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GENETIC ARCHITECTURE OF INBREEDING DEPRESSION AND THE MAINTENANCE OF GAMETOPHYTIC SELF-INCOMPATIBILITY

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Gametophytic self-incompatibility (GSI) is a widespread genetic system, which enables hermaphroditic plants to avoid self-fertilization and mating with close relatives. Inbreeding depression is thought to be the major force maintaining SI; however, inbreeding depression is a dynamical variable that depends in particular on the mating system. In this article we use multilocus, individual-based simulations to examine the coevolution of SI and inbreeding depression within finite populations. We focus on the conditions for the maintenance of SI when self-compatible (SC) mutants are introduced in the population by recurrent mutation, and compare simulation results with predictions from an analytical model treating inbreeding depression as a fixed parameter (thereby neglecting effects of purging within the SC subpopulation). In agreement with previous models, we observe that the maintenance of SI is associated with high inbreeding depression and is facilitated by high rates of self-pollination. Purging of deleterious mutations by SC mutants has little effect on the spread of those mutants as long as most deleterious alleles have weak fitness effects: in this case, the genetic architecture of inbreeding depression has little effect on the maintenance of SI. By contrast, purging may greatly enhance the spread of SC mutants when deleterious alleles have strong fitness effects.

KEY WORDS: **Deleterious mutation, inbreeding depression, purging, self-incompatibility.**

Self-incompatibility (SI) is a genetic system that enables hermaphroditic plants to avoid self-fertilization and limit mating with close relatives by recognition and rejection by the pistil of pollen expressing cognate specificities. In many species, SI specificity is controlled by a single multiallelic locus, the S-locus. SI is widespread, found in more than 100 families of angiosperms (Igic et al. 2008) despite the fact that it entails a transmission disadvantage. Indeed, a self-compatible (SC) mutant occurring in an SI population should benefit from a higher number of potential mates, and from a transmission advantage through self-fertilization. This last advantage is equal to two-thirds (Charlesworth and Charlesworth 1979), and is thus higher than the 50% advantage of an allele coding for selfing in an outcrossing population (Fisher 1941), because only the SC pollen contributes to the selfed offspring in heterozygous individuals for SC. Recently, it has been argued that SI may be maintained by selection acting at the species level, due to the fact that SI species diversify at higher rates (Goldberg et al. 2010). This form of selection only acts in the long term, however, and implies that SC mutations should occur very rarely. The main advantage of SI that could possibly explain its maintenance in the short term is the avoidance of inbreeding depression (e.g., Charlesworth and Charlesworth 1987). However, Charlesworth and Charlesworth (1979) showed that for SI to be maintained in the presence of SC mutants, inbreeding depression has to be high; its minimal value depends on the number of SI alleles segregating in the population and on the selfing rate of SC mutants, but is often close to Two-thirds when the number of SI alleles is large—this minimal

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value is higher and may even reach 1 when the number of SI alleles is not large and the selfing rate of SC mutants is small to moderate, as SC mutants also benefit from a higher number of potential mates. Furthermore, the minimal value of inbreeding depression needed to maintain SI may be underestimated by Charlesworth and Charlesworth's (1979) model because inbreeding depression was treated as a fixed variable, therefore neglecting the effect of purging of deleterious alleles by the self-fertilizing SC individuals. Purging is expected to facilitate the spread of SC mutants, as these mutants tend to better eliminate partially recessive deleterious alleles, thereby reducing the magnitude of inbreeding depression experienced by their selfed offspring (Uyenoyama and Waller 1991; Glémin 2003). This was confirmed by a deterministic simulation model by Porcher and Lande (2005), assuming that a given proportion of self-pollen lands on the stigma ("mass-action" pollination model, Holsinger 1991) and that inbreeding depression results from recessive lethal mutations segregating at a very large (effectively infinite) number of loci (Kondrashov 1985). In this model, invasion of an SI population by an SC mutant (i.e., the breakdown of SI) is easier than expected from results of Charlesworth and Charlesworth (1979), in particular when the selfing rate of SC mutants is moderate to high (so that purging can occur). Porcher and Lande (2005) also observed that in a small region of parameter space (namely, for high values of inbreeding depression and low selfing rates), the population may reach a stable, polymorphic equilibrium in which both SI and SC individuals are present. This observation is important in the context of how new SI specificities may arise through SC intermediates, assuming that compensatory mutations may secondarily restore a novel SI functionality (Uyenoyama et al. 2001; Gervais et al. 2011).

Although Porcher and Lande (2005) model showed that considering the joint dynamics of SI and inbreeding depression may strongly affect predictions concerning the maintenance of SI, the fact that they considered lethal mutations may overestimate the importance of purging in situations in which inbreeding depression is (at least partly) generated by mildly recessive deleterious alleles. Indeed, analytical models have shown that the advantage of a selfing modifier through purging is expected to increase with the strength of selection against deleterious alleles (Uyenoyama and Waller 1991; Epinat and Lenormand 2009), which was also observed in deterministic simulations representing the spread of a mutation affecting the selfing rate (Charlesworth et al. 1990). More recently, Porcher and Lande (2013) showed that the effect of purging on the spread of a mutation affecting selfing is much lower when the strength of selection against deleterious alleles is mild ($s = 0.05$) than when it is strong ($s = 1$). However, Porcher and Lande (2013) only considered weak-effect selfing modifiers (changing the selfing rate by 10^{-6}), and the effect of purging may be stronger in the case of a mutation having a large effect on the selfing rate (Charlesworth et al. 1990) such as a mutation disrupting SI. Because the results of Porcher and Lande (2005) showed that purging may strongly limit conditions for the maintenance of SI in the presence of lethal recessive mutations, it is important to assess the generality of this result (in particular to situations in which a substantial proportion of mutations are mildly deleterious) to better understand how SI can be maintained in natural populations (note that Porcher and Lande (2005) also considered situations in which inbreeding depression is partly due to mildly deleterious mutations, but this component of inbreeding depression was not dynamic in their model).

All previous simulation models explicitly considering the genetic basis of inbreeding depression (Charlesworth et al. 1990; Porcher and Lande 2005, 2013) were based on Kondrashov (1985) model, representing the dynamics of deleterious alleles at an infinite number of unlinked loci, in an infinite population. In principle, genetic linkage should increase the effect of purging, by increasing the association between SC alleles and purged genetic backgrounds; however, whether the effect of linkage is substantial for realistic values of genomic recombination rates is unclear. Furthermore, genetic linkage to the S-locus may affect the dynamics of deleterious alleles ("sheltered load," Glémin et al. 2001; Porcher and Lande 2005), in turn affecting the conditions for the maintenance of SI. Finite population size is expected to affect the number of SI alleles maintained in the population—which depends both on population size and on the mutation rate toward new SI alleles (Yokoyama and Hetherington 1982). Because conditions for the maintenance of SI depend on the number of SI alleles segregating (Charlesworth and Charlesworth 1979; Porcher and Lande 2005; Gervais et al. 2011), they should thus be affected by population size. Furthermore, the number of SI alleles may also change as SC mutants increase in frequency, which may in turn affect the conditions needed to maintain SI and SC individuals at a polymorphic equilibrium (Gervais et al. 2011).

In this article, we use a multilocus individual-based simulation program to explore the conditions for the maintenance of SI when inbreeding depression is generated by deleterious alleles segregating at a large number of partially linked loci in a finite population. Our model also differs from the previous models cited above by assuming that inbreeding depression affects both seed and pollen production, which in turn affects the selfing rate of SC individuals (as it depends on the quantity of self-pollen relative to the quantity of pollen received from other individuals). We show that in many cases, conditions for the maintenance of SI are similar to those obtained from an analytical model assuming fixed inbreeding depression (i.e., the effect of purging on the spread of SC mutants remains small), unless a substantial proportion of deleterious mutations have strong fitness effects. Linkage has only little effect for the parameter values tested, as long as the mean number of crossovers per genome (i.e., genetic map length)

is not too small. Finally, we almost never observe a polymorphic equilibrium, which is probably due to the fact that the number of SI alleles decreases as SC individuals increase in frequency, further enhancing the advantage of self-compatibility.

Methods

We consider a population with a GSI system, that is, fertilization is possible only if the specificity expressed by the pollen is different from the two specificities codominantly expressed in the style. Specificities are subject to negative frequency-dependent selection, because pollen bearing rare specificities can fertilize more individuals than pollen bearing more common specificities (Wright 1939). We assume that SI is coded by a single S-locus with many alleles (denoted S_i): a plant with genotype S_iS_j ($i \neq j$) is self-incompatible and can be fertilized by pollen of genotype S_l, with $l \neq i$ and $l \neq j$. We also consider a mutant, SC allele S_C segregating at the same locus: pollen carrying S_C can fertilize all plants, whereas a plant with genotype S_iS_C is partially SC (through its S_C pollen) and can be fertilized by any pollen whose genotype is different from S_i. Finally, S_CS_C individuals are fully SC and can be fertilized by any pollen. A parameter α measures the proportion of pollen produced by a plant that stays on the same plant ("self-pollen"), leading to self-fertilization if it carries the S_C allele. We assume that selfed offspring suffer from inbreeding depression, generated by partially recessive deleterious alleles segregating at a number of different loci. Several selective forces may affect the frequency of the S_C allele: (1) automatic transmission advantage through selfing, when $\alpha > 0$; (2) transmission advantage through outcrossing, as S_C pollen can fertilize all plants; (3) negative consequences of increased homozygosity due to selfing on the mean fitness of offspring (inbreeding depression); and (4) indirect benefits stemming from a better elimination of deleterious alleles as a consequence of increased homozygosity (purging). This last effect occurs more rapidly when deleterious alleles have stronger effects (e.g., Charlesworth and Willis 2009). S_C is thus favored by effects (1), (2), and (4), and disfavored by effect (3); but note that purging also tends to reduce inbreeding depression. In the following, we use a multilocus, individual-based simulation model to represent explicitly the genetic causes of effects (3) and (4) (inbreeding depression and purging). Results on the spread of S_C are compared to the predictions of a simple analytical model in which effect (4) is ignored by treating inbreeding depression as a fixed parameter.

ANALYTICAL MODEL

Our analytical model represents an infinite population with discrete, nonoverlapping generations. We assume that $n + 1$ alleles segregate at the S-locus: n self-incompatible alleles and the SC S_C allele. We denote x_1 and x_2 the frequencies of S_CS_C individuals produced by selfing (x_1) and by outcrossing (x_2), and x_3 and x_4 the frequencies of S_iS_C individuals produced by selfing (x_3) and by outcrossing (x_4), where S_i can be any SI allele. We suppose that selfed individuals produce fewer gametes (inbreeding depression), the number of male and female gametes produced by outcrossed individuals being proportional to $W_2 = W_4 = 1$, whereas the number of gametes produced by selfed individuals is proportional to $W_1 = W_3 = 1 - \delta$; mean fecundity $\overline{W}$ is thus given by $1 - \delta(x_1 + x_3)$. The selfing rate a_i (proportion of selfed seeds) of an individual of type i (1, 2, 3 or 4) is given by

$$a_i = \frac{\alpha\,\theta_i\,W_i}{\alpha W_i + (1-\alpha)\overline{W}}, \tag{1}$$

where $\theta_i = 1$ for $i = 1, 2$ and $\theta_i = 1/2$ for $i = 3, 4$. The numerator of equation (1) represents the quantity of compatible self-pollen (bearing allele S_C), whereas the denominator is the total quantity of pollen received by the individual. The frequency of allele S_C among gametes is given by $q = \sum_i \theta_i\,W_i\,x_i/\overline{W}$, whereas, by symmetry, each SI allele is present in frequency $p = (1 - q)/n$. From this, frequencies at the next generation are given by the following:

$$\begin{aligned}
\overline{W}x_1' &= W_1 a_1 x_1 + W_2 a_2 x_2 + \frac{1}{2}W_3 a_3 x_3 + \frac{1}{2}W_4 a_4 x_4,\\
\overline{W}x_2' &= W_1(1-a_1)q\,x_1 + W_2(1-a_2)q\,x_2\\
&\quad + \frac{[W_3(1-a_3)x_3 + W_4(1-a_4)x_4]\,q}{2(1-p)},\\
\overline{W}x_3' &= \frac{1}{2}W_3 a_3 x_3 + \frac{1}{2}W_4 a_4 x_4,\\
\overline{W}x_4' &= W_1(1-a_1)(1-q)\,x_1 + W_2(1-a_2)(1-q)\,x_2\\
&\quad + \frac{1}{2}W_3(1-a_3)x_3 \quad + \frac{1}{2}W_4(1-a_4)x_4\\
&\quad + (1-x_1-x_2-x_3-x_4)\,\frac{q}{2(1-p)}\,.
\end{aligned} \tag{2}$$

In the Supplementary Material, we use a local stability analysis to determine the values of α, n, and δ for which S_C increases in frequency when rare (which involves solving a fourth-order equation in δ numerically).

MULTILOCUS SIMULATIONS

Individual-based, multilocus simulations were used to explore the conditions for the maintenance of SI when deleterious alleles segregate at a large number of partly linked loci, and when the number of SI alleles evolves freely by mutation, selection, and drift. The simulation program (written in C++, and available from Dryad) corresponds to a modified version of the program described in Roze and Michod (2010), representing a population of N diploid individuals (the parameters used in the simulation

Table 1. Parameters and default values used in simulations.

Description	Symbol	Default Value
Population size	N	2000
Mean number of crossovers per genome per generation	L	10
Proportion of self-pollen	α	
Selection coefficient of deleterious mutations	s	0.05
Dominance coefficient of deleterious mutations	h	0.2
Rate of deleterious mutation per haploid genome	U	
Rate of mutation from S_i to any S_j (with $j \neq i$)	U_{SI}	10^{-5}
Rate of mutation from S_i to S_C	U_{SC}	10^{-4}

model are summarized in Table 1). Each individual possesses two copies of a linear chromosome, and an S-locus located at the midpoint of the chromosome. We assume that a maximum of $k + 1$ alleles can segregate at the S-locus: k self-incompatible alleles S_i ($1 \leq i \leq k$) and an SC allele S_C; k is fixed at 100 in all simulations. Every generation, each S_i allele mutates to any of the $k - 1$ other SI alleles with probability U_{SI} and to allele S_C with probability U_{SC} (loss of SI). There is no reverse mutation from S_C to S_i, that is, loss of SI is irreversible. Deleterious mutations occur at a rate U per haploid genome, that is, the number of new deleterious mutations on each chromosome is drawn from a Poisson distribution with parameter U, whereas the position of each new mutation along the chromosome is sampled from a (continuous) uniform distribution—the number of sites at which deleterious alleles may segregate is thus effectively infinite. All deleterious mutations have the same selection and dominance coefficients (s and h respectively), although we also consider cases in which a given proportion of mutations are lethal (as detailed below). Reproduction occurs as follows: for each of the N individuals of the next generation the maternal parent is sampled randomly among all individuals of the previous generation, the probability of sampling parent i being proportional to its fecundity $W_i = (1 - hs)^{N_{\text{he}}}(1 - s)^{N_{\text{ho}}}$, where N_{he} and N_{ho} are the number of mutations in the heterozygous and homozygous state within its genome. If the maternal plant carries at least one SC allele S_C, its selfing rate a_i is calculated as follows:

$$a_i = \frac{\alpha\, \gamma_{ii}\, W_i}{\alpha\, \gamma_{ii}\, W_i + \frac{1-\alpha}{N-1} \sum_{j \neq i} \gamma_{ij}\, W_j}, \tag{3}$$

where γ_{ij} is 0, 1, or 2 and represents the number of individual j's S-alleles that are compatible with individual i. In the case of selfing, the offspring's genome is formed from two of i's recombinant gametes; otherwise an individual j is sampled randomly with a probability proportional to W_j, and contributes as a father only if one of its S-alleles is compatible with those of the mother (if not, another individual is sampled until a compatible partner is found). To form a recombinant gamete, the number of crossovers occurring along the chromosome is drawn from a Poisson distribution with parameter L (genome map length, in Morgans) and the position of each crossover is sampled from a uniform distribution.

At the beginning of each simulation, individuals are free of deleterious mutations and heterozygous for randomly sampled SI alleles. During the first 2000 generations, the number of SI alleles segregating in the population is allowed to reach equilibrium by considering only mutation between SI alleles ($U_{SC} = 0$, $U = 0$). Deleterious mutations are then introduced and allowed to reach mutation-selection balance over the next 2000 generations. Finally, during the next 500,000 generations, SC mutants are also introduced. Because loss of SI is irreversible, simulations are stopped after 50,000 generations if S_C is fixed in the population. Every 100 generations, different variables are measured from the population: the frequency of allele S_C, the effective number of SI alleles present and the level of inbreeding depression. The effective number of SI alleles n_e (measured before allele S_C is introduced) corresponds to the number of alleles that would yield the same genetic diversity at the S-locus if all alleles were present in frequency $1/n_e$; it is calculated as $n_e = 1/\sum_{i=1}^{k} p_i^2$, where p_i is the frequency of allele S_i. Inbreeding depression is measured as $\delta = 1 - W_s/W_o$, where W_s and W_o are the mean fecundities of selfed and outcrossed offspring, respectively (estimated by creating 100 selfed and 100 outcrossed offspring from randomly sampled parents, without taking into account the compatibility between their S-alleles). For each simulation run, δ and n_e are averaged over the last 50 samples before introduction of SC mutants, whereas the frequency of S_C is averaged over the last 300 samples of the simulation (last 30,000 generations). The minimal value of δ necessary to maintain SI in the population is determined by running simulations with increasing values of U for each set of parameters values (U_{SI}, U_{SC}, s, h, N, L, and α). When the frequency of S_C stays lower than 0.05 throughout the simulation, SI is considered maintained.

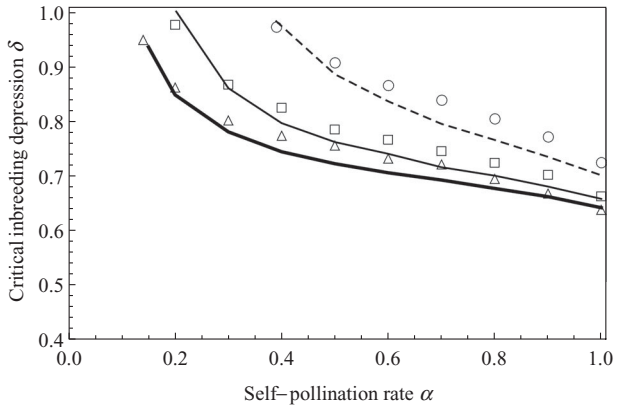

Figure 1. Minimal inbreeding depression needed to prevent invasion of an SI population by an SC mutant, when the genetic load depends only on small-effect deleterious alleles, and for different population sizes *N*. The points correspond to multilocus simulation results and the curves to analytical predictions. Circles, dashed curve: $N = 500$; squares, solid curve: $N = 2000$; triangles, thick curve: $N = 5000$. Other parameter values: $L = 10$, $s = 0.05$, $h = 0.2$.

Results

MILDLY DELETERIOUS MUTATIONS

Figure 1 shows the minimal value of inbreeding depression δ necessary to maintain SI in the population as a function of the rate of self-pollination α, for different values of population size N. In all figures, the highest value of inbreeding depression (in the absence of S_C) for which we observed that S_C invades the population (i.e., reaches frequency 0.05) is just slightly below the points (see Fig. S3 for more detailed results). In almost all simulations the frequency of S_C at equilibrium was either close to zero or equal to 1. Note that because the loss of SI is irreversible in our model (no back mutation from SC to SI), one expects that allele S_C should necessarily become fixed after a sufficiently long time. However, changing the number of generations with $U_{SC} > 0$ to 10^5 or to 10^6 did not lead to significant differences in the threshold values of δ shown in Figure 1 (results not shown), suggesting that as one enters the area above the points, the expected fixation time of S_C quickly reaches extremely high values (i.e., SI is stably maintained). In the same vein, increasing the mutation rate towards S_C (U_{SC}) from 10^{-5} to 10^{-4} has very little effect on the results (not shown). In a few cases, S_C was still polymorphic at the end of the simulation (at frequency >0.05), or the time to fixation of S_C was higher than the average time to fixation of a neutral allele ($4N$ generations), suggesting that selection may maintain polymorphism for these parameter values. However, this was only observed for narrow parameter ranges at the leftmost limit of the region in which SI is maintained (see Fig. S3).

Curves on Figure 1 correspond to the predictions derived from the analytical model (neglecting the effect of genetic associations between the S-locus and selected loci), in which the number of SI alleles n is set to the average effective number of alleles n_e measured in simulations corresponding to the critical δ. Overall, simulation results are qualitatively and quantitatively consistent with these analytical expectations: maintenance of SI is always observed when inbreeding depression is high ($\delta > 2/3$), the critical δ being lower when the self-pollination rate α is higher, in agreement with previous results neglecting effects of purging (Charlesworth and Charlesworth 1979; Uyenoyama et al. 2001). The effect of population size N on the critical δ is due to the fact that the effective number of SI alleles is reduced in smaller populations through the loss of low-frequency alleles by drift (e.g., Yokoyama and Hetherington 1982): on average n_e at the critical δ equals 11.9, 23.0, and 36.4 for $N = 500$, 2000, and 5000, respectively. Lower effective numbers of SI alleles favor the spread of S_C by increasing the transmission advantage of S_C through outcrossing, as S_C pollen never encounters incompatible pistils and can fertilize every potential mate in the population (Charlesworth and Charlesworth 1979; Porcher and Lande 2005; Gervais et al. 2011). Simulations for different values of U_{SI} (rate of mutation toward new SI alleles) show that increasing U_{SI} (with $NU_{SI} = 0$, 0.02, and 0.2) has similar effects as increasing N (Fig. S1).

Overall, the good match between the simulation results (with purging) and predictions from the analytical model (without purging) indicates that purging has little effect on the spread of S_C for these parameter values. Note that the analytical model systematically underestimates the critical δ for SI to be maintained, which suggests that some purging may still be taking place. In most cases however, the discrepancy remains slight, suggesting that the magnitude of this effect is low, except when α increases and hence the selfing rate of SC individuals becomes more important. The effect of purging on the spread of S_C should be more important when selection against deleterious alleles is stronger (e.g., Charlesworth et al. 1990), as deleterious alleles are eliminated more rapidly when present in homozygotes, and as the benefit of being associated with chromosomes carrying fewer deleterious alleles is stronger. In agreement with this prediction, Figure 2 shows that discrepancies between analytical and simulation results becomes more important for higher values of s and h. One can also see from Figure 2 that, at the critical δ, s has little effect on the effective number of SI alleles n_e maintained in the population (the curves on Fig. 2 A are almost superposed), whereas higher values of h lead to lower values of n_e. This is likely due to the fact that n_e is affected by background selection (reduction in diversity due to selection at linked sites, e.g., Charlesworth 1993). Indeed, background selection is stronger when the deleterious mutation rate U is higher (e.g., Hudson and Kaplan 1995), and higher values of U are needed to reach the critical δ when h is increased,

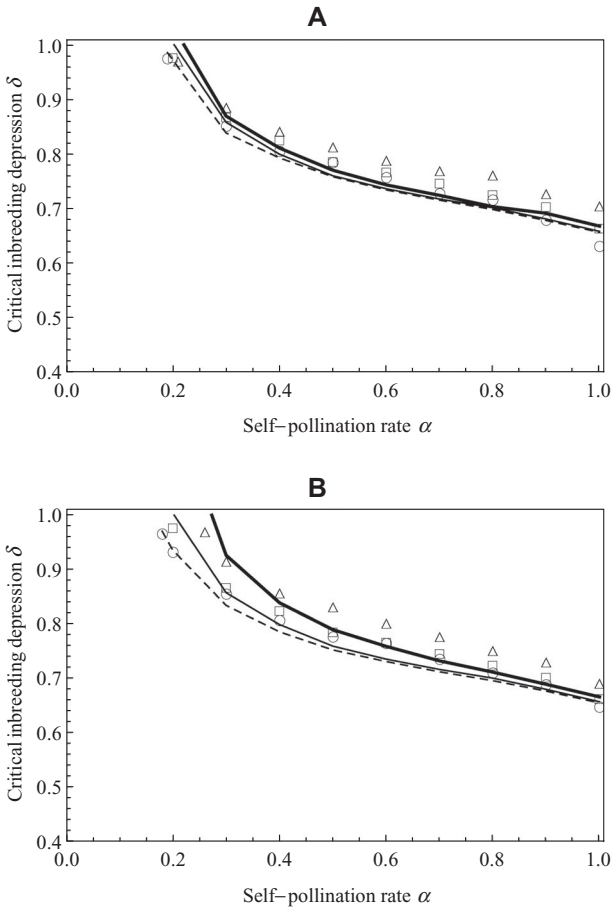

Figure 2. Minimal inbreeding depression needed to prevent invasion of an SI population by an SC mutant, when the genetic load depends only on small-effect deleterious alleles, and for different selection (A) and dominance (B) coefficients of deleterious alleles. The points correspond to multilocus simulation results and the curves to analytical predictions. (A) circles, dashed curve: $s = 0.02$; squares, solid curve: $s = 0.05$; triangles, thick curve: $s = 0.1$. (B) Circles, dashed curve: $h = 0.1$; squares, solid curve: $h = 0.2$; triangles, thick curve: $h = 0.3$. Other parameter values: $N = 2000$, $L = 10$, $h = 0.2$ (in A), $s = 0.05$ (in B).

leading to stronger background selection effects at the critical δ. By contrast, δ is only weakly dependent on s (as long as population size is sufficiently large, e.g., Bataillon and Kirkpatrick 2000), and s has thus little effect on the strength of background selection at the critical δ. Finally, we find that varying map length L has relatively little effect on the results as long as it is sufficiently large (roughly, $L > 5$ using our default parameter values shown in Table 1). Figure S2 shows that reducing L decreases the effective number of SI alleles (background selection) and increases selection for S_C through purging (higher discrepancy between analytical and simulation results when L is lower), both effects reducing the parameter range in which SI is maintained.

ADDING A PROPORTION OF NEARLY RECESSIVE LETHAL MUTATIONS

Using a deterministic model in which mutations generating inbreeding depression are lethal and nearly recessive, Porcher and Lande (2005) found much more stringent conditions for the maintenance of SI than those shown on Figures 1 and 2. We modified our simulation program so that a proportion λ of deleterious mutations are nearly recessive lethals (selection and dominance coefficients: $s_l = 1$ and $h_l = 0.02$, respectively) whereas the other mutations (in proportion $1 - \lambda$) are mildly deleterious ($s = 0.05$ and $h = 0.2$). As shown by Figure 3, the discrepancy between analytical and simulation results becomes stronger as λ increases, and the parameter range in which SI is maintained is considerably reduced. In particular, allele S_C invades the population for much larger values of inbreeding depression when the rate of self-pollination α is high, so that individuals carrying S_C frequently self. The proportion of lethal mutations has almost no effect on the effective number of SI alleles maintained in the absence of S_C, and therefore the analytical predictions are nearly unaffected by λ (curves on Fig. 3 are nearly superposed).

Discussion

SI (and especially GSI) is widespread among angiosperms, despite the fact that SC mutants should benefit from a direct transmission advantage. Different models have shown that, provided that it is sufficiently high, inbreeding depression can allow the stability of SI despite the recurrent occurrence of SC mutants (Charlesworth and Charlesworth 1979; Uyenoyama et al. 2001; Porcher and Lande 2005; Gervais et al. 2011). However, these models differ in the way inbreeding depression is introduced: some models treat inbreeding depression as a fixed parameter, thereby neglecting the effects of purging within SC backgrounds (Charlesworth and Charlesworth 1979; Uyenoyama et al. 2001; Gervais et al. 2011), whereas the model by Porcher and Lande (2005) explicitly represents the genetic architecture of inbreeding depression (infinite number of unlinked loci subject to recessive lethal mutations) and shows that purging can dramatically decrease the parameter range in which SI is maintained, in particular when the selfing rate of SC mutants is high. The importance of this effect should, in principle, depend on the genetic basis of inbreeding depression, because purging may occur over just a few generations when deleterious alleles are highly deleterious, but much more slowly when mutations tend to have weak fitness effects. In this article, we compare predictions from an analytical model assuming fixed inbreeding depression to the results of multilocus simulations in which deleterious alleles occur along a linear genetic map, to assess the importance of purging on the spread of SC mutants. When inbreeding depression is mainly due to weak-effect mutations, purging has limited effects. In most

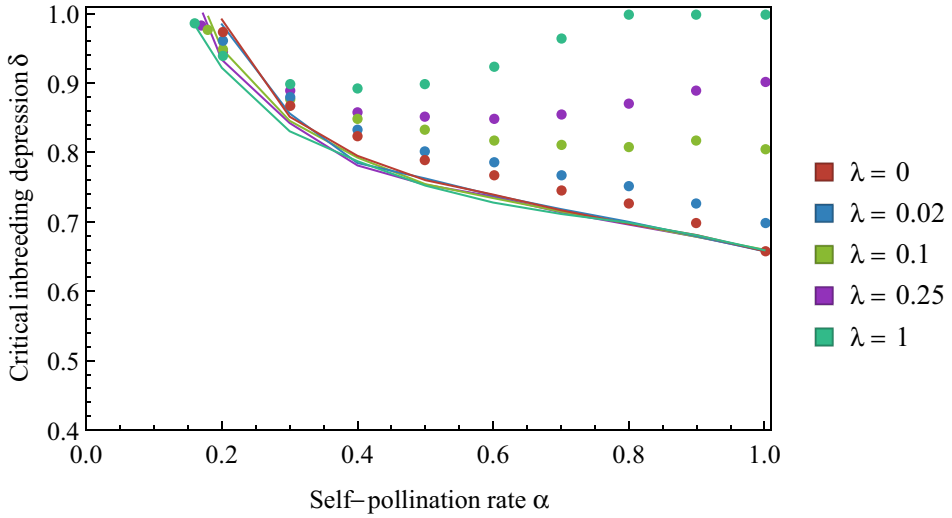

Figure 3. Minimal inbreeding depression needed to prevent invasion of an SI population by an SC mutant, when the genetic load depends on a mix of small-effect and nearly recessive lethal deleterious alleles, and for different proportions λ of lethal mutations. The points correspond to multilocus simulation results and the curves to analytical predictions. Mildly deleterious mutations: $s = 0.05$ and $h = 0.2$. Nearly recessive lethal mutations: $s = 1$ and $h = 0.02$. Other parameter values: $N = 2000$, $L = 10$.

cases, maintenance of SI mainly depends on the number of SI alleles segregating in the population, the rate of self-pollination, and inbreeding depression, independently of population size and the genetic architecture of inbreeding depression—a similar result was obtained recently by Porcher and Lande (2013) on the evolution of self-fertilization through weak-effect modifiers. Note that our model does not incorporate pollen limitation, which would tend to favor the loss of SI (Porcher and Lande 2005). However, our results relative to the effect of purging should remain valid in the presence of pollen limitation: pollen limitation adds direct selection for self-compatibility, but should not modify the indirect effect of deleterious alleles on SC mutants.

Although our current knowledge on the genetic basis of inbreeding depression remains fragmentary, several lines of evidence suggest an important role of mutations of small effects (Carr and Dudash 2003; Charlesworth and Willis 2009), although a study by Fox et al. (2010) showed a rapid reduction of inbreeding depression after several generations of inbreeding, indicating a potentially important effect of strongly deleterious mutations. More experimental work is thus necessary to assess whether purging is susceptible to significantly affect the spread of SC mutants within self-incompatible populations.

Finally, we almost never observe stable polymorphic equilibria involving both SI and SC alleles (except for restricted cases involving very high inbreeding depression and low rates of self-pollination). This stands in contrast to previous models involving infinite populations (Uyenoyama et al. 2001; Porcher and Lande 2005; Gervais et al. 2011), in which wider regions of parameter space allowing polymorphism were observed. A possible explanation for this discrepancy is that, in infinite populations, the number of SI alleles stays constant and is not affected by the frequency of SC, whereas in our model the number of SI alleles decreases as SC increases in frequency (because the size of the SI subpopulation decreases). The decrease in number of SI alleles tends to favor SC, whose frequency can further increase until reaching fixation. This result is consistent with the fact that SC alleles are rarely found in natural SI populations (Stone 2002), although some cases have been reported in which SI appears to be quantitative rather than qualitative, with some partially SC alleles (Mena-Ali and Stephenson 2007; Paape et al. 2011). The lack of polymorphic equilibria should impose restrictions on the evolution of new SI specificities. In the present model we assume that new SI alleles appear in a single mutational step, but in reality the evolution of a new specificity involves at least two mutations: one affecting the protein expressed by the pollen and the other the receptor expressed by the pistil (both genes being part of the S-locus). Most scenarios for the evolution of new specificities rely on an intermediate step involving a SC mutant present at an intermediate frequency in the population (e.g., Uyenoyama et al. 2001; Gervais et al. 2011), which should become more difficult in the absence of polymorphic equilibrium (unless the mutation rate at the S-locus is sufficiently high, so that a compensatory mutation can appear before SC reaches fixation). Furthermore, SC mutations occurring in the receptor part of the S-locus can spread under more restricted conditions than SC mutations in the pollen part, because they do not benefit from a fertilization advantage under outcrossing. Modifying our simulation model to explicitly

represent the pollen and pistil components of the S-locus (to explore conditions for the evolution of new SI specificities with dynamical inbreeding depression) would be an interesting extension of the present work.

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DATA ARCHIVING

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Supporting Information

Additional Supporting Information may be found in the online version of this article at the publisher's website:

Figure S1. Effect of mutation rate towards new SI alleles U_{SI}.
Figure S2. Effect of map length L.
Figure S3. Full simulation results.
Text S1. Condition for increase of the SC mutant in the absence of purging.