Genetic architecture of inbreeding depression and the maintenance of gametophytic self-incompatibility
Camille Gervais, Diala Abu Awad, Denis Roze, Vincent Castric, Sylvain Billiard

To cite this version:

HAL Id: hal-01137473
https://hal.archives-ouvertes.fr/hal-01137473
Submitted on 31 Mar 2015

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
Genetic architecture of inbreeding depression and the maintenance of gametophytic self-incompatibility

Camille Gervais\textsuperscript{1,2}, Diala Abu Awad\textsuperscript{3}, Denis Roze\textsuperscript{1,2}, Vincent Castric\textsuperscript{3}, Sylvain Billiard\textsuperscript{3}

1- CNRS, UMI 3614, Evolutionary Biology and Ecology of Algae, 29680 Roscoff, France
2- Sorbonne Universités, UPMC University Paris 06, 29680 Roscoff, France
3- UMR CNRS 8198, Université Lille 1, Sciences et Technologies, Laboratoire de Génétique et Evolution des Populations Végétales, 59655 Villeneuve d’Ascq, France

Corresponding author: Sylvain Billiard
Laboratoire de Génétique et Evolution des Populations Végétales
Bâtiment SN2
Université des Sciences et Technologies de Lille 1
F-59655 Villeneuve d’Ascq Cedex, France
Ph: (+33)3 20 33 59 23 ; fax : (+33)3 20 43 69 79
sylvain.billiard@univ-lille1.fr

Running title: purging and the maintenance of SI
Word count: 4368
Gametophytic self-incompatibility 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 self-incompatibility; however, inbreeding depression is a dynamical variable that depends in particular on the mating system. In this paper we use multilocus, individual based simulations to examine the co-evolution of self-incompatibility and inbreeding depression within finite populations. We focus on the conditions for the maintenance of self-incompatibility when self-compatible 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 self-compatible sub-population). In agreement with previous models, we observe that the maintenance of self-incompatibility is associated with high inbreeding depression and is facilitated by high rates of self-pollination. Purging of deleterious mutations by self-compatible 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 self-incompatibility. By contrast, purging may greatly enhance the spread of self-compatible mutants when deleterious alleles have strong fitness effects.

*Keywords*: deleterious mutation, inbreeding depression, self-incompatibility, purging.
INTRODUCTION

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 a 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 2/3, 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 self-compatible (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 2/3 when the number of SI alleles is large — this minimal value is higher and may even reach 1 when the number of SI alleles is not large and the selfing rate of self-compatible 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 (1979)'s model because inbreeding depression was treated 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; Glémín, 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 a SI population by a SC mutant (i.e. the breakdown of SI) is easier than expected from Charlesworth and Charlesworth (1979)'s results, 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 where both SI and SC individuals are present. This observation is important in the context of how new self-incompatibility specificities may arise through self-compatible 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)'s 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 where 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 where a substantial proportion of mutations are mildly
deleterious) in order to better understand how self-incompatibility can be maintained
in natural populations (note that Porcher and Lande (2005) also considered situations
where inbreeding depression is partly due to mildly deleterious mutations, but this
component of inbreeding depression is not dynamic in their model).

All previous simulation models explicitly considering the genetic basis of in-
breeding depression [Charlesworth et al. 1990; Porcher and Lande 2005, 2013] were
based on Kondrashov (1985)'s 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
self-compatible alleles and purged genetic backgrounds; however, whether the effect
of linkage is substantial for realistic values of genomic recombination rates is unclear.
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
towards new SI alleles (Yokoyama and Hetherington, 1982). Since 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 self-compatible mutants increase in frequency, which may in turn affect the condi-
tions needed to maintain SI and SC individuals at a polymorphic equilibrium (Gervais
et al., 2011).

In this paper, we use a multilocus individual-based simulation program to ex-
probe 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 assum-
ing 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 (that is, 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

5
values tested, as long as the mean number of cross-overs 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 gametophytic self-incompatibility (GSI) system, i.e. 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, since pollen bearing rare specificities can fertilize more individuals than pollen bearing more common specificities (Wright, 1939). We assume that self-incompatibility 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, self-compatible allele $S_C$ segregating at the same locus: pollen carrying $S_C$ can fertilize all plants, while a plant with genotype $S_iS_C$ is partially self-compatible (through its $S_C$ pollen) and can be fertilized by any pollen whose genotype is different from $S_i$. Finally, $S_C S_C$ individuals are fully self-compatible and can be fertilized by any pollen.

A parameter $\alpha$ 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: (i) automatic transmission advantage
through selfing, when $\alpha > 0$, (ii) transmission advantage through outcrossing, as $S_C$
pollen can fertilize all plants, (iii) negative consequences of increased homozygosity
due to selfing on the mean fitness of offspring (inbreeding depression) and (iv) indirect
benefits stemming from a better elimination of deleterious alleles as a consequence of
increased homozygosity (purging). This last effect occurs more rapidly when deleter-
iou progeny have stronger effects (e.g., Charlesworth and Willis, 2009). $S_C$ is thus
favoured by effects (i), (ii) and (iv), and disfavoured by effect (iii); but note that purg-
ing 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
(iii) and (iv) (inbreeding depression and purging). Results on the spread of $S_C$ are
compared to the predictions of a simple analytical model where effect (iv) is ignored
by treating inbreeding depression as a fixed parameter.

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

\[
a_i = \frac{\alpha \theta_i W_i}{\alpha W_i + (1 - \alpha)W}
\]  

(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 \(S_C\)), while the denominator is the total quantity of pollen received by the individual. The frequency of allele \(S_C\) among gametes is given by \(q = \sum_i \theta_i W_i x_i / W\), while, by symmetry, each SI allele is present in frequency \(p = (1 - q)/n\). From this, frequencies at the next generation are given by:

\[
Wx' = \begin{align*}
Wx'_1 &= W_1 a_1 x_1 + W_2 a_2 x_2 + \frac{1}{2} W_3 a_3 x_3 + \frac{1}{2} W_4 a_4 x_4 \\
Wx'_2 &= W_1 (1 - a_1) q x_1 + W_2 (1 - a_2) q x_2 + \frac{1}{2} \frac{W_3 (1 - a_3) x_3 + W_4 (1 - a_4) x_4 q}{2 (1 - p)} \\
Wx'_3 &= \frac{1}{2} W_3 a_3 x_3 + \frac{1}{2} W_4 a_4 x_4 \\
Wx'_4 &= W_1 (1 - a_1) (1 - q) x_1 + W_2 (1 - a_2) (1 - q) x_2 + \frac{1}{2} W_3 (1 - a_3) x_3 \\
&\quad + \frac{1}{2} W_4 (1 - a_4) x_4 + (1 - x_1 - x_2 - x_3 - x_4) \frac{q}{2 (1 - p)}.
\end{align*}
\]  

(2)

In the Supplementary Material, we use a local stability analysis to determine the values of \(\alpha\), \(n\) and \(\delta\) for which \(S_C\) increases in frequency when rare (which involves solving a fourth-order equation in \(\delta\) 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)](http://example.com), representing a population of \(N\) diploid individuals (the parameters
used in the simulation model are summarized in Table 1). Each individual possesses
two copies of a linear chromosome, and a S-locus located at the mid-point of the chro-
mosome. 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 a self-compatible 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 $S_i$, i.e. loss of self-incompatibility 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 $U$, while the position of each new mutation along the chro-
mosome 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 where 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 $W_i = (1 - hs)^{N_{he}}(1 - s)^{N_{ho}}$, 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 self-compatible allele $S_C$, its selfing rate $a_i$ is calculated as:

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

(3)

where $\gamma_{ij}$ is 0, 1 or 2, and represents the number of individual $j$’s S-alleles which 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 cross-overs occurring along the chromosome is drawn from a Poisson distribution with parameter \(L\) (genome map length, in Morgans) and the position of each cross-over 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 7,500 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 7,500 generations. Finally, during the next 500,000 generations, self-compatible 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, \( \delta \) and \( n_e \) are averaged over the last 50 samples before introduction of self-compatible mutants, while the frequency of \( S_C \) is averaged over the last 300 samples of the simulation (last 30,000 generations). The minimal value of \( \delta \) 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 \( \alpha \)). When the frequency of \( S_C \) stays lower than 0.05 throughout the simulation, SI is considered maintained.

**RESULTS**

**Mildly deleterious mutations.** Figure 1 shows the minimal value of inbreeding depression \( \delta \) necessary to maintain SI in the population as a function of the rate of self-pollination \( \alpha \), 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 \( (i.e., \text{reaches frequency } 0.05) \) is slightly below the points, at a distance equivalent to the size of points (not shown). In almost all simulations the frequency of \( S_C \) at equilibrium was either close to zero or equal to 1, \( i.e. \) polymorphic equilibria for \( S_C \) were almost never observed; we will return to this point in the Discussion. 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 \( \delta \) (results not shown), suggesting that as one enters the area above the points in Figure 1, 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).

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), where the number of SI alleles $n$ is set to the average effective number of alleles $n_e$ measured in simulations corresponding to the critical $\delta$. 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 $\delta$ being lower when the self-pollination rate $\alpha$ 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 $\delta$ 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 $\delta$ equals 11.9, 23.0 and 36.4 for $N = 500$, 2000 and 5000, respectively. Lower effective numbers of SI alleles favour 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 towards new SI alleles) show that increasing $U_{SI}$ (with $NU_{SI} = 0$, 0.02 and 0.2) has similar effects as increasing $N$ (Figure S1).

Overall, the match between the simulation results and predictions from the analytical model indicates that purging has little effect on the spread of $S_C$ for these parameter values; however, the analytical model systematically underestimates the
critical \( \delta \) for SI to be maintained, which is probably a consequence of purging (the discrepancy remains slight, but becomes more apparent as \( \alpha \) increases, and thus as the selfing rate of self-compatible 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 \( \delta \), \( s \) has little effect on the effective number of SI alleles \( n_e \) maintained in the population (the curves on Figure 2A are almost superposed), while 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 \( \delta \) when \( h \) is increased, leading to stronger background selection effects at the critical \( \delta \). By contrast, \( \delta \) 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 \( \delta \). 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 where SI is maintained.

Adding a proportion of nearly recessive lethal mutations. Using a deterministic model where 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 1-2. We modified our simulation program so that a proportion $\lambda$ of deleterious mutations are nearly recessive lethals (selection and dominance coefficients: $s_l = 1$ and $h_l = 0.02$, respectively) while 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 $\lambda$ increases, and the parameter range where 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 $\alpha$ 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 $\lambda$ (curves on Figure 3 are nearly superposed).

DISCUSSION

Self-incompatibility (and especially gametophytic SI) is widespread among angiosperms, despite the fact that self-compatible 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 \cite{Charlesworth1979, Uyenoyama2001, Porcher2005, Gervais2011}. 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 \cite{Charlesworth1979, Uyenoyama2001, Gervais2011}, while the model by Porcher and Lande \cite{Porcher2005} 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 where 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, since 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 paper, we compare predictions from an analytical model assuming fixed inbreeding depression to the results of multilocus simulations where deleterious alleles occur along a linear genetic map, in order 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 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 \cite{Porcher2013} on the evolution of self-fertilization through weak-effect modifiers. Note that our model does not incorporate pollen limitation, which would tend to favour the loss of SI \cite{Porcher2005}. 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.

Whilst 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 \(\text{[Carr and Dudash, 2003; Charlesworth and Willis, 2009]}\), although a study by \(\text{[Fox et al. (2010)]}\) 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 self-compatible 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 \(\text{[Uyenoyama et al., 2001; Porcher and Lande, 2005; Gervais et al., 2011]}\), where wider regions of parameter space allowing polymorphism are 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, while in our model the number of SI alleles decreases as SC increases in frequency (since the size of the SI sub-population decreases). The decrease in number of SI alleles tends to favour 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 \(\text{[Stone, 2002]}\), although some cases have been reported where self-incompatibility appears to be quantitative rather than qualitative, with some partially self-compatible alleles \(\text{[Mena-Ali and Stephenson, 2007; Paape et al., 2011]}\). 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). Extending our simulation model to explicitly represent the pollen and pistil components of the S-locus (in order to explore conditions for the evolution of new SI specificities with dynamical inbreeding depression) would be an interesting extension of the present work.

Acknowledgements. This work was supported by the French Agence Nationale de la Recherche (ANR-11-BSV7-013).


Figure 1. Critical inbreeding depression above which the SC mutant cannot increase in frequency in the SI population 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: $L = 10$, $s = 0.05$, $h = 0.2$. 
Figure 2. Critical inbreeding depression above which the SC mutant cannot increase in frequency in the SI population 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).
Figure 3. Critical inbreeding depression above which the SC mutant cannot increase in frequency in the SI population for different proportions $\lambda$ of nearly recessive 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: $N = 2000$, $L = 10$. 
<table>
<thead>
<tr>
<th>Description</th>
<th>Symbol</th>
<th>Default value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Population size</td>
<td>$N$</td>
<td>2000</td>
</tr>
<tr>
<td>Mean number of cross-overs per genome per generation</td>
<td>$L$</td>
<td>10</td>
</tr>
<tr>
<td>Proportion of self-pollen</td>
<td>$\alpha$</td>
<td></td>
</tr>
<tr>
<td>Selection coefficient of deleterious mutations</td>
<td>$s$</td>
<td>0.05</td>
</tr>
<tr>
<td>Dominance coefficient of deleterious mutations</td>
<td>$h$</td>
<td>0.2</td>
</tr>
<tr>
<td>Rate of deleterious mutation per haploid genome</td>
<td>$U$</td>
<td></td>
</tr>
<tr>
<td>Rate of mutation from $S_i$ to any $S_j$ (with $j \neq i$)</td>
<td>$U_{SI}$</td>
<td>$10^{-5}$</td>
</tr>
<tr>
<td>Rate of mutation from $S_i$ to $S_C$</td>
<td>$U_{SC}$</td>
<td>$10^{-4}$</td>
</tr>
</tbody>
</table>