

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

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Abstract

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

Introduction

Over the last 30 years, theoretical studies of plant mating systems have considered the role of inbreeding depression as central for the evolution of self-fertilization (Lloyd, 1979; Lande & Schemske, 1985; Charlesworth & Charlesworth, 1990). Inbreeding depression is the main evolutionary force that opposes the automatic 50% advantage of selfing (Fisher, 1941); it dictates the cost of seed discounting and determines the extent to which selfing causes reproductive assurance (Lloyd, 1992), so that the predicted outcome of mating system evolution critically depends on inbreeding depression values. Simple evolutionary models with a constant inbreeding

depression, δ , predict a dichotomous outcome of evolution: complete selfing when $\delta < 0.5$ and complete outcrossing when $\delta > 0.5$. Importantly, incorporating purging, i.e. a decrease in inbreeding depression with increasing population selfing rate due to the elimination of recessive deleterious mutations by selection, does not change these conclusions (Lande & Schemske, 1985; Charlesworth & Charlesworth, 1990; but see Uyenoyama & Waller, 1991a). Yet, the existence of natural populations with intermediate stable selfing rates is now widely acknowledged and a variety of theoretical models have been proposed to account for the maintenance of such mixed mating systems (reviewed in Goodwillie *et al.*, 2005). Although several models rely on ecology (e.g. pollination biology, Holsinger, 1991; Johnston, 1998; Vallejo-Marin & Uyenoyama, 2004; Porcher & Lande, 2005; Johnston *et al.*, 2009; or population dynamics, Morgan *et al.*, 2005) to explain mixed mating systems, numerous studies have elaborated on the prominent

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role of inbreeding depression by examining various genetic mechanisms (including overdominance, biparental inbreeding in isolated or structured populations, or decline in fitness with generations of selfing, Lloyd, 1979; Uyenoyama, 1986; Holsinger, 1988; Uyenoyama & Waller, 1991b; Latta & Ritland, 1993; Ronfort & Couvet, 1995; Rausher & Chang, 1999).

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

Here, we use a common genetic model of inbreeding depression to examine one possible genetic mechanism of fluctuating inbreeding depression and to test whether such fluctuations can maintain mixed mating systems when purging occurs. Consistent with the bulk of experimental data (Charlesworth & Charlesworth, 1999), we assume that inbreeding depression is caused by partly recessive, deleterious mutations. Such a mutation can be characterized by its selection coefficient (S) and its dominance coefficient (h). From this genetic perspective, environmental variation in inbreeding depression could result from fluctuations in either S or h or both (Bijlsma *et al.*, 1999; Armbruster & Reed, 2005), but little is known so far regarding the most likely source(s) of variation in inbreeding depression (Cheptou, 2006). Numerous experimental observations of larger inbreeding depression in stressful environments (e.g. Bijlsma *et al.*, 1999; and reviews in Armbruster & Reed, 2005; Willi *et al.*, 2007) suggest that environmental conditions may influence the selection coefficient of deleterious alleles, although other experiments comparing the mean fitness of *Arabidopsis thaliana* mutation accumulation lines across light and nutrient gradients failed to demonstrate any environment-specific effects of spontaneous mutations (Chang & Shaw, 2003; Kavanagh & Shaw, 2005). In the present study, we assume

that fluctuations in inbreeding depression are caused by temporal changes in the selection coefficient of deleterious mutations. We apply an analytical approach assuming an infinite population size. We address (1) the effect of temporal fluctuations of selection coefficients on the temporal variation in inbreeding depression, and compare this predicted variation to that observed in natural populations, (2) the effectiveness of purging under fluctuating selection and (3) the evolution of mating systems. We specifically investigate whether intermediate selfing rates are evolutionarily stable when inbreeding depression is subjected to fluctuating selection and is allowed to co-evolve with the mating system.

The model

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

Inbreeding depression with a fluctuating selection environment

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

Each generation, the modelled population undergoes mating, followed by mutation to deleterious alleles and selection. Recursion equations describing the distribution of number of homozygous and heterozygous mutations per individual are detailed in an online appendix and can also be found in Kondrashov (1985) or Charlesworth *et al.* (1990). These equations were iterated for 1000 generations (C++ code for numerical iterations available upon request from E.P.), by which time the population had reached steady state for all parameter combinations. To identify steady state, we considered the growth rate in the number of mutations across generations, N_{t+1}/N_t ; the population was considered at steady state when the

average growth rate over 50 generations did not differ significantly from 1 (one sample Student's *t*-test). Equations were subsequently iterated for another 1000 generations to record fluctuations in inbreeding depression at (statistical) steady state. For each set of parameter values, we recorded (1) the mean and variance of the number of homozygous and heterozygous deleterious mutations per individual and (2) the mean and variance of inbreeding depression, measured over the last 1000 generations. Because inbreeding depression is constrained between 0 (in the present study) and 1, the variance in inbreeding depression depends on the mean (e.g. the variance must be 0 if the mean is 0 or 1). To account for this dependence on the mean, we compared the simulated variance in inbreeding depression to the maximum possible variance:

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

where μ_{ID} is the mean inbreeding depression.

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

$$s^2 = \frac{1}{n-1} \sum (x_i - \bar{x})^2.$$

We thus chose to calculate the sample variance,

$$\sigma_{\text{ID}}^2 = \frac{1}{n} \sum (x_i - \bar{x}_{\text{ID}})^2.$$

Due to small sample sizes and nonrandom sampling, this crude procedure provides an order of magnitude estimate for the actual variance in inbreeding depression.

Evolutionarily stable mating systems

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

We deduce stable selfing rates using pairwise invasibility plots (PIP), in which regions of invasion (in grey)

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

Parameter values

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

Analytical approximation

To characterize the effect of purging on the selection of self-fertilization in a fluctuating environment, we

compared the results of the Kondrashov model with stochastic variation in selection coefficients to Cheptou & Schoen's (2002) analytical phenotypic approach. Following Lande & Schemske (1985), an approximate measure of the strength of selection on a rare genotype with selfing rate r' is given by the expected fitness of such genotypes:

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

where r is the mean selfing rate in the population and δ is the inbreeding depression.

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

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

Assuming small effects of mutation on the selfing rate, the evolution of self-fertilization can be analysed by modelling the invasion of a rare genotype with selfing r' in a population with selfing rate r . The success of invasion can be evaluated via $D(r)$, the selection gradient $\partial s / \partial r'$ at r : if the latter is positive (negative) mutants with slightly higher (lower) selfing rate may successfully invade. The selection gradient $D(r)$ for an inbreeding depression distribution with mean μ_δ and variance σ_δ^2 is given by (see Cheptou & Schoen, 2002 for details):

$$D(r) = \frac{0.5 - \mu_\delta}{1 - \mu_\delta r} - \frac{(1 - \frac{r}{2})r}{(1 - \mu r)^3} \sigma_\delta^2 \quad (4)$$

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

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

We incorporated purging in this analytical approach by making both μ_δ and σ_δ^2 functions of the population selfing rate, r . This and eqn (4) yield the following conditions for maintenance of mixed mating:

$$\mu_\delta(0) < 0.5, \quad (5)$$

$$\sigma_\delta^2(1) > 2[1 - \mu_\delta(1)]^2 [0.5 - \mu_\delta(1)]. \quad (6)$$

We tested whether the values generated by the Kondrashov model with fluctuating selection (mean and

variance of inbreeding depression at $r = 0$ and 1) met these conditions for the maintenance of mixed mating.

Results

Effectiveness of purging under fluctuating inbreeding depression

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

Magnitude of variation in inbreeding depression

As expected, temporal fluctuations in the selection coefficient of deleterious mutations generated variation in inbreeding depression across generations. Variation in inbreeding depression increased with the selection coefficient, σ_S^2 up to ca. 0.05. It was also affected by the population selfing rate and the purging process, with a peak in variance when the average inbreeding depression was closest to 0.5. Because mean and variance of inbreeding depression are not independent (eqn 1), the changes in variance under different population selfing rates were in great part attributable to changes in mean inbreeding depression. Depending on the mutation rate and dominance coefficient of deleterious mutations, variation in mean inbreeding depression explained 51–97% of the variance of inbreeding depression (these values were obtained by examining the correlation between the variance in the simulations and the maximum variance in inbreeding depression calculated from eqn 1).

Comparison of simulated vs. observed variation in inbreeding depression

Overall, the empirical data generally exhibited more variation in inbreeding depression than simulations

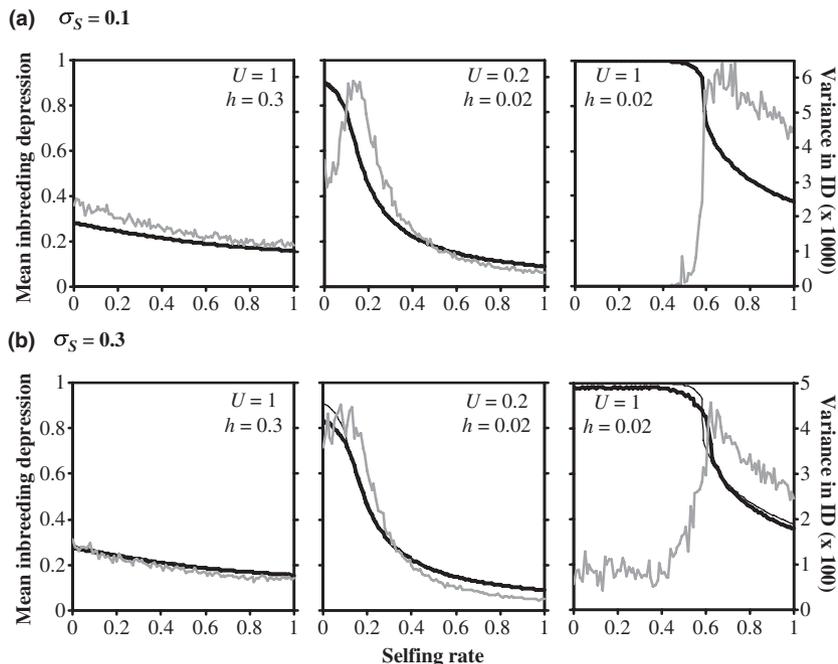


Fig. 1 Equilibrium inbreeding depression under fluctuating selection. Mean inbreeding depression (thick black lines) and variance in inbreeding depression (grey lines, measured over generations) are calculated over 1000 generations at steady state. The average selection coefficient of deleterious mutations 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.

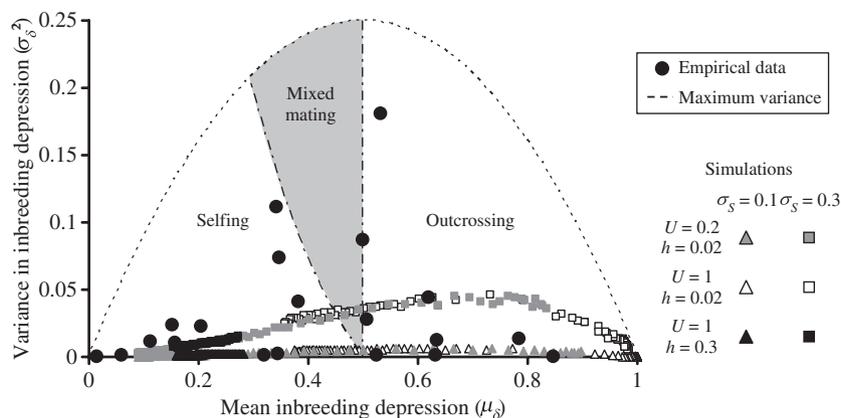


Fig. 2 Predicted and empirically derived estimates of the mean and variance in inbreeding depression. Empirical data (black circles) are from Armbruster & Reed (2005). Predicted values (squares and triangles) are from our simulation approach and are the same as in Fig. 1. The shaded area corresponds to combinations of mean and variance in inbreeding depression for which mixed mating systems are expected to be stable under Cheptou & 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 $\mu_{ID}(1 - \mu_{ID})$, as a function of the mean inbreeding depression, μ_{ID} ($0 < \mu_{ID} < 1$).

(Fig. 2, σ_{ID}^2 up to 0.18 and 0.046 respectively). The parameter space of μ_{ID} (mean inbreeding depression) and σ_{ID}^2 (variance in inbreeding depression) where the analytical model of Cheptou & Schoen (2002) predicts stable mixed mating systems (eqn 4, $D(r) = 0$) are plotted on Fig. 2 (shaded area). Interestingly, none of the empirical points fall within this parameter space. Despite relatively low variance in inbreeding depression generated by our theoretical approach, the simulations nonetheless generated some situations for which Cheptou & Schoen’s

(2002) model predicts stable mixed mating: this was the case with $U = 0.2, h = 0.02, \sigma_S = 0.3$ and $U = 1, h = 0.02, \sigma_S = 0.3$ (combination of μ_{ID} and σ_{ID}^2 within the shaded area, Fig. 2).

Evolution of self-fertilization under fluctuating inbreeding depression

Evolutionarily stable selfing rates can be deduced from PIP (Fig. 3), where regions of invasion (in grey) and

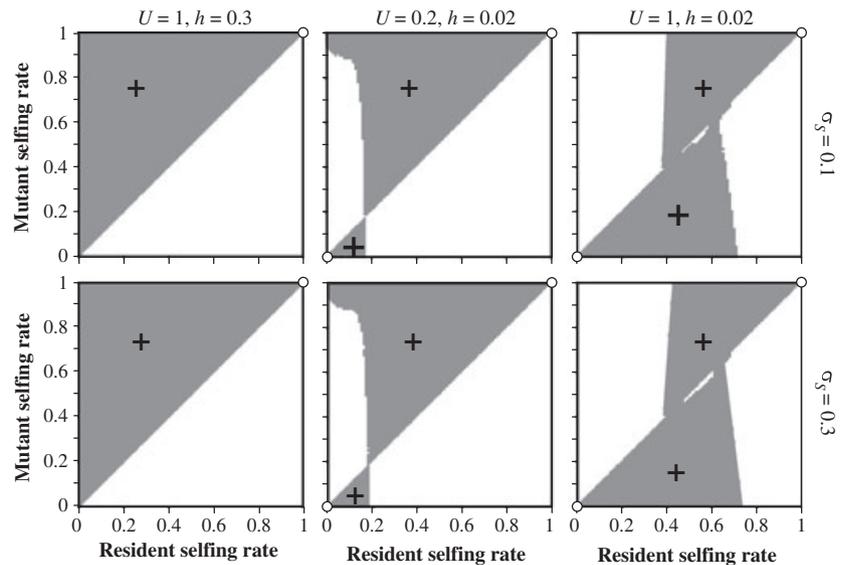


Fig. 3 Evolutionarily stable selfing rates under fluctuating inbreeding depression. The average selection coefficient of deleterious mutations is $\mu_S = 0.5$. Regions where the mutant invades ('+') are in grey, regions where it does not invade are in white. White circles indicate evolutionarily stable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

noninvasion (in white) of a rare mutant are plotted against the selfing rate of the resident genotype, r and that of the mutant, r' . Evolutionarily stable selfing rates are located at the intersection of the $r = r'$ line and a line separating regions of invasion and noninvasion, and are characterized by the fact that no mutant can invade (i.e. the areas just above and below are white on the PIP). The main result of our study is that intermediate selfing rates were never evolutionarily stable (Fig. 3), even though large variances in the selection coefficient of deleterious mutations generated fluctuations in the magnitude of inbreeding depression. This was true regardless of the mutation rate, the dominance coefficient of deleterious mutation, as well as the mean and variance of the selection coefficient of mutations (and hence variance in inbreeding depression). The only stable mating systems were complete outcrossing with nearly codominant deleterious mutations ($h = 0.3$, Fig. 3) and complete outcrossing or complete selfing (depending on the initial conditions) with nearly recessive mutations ($h = 0.02$, Fig. 3). In addition, the threshold for the selection of pure selfing or pure outcrossing did not depend on the variance in inbreeding depression. Thus, in our genetic model, fluctuations in inbreeding depression do not favour the maintenance of mixed mating.

This was confirmed by considering the modified version of Cheptou & Schoen (2002) analytical approach, accounting for purging via selfing rate dependent inbreeding depression. Under this model, condition (2) for the maintenance of stable mixed mating (namely $D(1) < 0$, invasion of a mutant with selfing rate < 1 in a completely selfing population) requires substantial variance in inbreeding depression in a completely selfing population where average inbreeding depression is generally low. Under the Kondrashov model, high variance is generated by a high mutation rate (e.g. $U = 1$, Fig. 1).

However, this set of parameters also generates high average inbreeding depression (μ_δ close to 1) at $r = 0$, which invalidates condition (1) for the maintenance of mixed mating (namely $D(0) > 0$, invasion of a mutant with the selfing rate > 0 in a completely outcrossing population, $\Leftrightarrow \mu_\delta < 0.5$). Hence, although some combinations of μ_δ and σ_δ fell within the 'mixed mating' window of Fig. 2, sufficient conditions for stable mixed mating (1) and (2) were never met. Mixed mating can therefore never be maintained when inbreeding depression is modelled with partly recessive deleterious mutations in an infinite population (as in Kondrashov, 1985).

Discussion

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

Fluctuations in selection coefficients have little effect on purging

Temporal variation in the selection coefficient of the deleterious mutations has very little effect on the average equilibrium inbreeding depression. This is consistent with single locus theory in randomly mating populations: Crow & Kimura (1970) showed that with incompletely recessive ($h > 0$), mildly deleterious mutations ($S \gg u$) mutant homozygotes are kept sufficiently rare by selection so that most selection occurs against mutant heterozygotes. As a result, the dynamics of the mutant allele in a constant environment are approximately a

linear function of the selection coefficient, S , and can be written $dq/dt \approx u - hSq$ (Crow & Kimura, 1970; Lande & Schemske, 1985), where q is the mutant allele frequency and u is the per locus mutation rate. With fluctuating selection, this yields $E(dq/dt) = u - E(hS)q$. At equilibrium ($dq/dt = 0$), $q = u/E(hS)$. Hence, in randomly mating populations under fluctuating selection, inbreeding depression at a single locus depends solely on the mean selection coefficient (or dominance coefficient) of the deleterious mutation, not on its variance. Our results extend these predictions with a single locus to many loci, as well as nonrandom mating. Similarly, when selfing is enforced in a previously completely outcrossing population, fluctuations do not affect the time required for the population to reach the new equilibrium inbreeding depression (data not shown), which is due to the fact that, under complete selfing, highly recessive deleterious mutations are quickly exposed to selection and a few generations of strong selection are enough to purge most of the load (e.g. Lande & Schemske, 1985).

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

Fluctuations in selection coefficients can generate substantial variation in inbreeding depression

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

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

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

Based on a phenotypic model with no purging of deleterious mutations, Cheptou & Schoen (2002) predicted that intermediate selfing rates can be stable with fluctuating inbreeding depression under some combinations of mean and variance in inbreeding depression (see Fig. 2). Our results with an explicit genetic model of inbreeding depression contrast with their predictions: mixed mating systems were never evolutionarily stable, although some parameter combinations appear to generate a mean and variance of inbreeding depression consistent with stable mixed mating systems under Cheptou and Schoen's approach [Fig. 2, e.g. a high mutation rate to deleterious alleles ($U = 1$), nearly recessive mutations ($h = 0.02$) and substantial fluctuation in the selection coefficient of deleterious mutations]. Evidently, it is purging in our model that makes mixed mating unstable. Although the mean and variance are independent parameters in Cheptou and Schoen's model, these quantities intrinsically covary in an explicit genetic model. Purging creates a strong positive feedback that

selects for selfing (Lande & Schemske, 1985) and that overwhelms the negative feedback produced by fluctuating inbreeding depression (Cheptou & Schoen, 2002).

A heuristic understanding of why the genetic architecture of inbreeding depression can disrupt the maintenance of intermediate selfing rates was seen using an analytical approach. By incorporating selfing rate-dependent mean and variance of inbreeding depression into Cheptou & Schoen's (2002) analytical approach, we derived sufficient conditions for mixed mating: moderate mean inbreeding depression under complete outcrossing ($\mu_\delta < 0.5$) together with appreciable variance in inbreeding depression under complete selfing. In our simulations, these conditions were never met because the genetic architecture of inbreeding depression generates two contrasting situations that depend on the characteristics of the deleterious mutation. First, a low mutation rate (data not shown) or nearly codominant deleterious mutations that can be eliminated by selection even in a heterozygous state ($h = 0.3$, Fig. 1) result in moderate inbreeding depression in a completely outcrossing population [condition (1)]. However, this also generates a low inbreeding depression (and hence a low variance in inbreeding depression) under complete selfing, due to extensive purging, so that condition (2) is not met. Alternatively, a high mutation rate to nearly recessive mutations ($U = 1$ and $h = 0.02$, Fig. 1) creates situations in which the mean inbreeding depression under complete selfing is close to 0.5, so that the variance in inbreeding depression can be large [condition (2)]. However, with this characteristic of mutations, condition (1) is not met due to the absence of purging in a completely outcrossing population, generating large mean inbreeding depression.

Some limits of the model

Although fluctuating selection coefficients can generate substantial inbreeding depression, our approach suggests that when purging occurs, fluctuating inbreeding depression is very unlikely to maintain intermediate selfing rates. This probably depends strongly on several assumptions of our model. First, Kondrashov's (1985) approach assumes infinite population size, whereas in natural populations purging is a stochastic process (Byers & Waller, 1999) that can be slowed down in small populations (Glémin, 2003), but should also be reinforced by the possibility of biparental inbreeding in finite populations. The role of demographic stochasticity in the evolution of genetic load and mating systems has been addressed in a limited number of studies (e.g. Charlesworth *et al.*, 1992; Wang *et al.*, 1999; Bataillon & Kirkpatrick, 2000; Theodorou & Couvet, 2002; Glémin, 2003; Guillaume & Perrin, 2006) but the interaction between demography, genetics and environmental variation remains to be explored. Second, we assumed that environmental variation affected the selection coefficient

of a large number of strictly identical, unlinked deleterious mutations. Although little is known regarding the actual mechanisms for environment-dependent inbreeding depression (Armbruster & Reed, 2005), recent studies suggest the existence of environment-specific deleterious alleles (e.g. Vermeulen & Bijlsma, 2004), i.e. alleles that are usually neutral but become deleterious in specific (e.g. stressful) environments. Such environment-specific alleles, which are rarely submitted to selection, may accumulate in the genome and eventually add up to environment-independent inbreeding depression in stressful environments, which can affect the evolution of mating systems. However, our model suggests that their effects are likely to remain minor if these alleles are expressed frequently enough, because purging occurs within a couple of generations under selection. Lastly, other genetic mechanisms such as variation in dominance or even purely additive gene action when the strength of stabilizing selection varies may create inbreeding depression variance under heterogeneous environments (Lande & Schemske, 1985).

Conclusion

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

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Supporting information

Additional Supporting Information may be found in the online version of this article:

Appendix S1 Recursion equations for Kondrashov's model with fluctuating selection.

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