 As a result, the dynamics of the mutant allele in a constant environment are approximately a  
15 linear function of the selection coefficient,  $S$ , and can be written  $dq/dt \approx u - hSq$  (Crow &  
16 Kimura, 1970; Lande & Schemske, 1985), where  $q$  is the mutant allele frequency and  $u$  is the  
17 per locus mutation rate. With fluctuating selection, this yields  $E(dq/dt) = u - E(hS)q$ . At  
18 equilibrium ( $dq/dt = 0$ ),  $q = u/E(hS)$ . Hence, in randomly mating populations under fluctuating  
19 selection, inbreeding depression at a single locus depends solely on the mean selection  
20 coefficient (or dominance coefficient) of the deleterious mutation, not on its variance. Our  
21 results extend these predictions with a single locus to many loci, as well as non-random  
22 mating. Similarly, when selfing is enforced in a previously completely outcrossing  
23 population, fluctuations do not affect the time required for the population to reach the new  
24 equilibrium inbreeding depression (not shown), which is due to the fact that, under complete  
25 selfing, highly recessive deleterious mutations are quickly exposed to selection and a few

1 generations of strong selection are enough to purge most of the load (e.g. Lande & Schemske,  
2 1985).

3 A number of experimental approaches have demonstrated that inbreeding depression  
4 varies across environments and generally appears to be stronger in more stressful  
5 environments, generally defined as environments reducing mean fitness (Armbruster & Reed,  
6 2005). As a consequence, purging might be inefficient in relatively benign environments,  
7 where inbreeding depression is weak (e.g. Bijlsma et al., 1999; Keller & Waller, 2002;  
8 Armbruster & Reed, 2005). Such faster reduction in inbreeding depression was observed by  
9 Kristensen et al. (2003) and Swindell and Bouzat (2006) in inbred laboratory populations of  
10 *Drosophila* species submitted to stressful environments (high temperature, competition,  
11 chemical stress) vs. benign environments. Their *Drosophila* data are however not directly  
12 comparable to our theoretical results suggesting that variable selection has little effect on  
13 purging because in these experimental studies, environment-dependent purging was examined  
14 in two or more contrasting, but constant environments. In the variable environment simulated  
15 here, our results suggest that only five to ten generations of stress can increase inbreeding  
16 depression and are enough to purge most of the load (not shown), regardless of the average  
17 effects of mutations/stress in the environment, because the rate of purging is much faster than  
18 mutation accumulation (Lande & Schemske, 1985).

19

20 *Fluctuations in selection coefficients can generate substantial variation in inbreeding*  
21 *depression*

22 Although the time-averaged inbreeding depression is little affected by fluctuating  
23 selection, the *current* inbreeding depression can exhibit substantial variation across  
24 environments. In the present study, we considered mutations that were moderately deleterious  
25 on average ( $\mu_S = 0.5$ ), but this intermediate selection coefficient was allowed to vary between

1 0 (neutral mutations) and 1 (lethal mutations) following a truncated normal distribution with  
2 variance between 0.01 and 0.06. As a result, the observed variance in inbreeding depression  
3 ranged between  $5 \times 10^{-4}$  and 0.05, and was highest when the mean inbreeding depression was  
4 close to 0.5, which was generally observed at intermediate selfing rates (with nearly recessive  
5 deleterious mutations,  $h = 0.02$ , Fig. 1). Although empirical data on variation in inbreeding  
6 depression magnitude are scarce, several studies (e.g. Jiménez et al., 1994; Koelewijn, 1998;  
7 Cheptou et al., 2001; Haag et al., 2002) find that their study organisms exhibit more variation  
8 in inbreeding depression than any of our simulations (regardless of parameter values). This  
9 would suggest that varying  $S$  in time, as simulated here, might not be the only mechanism  
10 generating the observed variation in the experimental data. It is however important to keep in  
11 mind that experiments on inbreeding depression do not necessarily mimic natural conditions,  
12 and that the variance in inbreeding depression was generally estimated from two data points  
13 (i.e. two experimental conditions). Obviously there is a need for experimental studies that  
14 estimate inbreeding depression over wider ranges of environmental conditions. In addition,  
15 the magnitude of inbreeding depression in natural populations depends on the history of  
16 populations (Kristensen et al., 2003; Leimu et al., 2008), so that it could be less sensitive to  
17 environmental variation than suggested by greenhouse experiments (e.g. Galloway &  
18 Etterson, 2007). Comparison of inbreeding depression variation in the wild (see for instance  
19 Dole & Ritland, 1993) would be more relevant.

20

21 *Purging cancels out the role of fluctuating inbreeding depression in the maintenance of mixed*  
22 *mating systems*

23 Based on a phenotypic model with no purging of deleterious mutations, Cheptou and  
24 Schoen (2002) predicted that intermediate selfing rates can be stable with fluctuating  
25 inbreeding depression under some combinations of mean and variance in inbreeding

1 depression (see Fig. 2). Our results with an explicit genetic model of inbreeding depression  
2 contrast with their predictions: mixed mating systems were never evolutionarily stable,  
3 although some parameter combinations appear to generate a mean and variance of inbreeding  
4 depression consistent with stable mixed mating systems under Cheptou and Schoen's  
5 approach (Fig 2, e.g. a high mutation rate to deleterious alleles ( $U = 1$ ), nearly recessive  
6 mutations ( $h = 0.02$ ) and substantial fluctuation in the selection coefficient of deleterious  
7 mutations). Evidently, it is purging in our model that makes mixed mating unstable. While the  
8 mean and variance are independent parameters in Cheptou and Schoen's model, these  
9 quantities intrinsically covary in an explicit genetic model. Purging creates a strong positive  
10 feedback that selects for selfing (Lande & Schemske, 1985) and that overwhelms the negative  
11 feedback produced by fluctuating inbreeding depression (Cheptou & Schoen, 2002).

12         A heuristic understanding of why the genetic architecture of inbreeding depression can  
13 disrupt the maintenance of intermediate selfing rates was seen using an analytical approach.  
14 By incorporating selfing rate-dependent mean and variance of inbreeding depression into  
15 Cheptou and Schoen's (2002) analytical approach, we derived sufficient conditions for mixed  
16 mating: moderate mean inbreeding depression under complete outcrossing ( $\mu_s < 0.5$ )  
17 together with appreciable variance in inbreeding depression under complete selfing. In our  
18 simulations, these conditions were never met because the genetic architecture of inbreeding  
19 depression generates two contrasting situations that depend on the characteristics of the  
20 deleterious mutation. First, a low mutation rate (not shown) or nearly codominant deleterious  
21 mutations that can be eliminated by selection even in a heterozygous state ( $h = 0.3$ , Fig. 1)  
22 result in moderate inbreeding depression in a completely outcrossing population (condition  
23 (1)). However, this also generates a low inbreeding depression (and hence a low variance in  
24 inbreeding depression) under complete selfing, due to extensive purging, so that condition (2)  
25 is not met. Alternatively, a high mutation rate to nearly recessive mutations ( $U = 1$  and  $h =$

1 0.02, Fig. 1) creates situations in which the mean inbreeding depression under complete  
2 selfing is close to 0.5, so that the variance in inbreeding depression can be large (condition  
3 (2)). However, with this characteristic of mutations, condition (1) is not met due to the  
4 absence of purging in a completely outcrossing population, generating large mean inbreeding  
5 depression.

6

### 7 *Some limits of the model*

8       Although fluctuating selection coefficients can generate substantial inbreeding  
9 depression, our approach suggests that when purging occurs, fluctuating inbreeding  
10 depression is very unlikely to maintain intermediate selfing rates. This probably depends  
11 strongly on several assumptions of our model. First, Kondrashov's (1985) approach assumes  
12 infinite population size, whereas in natural populations purging is a stochastic process (Byers  
13 & Waller, 1999) that can be slowed down in small populations (Glémin, 2003), but should  
14 also be reinforced by the possibility of biparental inbreeding in finite populations. The role of  
15 demographic stochasticity in the evolution of genetic load and mating systems has been  
16 addressed in a limited number of studies (e.g. Charlesworth et al., 1992; Wang et al., 1999;  
17 Bataillon & Kirkpatrick, 2000; Theodorou & Couvet, 2002; Glémin, 2003; Guillaume &  
18 Perrin, 2006) but the interaction between demography, genetics and environmental variation  
19 remains to be explored. Second, we assumed that environmental variation affected the  
20 selection coefficient of a large number of strictly identical, unlinked deleterious mutations.  
21 Although little is known regarding the actual mechanisms for environment-dependent  
22 inbreeding depression (Armbruster & Reed, 2005), recent studies suggest the existence of  
23 environment-specific deleterious alleles (e.g. Vermeulen & Bijlsma, 2004), i.e. alleles that are  
24 usually neutral but become deleterious in specific (e.g. stressful) environments. Such  
25 environment specific alleles, which are rarely submitted to selection, may accumulate in the

1 genome and eventually add up to environment-independent inbreeding depression in stressful  
2 environments, which can affect the evolution of mating systems. However, our model  
3 suggests that their effects are likely to remain minor if these alleles are expressed frequently  
4 enough, because purging occurs within a couple of generations under selection. Lastly, other  
5 genetic mechanisms such as variation in dominance or even purely additive gene action when  
6 the strength of stabilizing selection varies may create inbreeding depression variance under  
7 heterogeneous environments (Lande & Schemske, 1985).

8

### 9 *Conclusion*

10 Our model attempts to link theoretical genetic models of inbreeding depression with the  
11 empirical observations that inbreeding depression is sensitive to environmental conditions.  
12 We extend Kondrashov's framework to heterogeneous environments and show that  
13 temporally varying selection on deleterious mutations maintains substantial variance in  
14 inbreeding depression. However, this mechanism cannot in itself maintain stable mixed  
15 selfing rates. Additional experimental and theoretical work is needed to elucidate the genetic  
16 basis of environmental variation in inbreeding depression and its consequences for the  
17 evolution of mating systems.

18

19

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## Figure Legends

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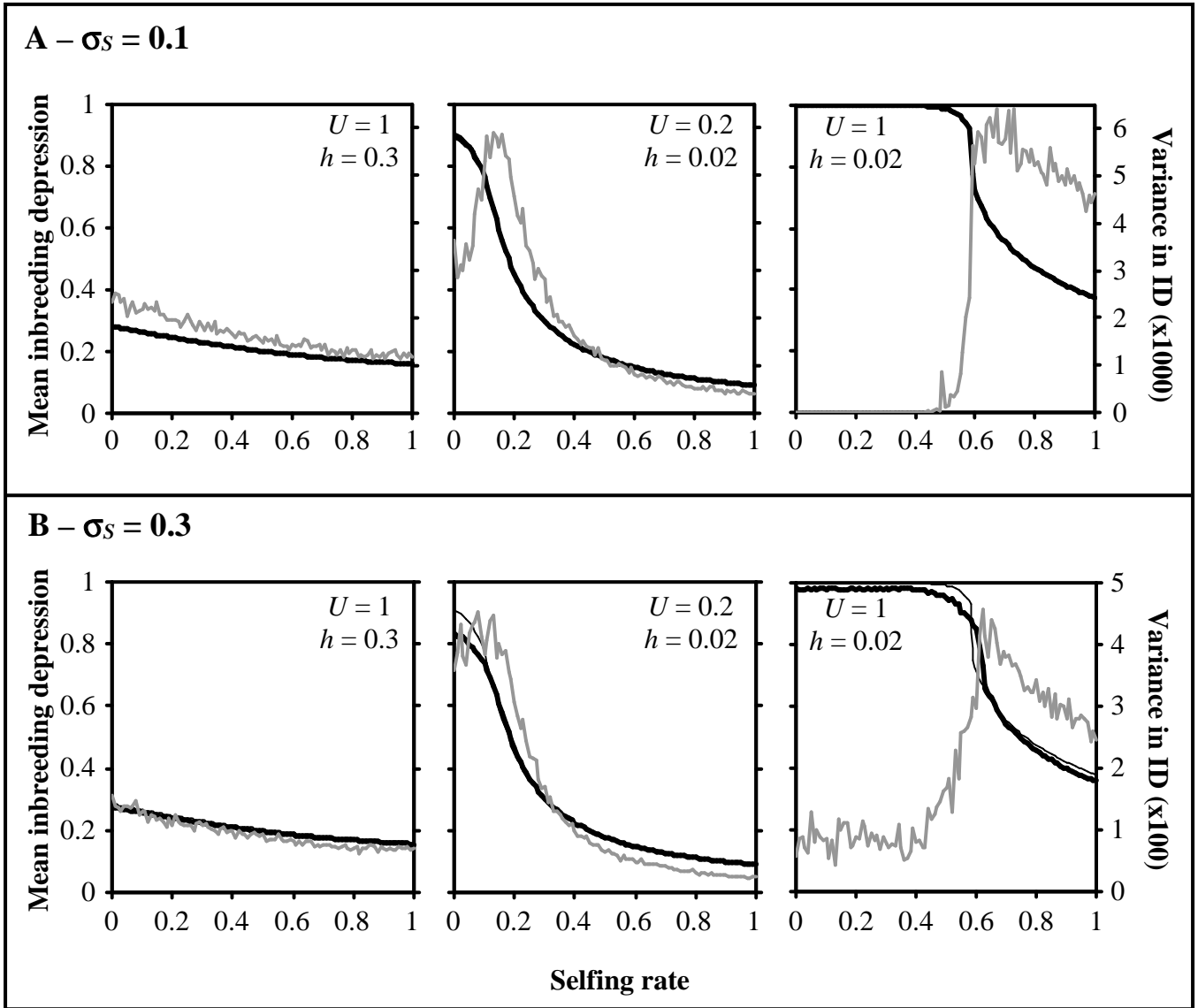
**Figure 1:** Equilibrium inbreeding depression under fluctuating selection.

Mean inbreeding depression (thick black lines) and variance in inbreeding depression (grey lines, measured over generations) are calculated over 1000 generations at steady state. The average selection coefficient of deleterious mutations is  $\mu_s = 0.5$ . Expected inbreeding depression in a constant environment ( $\sigma_s = 0$ , thin black lines) is sometimes exactly superimposed on the curves of mean inbreeding depression.

**Figure 2:** Predicted and empirically derived estimates of the mean and variance in inbreeding depression. Empirical data (black circles) are from Armbruster and Reed (2005). Predicted values (squares and triangles) are from our simulation approach and are the same as in Figure 1. The shaded area corresponds to combinations of mean and variance in inbreeding depression for which mixed mating systems are expected to be stable under Cheptou and Schoen's (2002) model, based on Jensen approximation (see Cheptou & Schoen, 2002 for a numerical example using a truncated Gaussian distribution). The dotted black envelope line represents the maximum variance in inbreeding depression  $\mu_s(1-\mu_s)$ , as a function of the mean inbreeding depression,  $\mu_s$  ( $0 < \mu_s < 1$ ).

**Figure 3:** Evolutionarily stable selfing rates under fluctuating inbreeding depression. The average selection coefficient of deleterious mutations is  $\mu_s = 0.5$ . Regions where the mutant invades ('+') are in grey, regions where it does not invade are in white. White circles indicate evolutionarily stable selfing rates.

Figure 1



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Figure 2

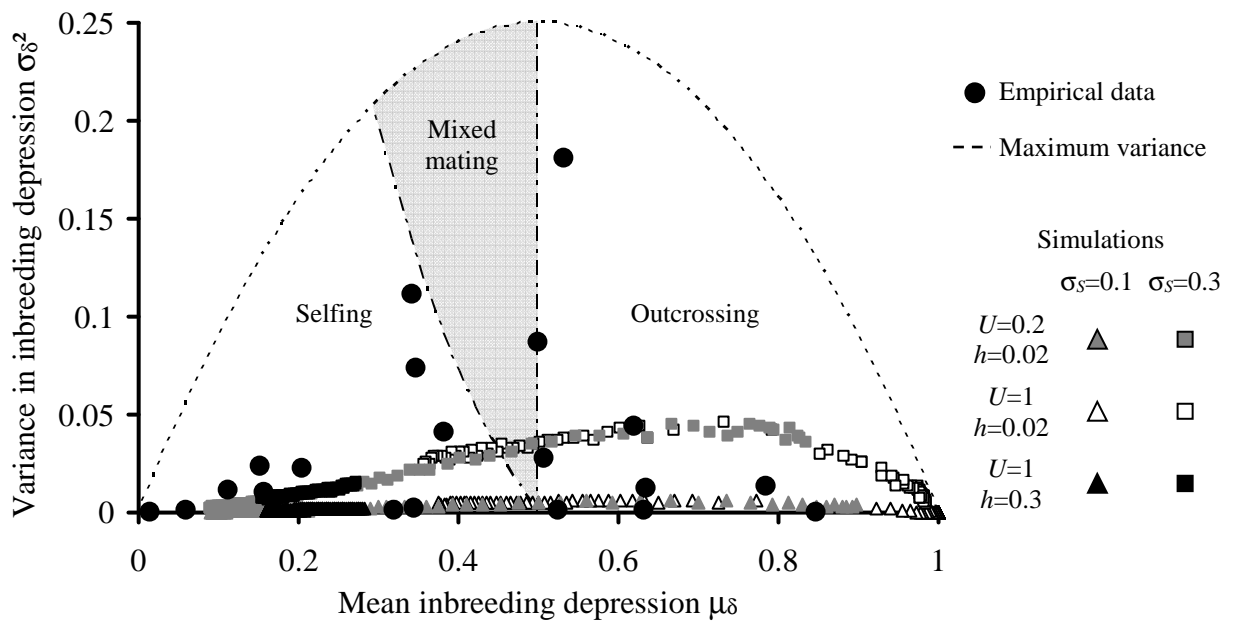
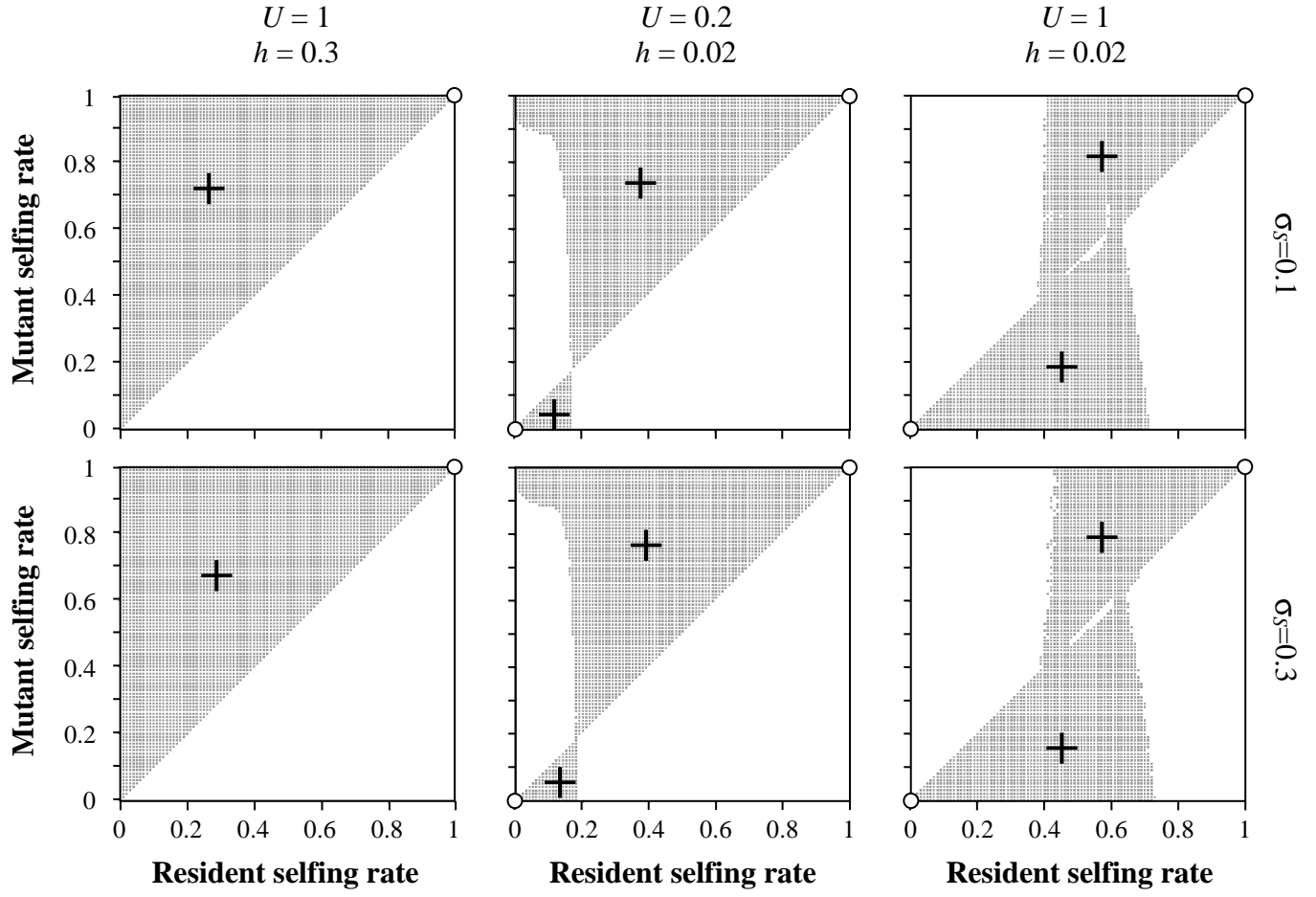




Figure 3



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## Supporting information

### Recursion equations for Kondrashov's model with fluctuating selection.

#### I. General equations

Here we derive recursion equations for the model describing the dynamics of inbreeding depression due partly recessive deleterious mutations in an infinite population with selfing rate  $r$  undergoing fluctuating selection. The dominance coefficient of mutations is  $h$  and their selection coefficient,  $S$ , is sampled at random each generation in a truncated Gaussian distribution with mean  $\mu_S$  and variance  $\sigma_S^2$ . Mutation occurs at an infinite number of loci, and affects the number of heterozygous loci only, i.e. it occurs exclusively at loci that do not already carry mutations.

Let  $q(ij)$  be the frequency of individuals carrying  $i$  mutations in the heterozygous state and  $j$  mutations in the homozygous state. Similarly,  $f(i)$  is the frequency of gametes carrying  $i$  deleterious mutations.

#### a. Selfing

The probability that a plant carrying  $n_1$  heterozygous loci and  $n_2$  homozygous loci produces by selfing an offspring carrying  $i$  ( $0 \leq i \leq n_1$ ) heterozygous loci and  $j$  ( $n_2 \leq j \leq n_1 + n_2$ ) homozygous loci is:

$$\binom{n_1}{i} \binom{n_1-i}{j-n_2} \left(\frac{1}{2}\right)^{2n_1-i}$$

Hence, the frequency of plants with  $i$  heterozygous loci and  $j$  homozygous loci obtained by selfing is:

$$q'(ij) = r \sum_{n_1=i}^{\infty} \sum_{n_2=0}^j \binom{n_1}{i} \binom{n_1-i}{j-n_2} \left(\frac{1}{2}\right)^{2n_1-i} q(n_1 n_2) \quad (\text{A1})$$

#### b. Outcrossing

The probability that a  $(n_1, n_2)$  plant produces a gamete with  $i$  mutations ( $n_2 \leq i \leq n_1 + n_2$ ) is:

$$\binom{n_1}{i-n_2} \left(\frac{1}{2}\right)^{i-n_2} \left(\frac{1}{2}\right)^{n_1-i+n_2}$$

Hence, the frequency of gametes carrying  $i$  mutations in the population is:

$$f(i) = \sum_{n_2=0}^i \sum_{n_1=i-n_2}^{\infty} \binom{n_1}{i-n_2} \left(\frac{1}{2}\right)^{n_1} q(n_1 n_2) \quad (\text{A2})$$

Because each mutation is unique, random mating in an infinite population never generates homozygous mutations. Therefore, the probability that an individual carrying  $n_1$  heterozygous

1 and  $n_2$  homozygous mutations produces by outcrossing a zygote with  $i$  heterozygous  
 2 mutations (and no mutation in the homozygous state) is:

$$3 \quad q(i0) = (1-r) \sum_{k=0}^i f_k f_{i-k} \quad (A3)$$

4  
 5 c. Mutation and selection  
 6

7 Mutation follows a Poisson process, with mean number of new heterozygous deleterious  
 8 mutations per genome of  $U$  per generation. The frequencies of zygotes after mutation are  
 9 therefore:

$$11 \quad q''(ij) = \sum_{k=0}^i \frac{U^{i-k} e^{-U}}{(i-k)!} q'(kj) \quad (A4)$$

12  
 13 The probability that a zygote with  $x$  homozygous mutations and  $y$  heterozygous mutations  
 14 survives to maturity is  $(1-S)^x(1-hS)^y$ . The frequency of mature plants with  $i$  heterozygous  
 15 loci and  $j$  homozygous loci in the next generation is then:

$$17 \quad q^*(ij) = \frac{(1-S)^j (1-hS)^i q''(ij)}{\bar{w}} \quad (A5)$$

18  
 19 where  $\bar{w}$  is the mean fitness of the population:

$$20 \quad \bar{w} = \sum_{i=0}^{\infty} \sum_{j=0}^{\infty} [(1-S)^j (1-hS)^i q''(ij)] \quad (A6)$$

21  
 22 Equations (A1–A6) completely define the recursion system. For each run, the initial  
 23 population contained no deleterious mutation. Fluctuating selection was modeled by sampling  
 24 each generation the selection coefficient of deleterious mutations,  $S$ , in a Gaussian distribution  
 25 with mean  $\mu_S$  and variance  $\sigma_S^2$  (equations A5 and A6). Simulations were run until the system  
 26 closely approached mutation-selection balance.

27  
 28  
 29 **II. Addition of a locus controlling the selfing rate**  
 30

31 We assume that selfing rate is controlled by a single locus (hereafter named ‘modifier  
 32 locus’), with two alleles: A is the resident and B is the mutant allele.

33  $f_{AA}(i,j)$ ,  $f_{AB}(i,j)$ , and  $f_{BB}(i,j)$  are the frequencies of the three diploid genotypes,  
 34 carrying  $i$  and  $j$  mutation in the heterozygous and homozygous state, respectively.

35  $f_A(i)$  and  $f_B(i)$  are the frequencies of gametes carrying allele A (respectively B) and  $i$   
 36 mutations.

37  
 38 a. Selfing  
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40  $q_J^G(ij)$  is the frequency of zygotes with genotype G at the modifier locus, carrying  $i$   
 41 heterozygous loci and  $j$  homozygous loci and originating from selfing of J genotypes. We  
 42 have:

43

$$1 \quad q_{AA}^{AA}(ij) = \sum_{n_1=i}^{\infty} \sum_{n_2=0}^j \binom{n_1}{i} \binom{n_1-i}{j-n_2} \left(\frac{1}{2}\right)^{2n_1-i} q_{AA}(n_1n_2) \quad (\text{A7})$$

$$2 \quad q_{AB}^{AA}(ij) = \frac{1}{4} \sum_{n_1=i}^{\infty} \sum_{n_2=0}^j \binom{n_1}{i} \binom{n_1-i}{j-n_2} \left(\frac{1}{2}\right)^{2n_1-i} q_{AB}(n_1n_2) \quad (\text{A8})$$

$$3 \quad q_{BB}^{BB}(ij) = \sum_{n_1=i}^{\infty} \sum_{n_2=0}^j \binom{n_1}{i} \binom{n_1-i}{j-n_2} \left(\frac{1}{2}\right)^{2n_1-i} q_{BB}(n_1n_2) \quad (\text{A9})$$

$$4 \quad q_{AB}^{BB}(ij) = \frac{1}{4} \sum_{n_1=i}^{\infty} \sum_{n_2=0}^j \binom{n_1}{i} \binom{n_1-i}{j-n_2} \left(\frac{1}{2}\right)^{2n_1-i} q_{AB}(n_1n_2) \quad (\text{A10})$$

$$5 \quad q_{AB}^{AB}(ij) = \frac{1}{2} \sum_{n_1=i}^{\infty} \sum_{n_2=0}^j \binom{n_1}{i} \binom{n_1-i}{j-n_2} \left(\frac{1}{2}\right)^{2n_1-i} q_{AB}(n_1n_2) \quad (\text{A11})$$

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7  
8 b. Outcrossing  
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10  $f_G^g(i)$  is the frequency of gametes with haploid genotype  $g$  at the modifier locus, carrying  $i$   
11 mutations and originating from plants with diploid genotypes  $G$ .  
12

$$13 \quad f_{AA}^A(i) = \sum_{n_2=0}^i \sum_{n_1=i-n_2}^{\infty} \binom{n_1}{i-n_2} \left(\frac{1}{2}\right)^{n_1} q_{AA}(n_1n_2) \quad (\text{A12})$$

$$14 \quad f_{AB}^A(i) = \frac{1}{2} \sum_{n_2=0}^i \sum_{n_1=i-n_2}^{\infty} \binom{n_1}{i-n_2} \left(\frac{1}{2}\right)^{n_1} q_{AB}(n_1n_2) \quad (\text{A13})$$

$$15 \quad f_{BB}^B(i) = \sum_{n_2=0}^i \sum_{n_1=i-n_2}^{\infty} \binom{n_1}{i-n_2} \left(\frac{1}{2}\right)^{n_1} q_{BB}(n_1n_2) \quad (\text{A14})$$

$$16 \quad f_{AB}^B(i) = \frac{1}{2} \sum_{n_2=0}^i \sum_{n_1=i-n_2}^{\infty} \binom{n_1}{i-n_2} \left(\frac{1}{2}\right)^{n_1} q_{AB}(n_1n_2) \quad (\text{A15})$$

17  
18  $p_g(i)$  is the frequency of pollen grains with genotype  $g$  at the modifier locus and carrying  $i$   
19 mutations.  
20

$$21 \quad p_A(i) = f_{AA}^A(i) + f_{AB}^A(i) \quad (\text{A16}) \quad p_B(i) = f_{AB}^B(i) + f_{BB}^B(i) \quad (\text{A17})$$

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23  
24  
25 c. Recursion equations for mating  
26

27 Let  $r_{AA}$ ,  $r_{AB}$ , and  $r_{BB}$  be the selfing rates of genotypes AA, AB and BB, respectively.  
28 In the main text,  $r_{AA} = r$  and  $r_{BB} = r'$ .  
29

$$30 \quad q_{AA}'(i0) = r_{AA} q_{AA}^{AA}(i0) + r_{AB} q_{AB}^{AA}(i0) + (1-r_{AA}) \left[ \sum_{k=0}^i f_{AA}^A(k) p_A(i-k) \right] + (1-r_{AB}) \left[ \sum_{k=0}^i f_{AB}^A(k) p_A(i-k) \right] \quad (\text{A18})$$

$$31 \quad q_{AA}'(ij) = r_{AA} q_{AA}^{AA}(ij) + r_{AB} q_{AB}^{AA}(ij), j > 0 \quad (\text{A19})$$

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$$q'_{BB}(i0) = r_{BB}q_{BB}^{BB}(i0) + r_{AB}q_{AB}^{BB}(i0) + (1-r_{BB}) \left[ \sum_{k=0}^i f_{BB}^B(k)p_B(i-k) \right] + (1-r_{AB}) \left[ \sum_{k=0}^i f_{AB}^B(k)p_B(i-k) \right] \quad (A20)$$

$$q'_{BB}(ij) = r_{BB}q_{BB}^{BB}(ij) + r_{AB}q_{AB}^{BB}(ij), j > 0 \quad (A21)$$

$$q'_{BB}(i0) = r_{AB}q_{AB}^{AB}(i0) + (1-r_{AA}) \left[ \sum_{k=0}^i f_{AA}^A(k)p_B(i-k) \right] + (1-r_{BB}) \left[ \sum_{k=0}^i f_{BB}^B(k)p_A(i-k) \right] + (1-r_{AB}) \left[ \sum_{k=0}^i (f_{AB}^A(k)p_B(i-k) + f_{AB}^B(k)p_A(i-k)) \right] \quad (A22)$$

$$q'_{AB}(ij) = r_{AB}q_{AB}^{AB}(ij), j > 0 \quad (A23)$$

### c. Mutation and selection

The frequencies of zygotes after mutation are, for any genotype G:

$$q_G''(ij) = \sum_{k=0}^i \frac{U^{i-k} e^{-U}}{(i-k)!} q_G'(kj) \quad (A24)$$

Selection acts both on mutations in heterozygous and homozygous state

$$q_G^*(ij) = \frac{(1-S)^j (1-hS)^i q_G''(ij)}{\bar{w}} \quad (A25)$$

where  $\bar{w}$  is the mean fitness of the population:

$$\bar{w} = \sum_{i=0}^{\infty} \sum_{j=0}^{\infty} \left[ (1-S)^j (1-hS)^i (q_{AA}''(ij) + q_{AB}''(ij) + q_{BB}''(ij)) \right] \quad (A26)$$

Equations (A7–26) completely define the recursion system. As before, fluctuating selection was modeled by sampling each generation the selection coefficient of deleterious mutations,  $S$ , in a Gaussian distribution with mean  $\mu_S$  and variance  $\sigma_S^2$  (equations A5 and A6). For each run, a small frequency of a mutant allele, with selfing rate  $r_{BB}$ , was introduced in linkage and identity equilibrium with deleterious mutations, into a population with selfing rate  $r_{AA}$  at mutation-selection equilibrium. Simulations were run for 1000 generations to detect invasion (or not) by the mutant.