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Genetic architecture of inbreeding depression and the maintenance of
gametophytic self-incompatibility

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ABSTRACT

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

1
2 Self-incompatibility (SI) is a genetic system that enables hermaphroditic plants
3 to avoid self-fertilization and limit mating with close relatives by recognition and re-
4 jection by the pistil of pollen expressing cognate specificities. In many species, SI
5 specificity is controlled by a single multiallelic locus, the S-locus. SI is widespread,
6 found in more than 100 families of angiosperms (Igic et al., 2008) despite the fact that
7 it entails a transmission disadvantage. Indeed, a self-compatible (SC) mutant occur-
8 ring in a SI population should benefit from a higher number of potential mates, and
9 from a transmission advantage through self-fertilization. This last advantage is equal
10 to $2/3$, and is thus higher than the 50% advantage of an allele coding for selfing in an
11 outcrossing population (Fisher, 1941), because only the SC pollen contributes to the
12 selfed offspring in heterozygous individuals for SC. Recently, it has been argued that
13 SI may be maintained by selection acting at the species level, due to the fact that SI
14 species diversify at higher rates (Goldberg et al., 2010). This form of selection only
15 acts in the long term, however, and implies that SC mutations should occur very rarely.
16 The main advantage of SI that could possibly explain its maintenance in the short term
17 is the avoidance of inbreeding depression (*e.g.*, Charlesworth and Charlesworth, 1987).
18 However, Charlesworth and Charlesworth (1979) showed that for SI to be maintained
19 in the presence of self-compatible (SC) mutants, inbreeding depression has to be high;
20 its minimal value depends on the number of SI alleles segregating in the population
21 and on the selfing rate of SC mutants, but is often close to $2/3$ when the number of SI
22 alleles is large — this minimal value is higher and may even reach 1 when the number
23 of SI alleles is not large and the selfing rate of self-compatible mutants is small to

24 moderate, as SC mutants also benefit from a higher number of potential mates. Fur-
25 thermore, the minimal value of inbreeding depression needed to maintain SI may be
26 underestimated by Charlesworth and Charlesworth (1979)'s model because inbreeding
27 depression was treated a fixed variable, therefore neglecting the effect of purging of
28 deleterious alleles by the self-fertilizing SC individuals. Purging is expected to facil-
29 itate the spread of SC mutants, as these mutants tend to better eliminate partially
30 recessive deleterious alleles, thereby reducing the magnitude of inbreeding depression
31 experienced by their selfed offspring (Uyenoyama and Waller, 1991; Glémin, 2003).
32 This was confirmed by a deterministic simulation model by Porcher and Lande (2005),
33 assuming that a given proportion of self-pollen lands on the stigma (“mass-action” pol-
34 lination model, Holsinger, 1991) and that inbreeding depression results from recessive
35 lethal mutations segregating at a very large (effectively infinite) number of loci (Kon-
36 drashov, 1985). In this model, invasion of a SI population by a SC mutant (*i.e.* the
37 breakdown of SI) is easier than expected from Charlesworth and Charlesworth (1979)'s
38 results, in particular when the selfing rate of SC mutants is moderate to high (so that
39 purging can occur). Porcher and Lande (2005) also observed that in a small region
40 of parameter space (namely, for high values of inbreeding depression and low selfing
41 rates), the population may reach a stable, polymorphic equilibrium where both SI and
42 SC individuals are present. This observation is important in the context of how new
43 self-incompatibility specificities may arise through self-compatible intermediates, as-
44 suming that compensatory mutations may secondarily restore a novel SI functionality
45 (Uyenoyama et al., 2001; Gervais et al., 2011).

46 Although Porcher and Lande (2005)'s model showed that considering the joint
47 dynamics of SI and inbreeding depression may strongly affect predictions concerning

48 the maintenance of SI, the fact that they considered lethal mutations may overestimate
49 the importance of purging in situations where inbreeding depression is (at least partly)
50 generated by mildly recessive deleterious alleles. Indeed, analytical models have shown
51 that the advantage of a selfing modifier through purging is expected to increase with
52 the strength of selection against deleterious alleles (Uyenoyama and Waller, 1991;
53 Epinat and Lenormand, 2009), which was also observed in deterministic simulations
54 representing the spread of a mutation affecting the selfing rate (Charlesworth et al.,
55 1990). More recently, Porcher and Lande (2013) showed that the effect of purging on
56 the spread of a mutation affecting selfing is much lower when the strength of selection
57 against deleterious alleles is mild ($s = 0.05$) than when it is strong ($s = 1$). However,
58 Porcher and Lande (2013) only considered weak-effect selfing modifiers (changing the
59 selfing rate by 10^{-6}), and the effect of purging may be stronger in the case of a
60 mutation having a large effect on the selfing rate (Charlesworth et al., 1990) such as
61 a mutation disrupting SI. Because the results of Porcher and Lande (2005) showed
62 that purging may strongly limit conditions for the maintenance of SI in the presence
63 of lethal recessive mutations, it is important to assess the generality of this result
64 (in particular to situations where a substantial proportion of mutations are mildly
65 deleterious) in order to better understand how self-incompatibility can be maintained
66 in natural populations (note that Porcher and Lande (2005) also considered situations
67 where inbreeding depression is partly due to mildly deleterious mutations, but this
68 component of inbreeding depression is not dynamic in their model).

69 All previous simulation models explicitly considering the genetic basis of in-
70 breeding depression (Charlesworth et al., 1990; Porcher and Lande, 2005, 2013) were
71 based on Kondrashov (1985)'s model, representing the dynamics of deleterious alleles

72 at an infinite number of unlinked loci, in an infinite population. In principle, genetic
73 linkage should increase the effect of purging, by increasing the association between
74 self-compatible alleles and purged genetic backgrounds; however, whether the effect
75 of linkage is substantial for realistic values of genomic recombination rates is unclear.
76 Finite population size is expected to affect the number of SI alleles maintained in
77 the population — which depends both on population size and on the mutation rate
78 towards new SI alleles (Yokoyama and Hetherington, 1982). Since conditions for the
79 maintenance of SI depend on the number of SI alleles segregating (Charlesworth and
80 Charlesworth, 1979; Porcher and Lande, 2005; Gervais et al., 2011), they should thus
81 be affected by population size. Furthermore, the number of SI alleles may also change
82 as self-compatible mutants increase in frequency, which may in turn affect the condi-
83 tions needed to maintain SI and SC individuals at a polymorphic equilibrium (Gervais
84 et al., 2011).

85 In this paper, we use a multilocus individual-based simulation program to ex-
86 plore the conditions for the maintenance of SI when inbreeding depression is generated
87 by deleterious alleles segregating at a large number of partially linked loci in a finite
88 population. Our model also differs from the previous models cited above by assum-
89 ing that inbreeding depression affects both seed and pollen production, which in turn
90 affects the selfing rate of SC individuals (as it depends on the quantity of self-pollen
91 relative to the quantity of pollen received from other individuals). We show that in
92 many cases, conditions for the maintenance of SI are similar to those obtained from an
93 analytical model assuming fixed inbreeding depression (that is, the effect of purging on
94 the spread of SC mutants remains small), unless a substantial proportion of deleterious
95 mutations have strong fitness effects. Linkage has only little effect for the parameter

106 values tested, as long as the mean number of cross-overs per genome (*i.e.*, genetic map
107 length) is not too small. Finally, we almost never observe a polymorphic equilibrium,
108 which is probably due to the fact that the number of SI alleles decreases as SC indi-
109 viduals increase in frequency, further enhancing the advantage of self-compatibility.

100 METHODS

101 We consider a population with a gametophytic self-incompatibility (GSI) sys-
102 tem, *i.e.* fertilization is possible only if the specificity expressed by the pollen is different
103 from the two specificities codominantly expressed in the style. Specificities are sub-
104 ject to negative frequency-dependent selection, since pollen bearing rare specificities
105 can fertilize more individuals than pollen bearing more common specificities (Wright,
106 1939). We assume that self-incompatibility is coded by a single S-locus with many
107 alleles (denoted S_i): a plant with genotype S_iS_j ($i \neq j$) is self-incompatible and can
108 be fertilized by pollen of genotype S_l , with $l \neq i$ and $l \neq j$. We also consider a mutant,
109 self-compatible allele S_C segregating at the same locus: pollen carrying S_C can fertilize
110 all plants, while a plant with genotype S_iS_C is partially self-compatible (through its
111 S_C pollen) and can be fertilized by any pollen whose genotype is different from S_i .
112 Finally, $S_C S_C$ individuals are fully self-compatible and can be fertilized by any pollen.
113 A parameter α measures the proportion of pollen produced by a plant that stays on
114 the same plant (“self-pollen”), leading to self-fertilization if it carries the S_C allele. We
115 assume that selfed offspring suffer from inbreeding depression, generated by partially
116 recessive deleterious alleles segregating at a number of different loci. Several selective
117 forces may affect the frequency of the S_C allele: (i) automatic transmission advantage

118 through selfing, when $\alpha > 0$, (ii) transmission advantage through outcrossing, as S_C
119 pollen can fertilize all plants, (iii) negative consequences of increased homozygosity
120 due to selfing on the mean fitness of offspring (inbreeding depression) and (iv) indirect
121 benefits stemming from a better elimination of deleterious alleles as a consequence of
122 increased homozygosity (purging). This last effect occurs more rapidly when deleterious
123 alleles have stronger effects (*e.g.*, Charlesworth and Willis, 2009). S_C is thus
124 favoured by effects (i), (ii) and (iv), and disfavoured by effect (iii); but note that purging
125 also tends to reduce inbreeding depression. In the following, we use a multilocus,
126 individual-based simulation model to represent explicitly the genetic causes of effects
127 (iii) and (iv) (inbreeding depression and purging). Results on the spread of S_C are
128 compared to the predictions of a simple analytical model where effect (iv) is ignored
129 by treating inbreeding depression as a fixed parameter.

130

131 **Analytical model.** Our analytical model represents an infinite population with discrete,
132 non-overlapping generations. We assume that $n + 1$ alleles segregate at the
133 S-locus: n self-incompatible alleles and the self-compatible S_C allele. We denote x_1
134 and x_2 the frequencies of $S_C S_C$ individuals produced by selfing (x_1) and by outcrossing
135 (x_2), and x_3 and x_4 the frequencies of $S_i S_C$ individuals produced by selfing (x_3) and by
136 outcrossing (x_4), where S_i can be any SI allele. We suppose that selfed individuals produce
137 fewer gametes (inbreeding depression), the number of male and female gametes produced
138 by outcrossed individuals being proportional to $W_2 = W_4 = 1$, while the number of gametes
139 produced by selfed individual is proportional to $W_1 = W_3 = 1 - \delta$;
140 mean fecundity \bar{W} is thus given by $1 - \delta(x_1 + x_3)$. The selfing rate a_i (proportion of

141 selfed seeds) of an individual of type i (1, 2, 3 or 4) is given by:

$$a_i = \frac{\alpha \theta_i W_i}{\alpha W_i + (1 - \alpha) \bar{W}} \quad (1)$$

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

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

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

151

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

158 used in the simulation model are summarized in Table 1). Each individual possesses
 159 two copies of a linear chromosome, and a S-locus located at the mid-point of the chro-
 160 mosome. We assume that a maximum of $k + 1$ alleles can segregate at the S-locus: k
 161 self-incompatible alleles S_i ($1 \leq i \leq k$) and a self-compatible allele S_C ; k is fixed at
 162 100 in all simulations. Every generation, each S_i allele mutates to any of the $k - 1$
 163 other SI alleles with probability U_{SI} and to allele S_C with probability U_{SC} (loss of
 164 SI). There is no reverse mutation from S_C to S_i , *i.e.* loss of self-incompatibility is
 165 irreversible. Deleterious mutations occur at a rate U per haploid genome, that is, the
 166 number of new deleterious mutations on each chromosome is drawn from a Poisson
 167 distribution with parameter U , while the position of each new mutation along the chro-
 168 mosome is sampled from a (continuous) uniform distribution — the number of sites
 169 at which deleterious alleles may segregate is thus effectively infinite. All deleterious
 170 mutations have the same selection and dominance coefficients (s and h respectively),
 171 although we also consider cases where a given proportion of mutations are lethal (as
 172 detailed below). Reproduction occurs as follows: for each of the N individuals of the
 173 next generation the maternal parent is sampled randomly among all individuals of
 174 the previous generation, the probability of sampling parent i being proportional to its
 175 fecundity $W_i = (1 - hs)^{N_{\text{he}}}(1 - s)^{N_{\text{ho}}}$, where N_{he} and N_{ho} are the number of mutations
 176 in the heterozygous and homozygous state within its genome. If the maternal plant
 177 carries at least one self-compatible allele S_C , its selfing rate a_i is calculated as:

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

178 where γ_{ij} is 0, 1 or 2, and represents the number of individual j 's S-alleles which are
 179 compatible with individual i . In the case of selfing, the offspring's genome is formed

180 from two of i 's recombinant gametes; otherwise an individual j is sampled randomly
181 with a probability proportional to W_j , and contributes as a father only if one of its
182 S-alleles is compatible with those of the mother (if not, another individual is sampled
183 until a compatible partner is found). To form a recombinant gamete, the number of
184 cross-overs occurring along the chromosome is drawn from a Poisson distribution with
185 parameter L (genome map length, in Morgans) and the position of each cross-over is
186 sampled from a uniform distribution.

187 At the beginning of each simulation individuals are free of deleterious mutations
188 and heterozygous for randomly sampled SI alleles. During the first 7,500 generations,
189 the number of SI alleles segregating in the population is allowed to reach equilibrium
190 by considering only mutation between SI alleles ($U_{SC} = 0$, $U = 0$). Deleterious mu-
191 tations are then introduced and allowed to reach mutation-selection balance over the
192 next 7,500 generations. Finally, during the next 500,000 generations, self-compatible
193 mutants are also introduced. Because loss of SI is irreversible, simulations are stopped
194 after 50,000 generations if S_C is fixed in the population. Every 100 generations, dif-
195 ferent variables are measured from the population: the frequency of allele S_C , the
196 effective number of SI alleles present and the level of inbreeding depression. The effec-
197 tive number of SI alleles n_e (measured before allele S_C is introduced) corresponds to
198 the number of alleles that would yield the same genetic diversity at the S-locus if all
199 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
200 the frequency of allele S_i . Inbreeding depression is measured as $\delta = 1 - W_s/W_o$, where
201 W_s and W_o are the mean fecundities of selfed and outcrossed offspring, respectively
202 (estimated by creating 100 selfed and 100 outcrossed offspring from randomly sampled
203 parents, without taking into account the compatibility between their S-alleles). For

204 each simulation run, δ and n_e are averaged over the last 50 samples before introduc-
205 tion of self-compatible mutants, while the frequency of S_C is averaged over the last 300
206 samples of the simulation (last 30,000 generations). The minimal value of δ necessary
207 to maintain SI in the population is determined by running simulations with increasing
208 values of U for each set of parameters values (U_{SI} , U_{SC} , s , h , N , L and α). When
209 the frequency of S_C stays lower than 0.05 throughout the simulation, SI is considered
210 maintained.

211

RESULTS

212 **Mildly deleterious mutations.** Figure 1 shows the minimal value of inbreeding
213 depression δ necessary to maintain SI in the population as a function of the rate of self-
214 pollination α , for different values of population size N . In all figures, the highest value
215 of inbreeding depression (in the absence of S_C) for which we observed that S_C invades
216 the population (*i.e.*, reaches frequency 0.05) is slightly below the points, at a distance
217 equivalent to the size of points (not shown). In almost all simulations the frequency of
218 S_C at equilibrium was either close to zero or equal to 1, *i.e.* polymorphic equilibria for
219 S_C were almost never observed; we will return to this point in the Discussion. Note
220 that because the loss of SI is irreversible in our model (no back mutation from SC
221 to SI), one expects that allele S_C should necessarily become fixed after a sufficiently
222 long time. However, changing the number of generations with $U_{SC} > 0$ to 10^5 or
223 to 10^6 did not lead to significant differences in the threshold values of δ (results not
224 shown), suggesting that as one enters the area above the points in Figure 1, the
225 expected fixation time of S_C quickly reaches extremely high values (*i.e.* SI is stably

226 maintained). In the same vein, increasing the mutation rate towards S_C (U_{SC}) from
227 10^{-5} to 10^{-4} has very little effect on the results (not shown).

228 Curves on Figure 1 correspond to the predictions derived from the analytical
229 model (neglecting the effect of genetic associations between the S-locus and selected
230 loci), where the number of SI alleles n is set to the average effective number of alleles n_e
231 measured in simulations corresponding to the critical δ . Overall, simulation results are
232 qualitatively and quantitatively consistent with these analytical expectations: main-
233 tenance of SI is always observed when inbreeding depression is high ($\delta > 2/3$), the
234 critical δ being lower when the self-pollination rate α is higher, in agreement with
235 previous results neglecting effects of purging (Charlesworth and Charlesworth, 1979;
236 Uyenoyama et al., 2001). The effect of population size N on the critical δ is due
237 to the fact that the effective number of SI alleles is reduced in smaller populations
238 through the loss of low-frequency alleles by drift (*e.g.*, Yokoyama and Hetherington,
239 1982): on average n_e at the critical δ equals 11.9, 23.0 and 36.4 for $N = 500$, 2000 and
240 5000, respectively. Lower effective numbers of SI alleles favour the spread of S_C by
241 increasing the transmission advantage of S_C through outcrossing, as S_C pollen never
242 encounters incompatible pistils and can fertilize every potential mate in the population
243 (Charlesworth and Charlesworth, 1979; Porcher and Lande, 2005; Gervais et al., 2011).
244 Simulations for different values of U_{SI} (rate of mutation towards new SI alleles) show
245 that increasing U_{SI} (with $NU_{SI} = 0, 0.02$ and 0.2) has similar effects as increasing N
246 (Figure S1).

247 Overall, the match between the simulation results and predictions from the an-
248 alytical model indicates that purging has little effect on the spread of S_C for these
249 parameter values; however, the analytical model systematically underestimates the

critical δ for SI to be maintained, which is probably a consequence of purging (the discrepancy remains slight, but becomes more apparent as α 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 δ , 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 δ when h is increased, 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

274 reducing the parameter range where SI is maintained.

275

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

291

DISCUSSION

292 Self-incompatibility (and especially gametophytic SI) is widespread among an-
293 giosperms, despite the fact that self-compatible mutants should benefit from a direct
294 transmission advantage. Different models have shown that, provided that it is suffi-
295 ciently high, inbreeding depression can allow the stability of SI despite the recurrent

296 occurrence of SC mutants (Charlesworth and Charlesworth, 1979; Uyenoyama et al.,
297 2001; Porcher and Lande, 2005; Gervais et al., 2011). However, these models differ in
298 the way inbreeding depression is introduced: some models treat inbreeding depression
299 as a fixed parameter, thereby neglecting the effects of purging within SC backgrounds
300 (Charlesworth and Charlesworth, 1979; Uyenoyama et al., 2001; Gervais et al., 2011),
301 while the model by Porcher and Lande (2005) explicitly represents the genetic archi-
302 tecture of inbreeding depression (infinite number of unlinked loci subject to recessive
303 lethal mutations) and shows that purging can dramatically decrease the parameter
304 range where SI is maintained, in particular when the selfing rate of SC mutants is
305 high. The importance of this effect should, in principle, depend on the genetic basis
306 of inbreeding depression, since purging may occur over just a few generations when
307 deleterious alleles are highly deleterious, but much more slowly when mutations tend
308 to have weak fitness effects. In this paper, we compare predictions from an analyti-
309 cal model assuming fixed inbreeding depression to the results of multilocus simulations
310 where deleterious alleles occur along a linear genetic map, in order to assess the impor-
311 tance of purging on the spread of SC mutants. When inbreeding depression is mainly
312 due to weak-effect mutations, purging has limited effects. In most cases, maintenance
313 of SI mainly depends on the number of SI alleles segregating in the population, the rate
314 of self-pollination and inbreeding depression, independently of population size and the
315 genetic architecture of inbreeding depression — a similar result was obtained recently
316 by Porcher and Lande (2013) on the evolution of self-fertilization through weak-effect
317 modifiers. Note that our model does not incorporate pollen limitation, which would
318 tend to favour the loss of SI (Porcher and Lande, 2005). However, our results rela-
319 tive to the effect of purging should remain valid in the presence of pollen limitation:

320 pollen limitation adds direct selection for self-compatibility, but should not modify the
321 indirect effect of deleterious alleles on SC mutants.

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

330 Finally, we almost never observe stable polymorphic equilibria involving both
331 SI and SC alleles (except for restricted cases involving very high inbreeding depression
332 and low rates of self-pollination). This stands in contrast to previous models involving
333 infinite populations (Uyenoyama et al., 2001; Porcher and Lande, 2005; Gervais et al.,
334 2011), where wider regions of parameter space allowing polymorphism are observed. A
335 possible explanation for this discrepancy is that, in infinite populations, the number of
336 SI alleles stays constant and is not affected by the frequency of SC, while in our model
337 the number of SI alleles decreases as SC increases in frequency (since the size of the SI
338 sub-population decreases). The decrease in number of SI alleles tends to favour SC,
339 whose frequency can further increase until reaching fixation. This result is consistent
340 with the fact that SC alleles are rarely found in natural SI populations (Stone, 2002),
341 although some cases have been reported where self-incompatibility appears to be quan-
342 titative rather than qualitative, with some partially self-compatible alleles (Mena-Ali
343 and Stephenson, 2007; Paape et al., 2011). The lack of polymorphic equilibria should

344 impose restrictions on the evolution of new SI specificities. In the present model we
345 assume that new SI alleles appear in a single mutational step, but in reality the evo-
346 lution of a new specificity involves at least two mutations: one affecting the protein
347 expressed by the pollen and the other the receptor expressed by the pistil (both genes
348 being part of the S-locus). Most scenarios for the evolution of new specificities rely
349 on an intermediate step involving a SC mutant present at an intermediate frequency
350 in the population (*e.g.*, Uyenoyama et al., 2001; Gervais et al., 2011), which should
351 become more difficult in the absence of polymorphic equilibrium (unless the mutation
352 rate at the S-locus is sufficiently high, so that a compensatory mutation can appear
353 before SC reaches fixation). Extending our simulation model to explicitly represent
354 the pollen and pistil components of the S-locus (in order to explore conditions for the
355 evolution of new SI specificities with dynamical inbreeding depression) would be an
356 interesting extension of the present work.

357

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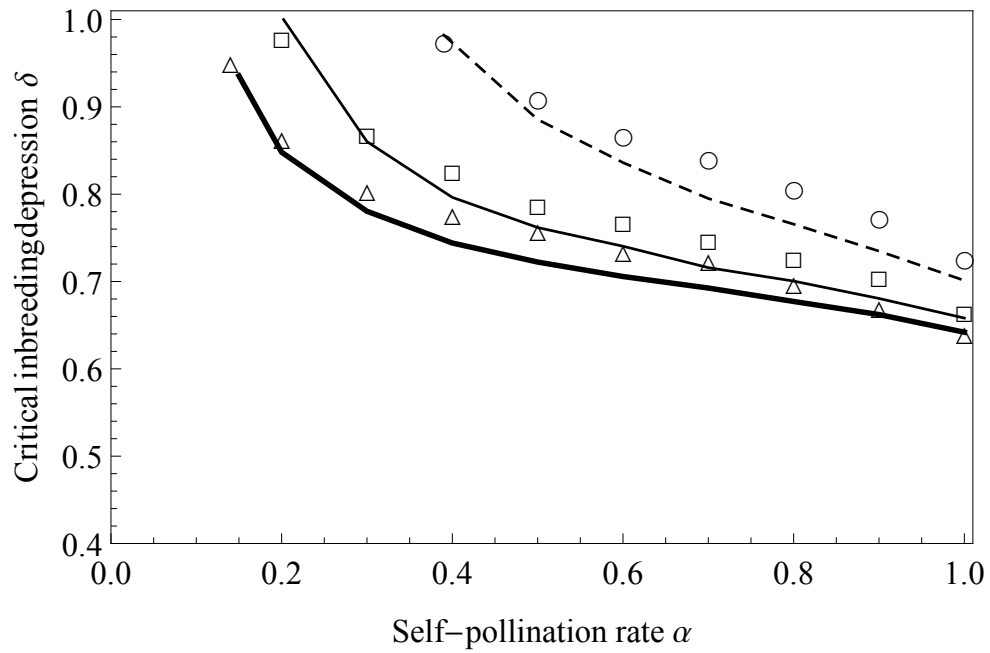
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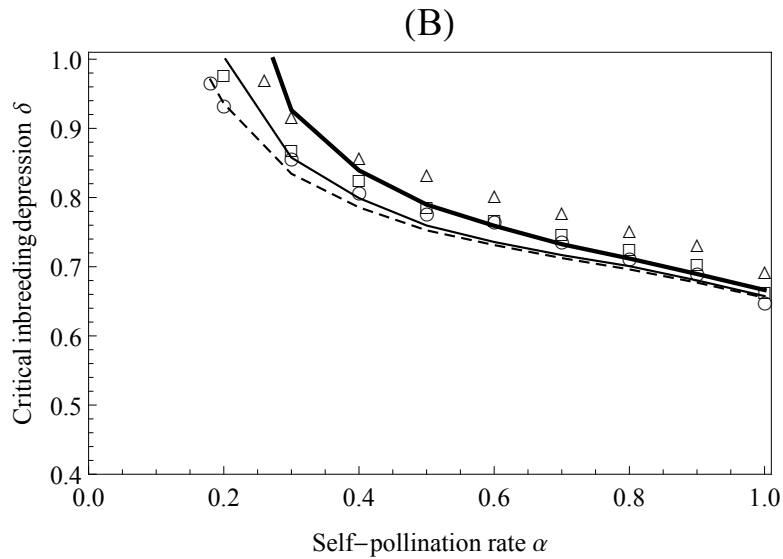
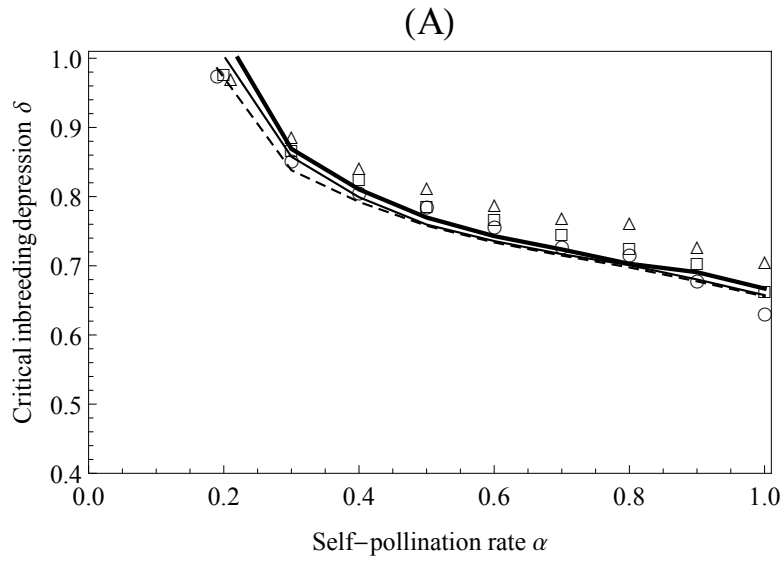
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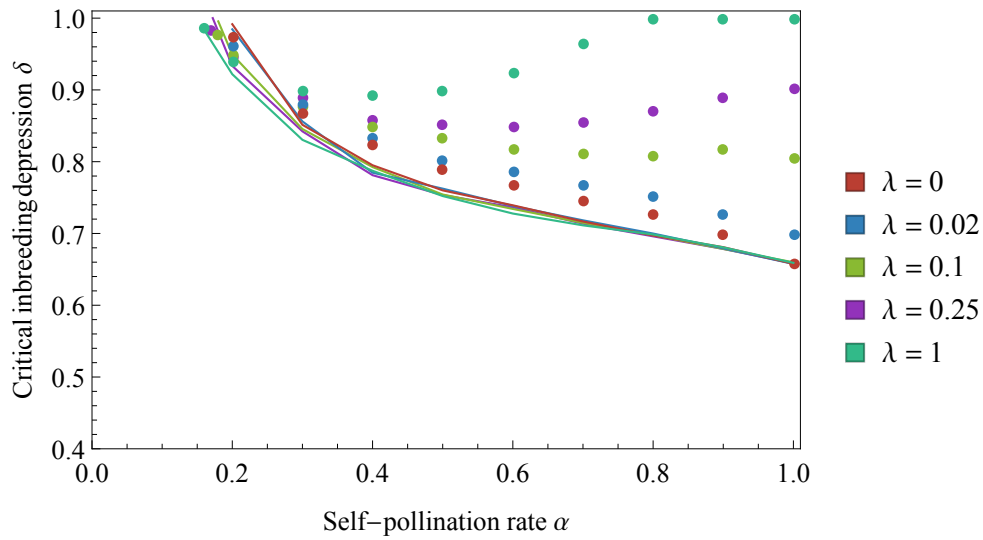
421

422 **Figure 1.** Critical inbreeding depression above which the SC mutant cannot in-
 423 crease in frequency in the SI population for different population sizes N . The points
 424 correspond to multilocus simulation results and the curves to analytical predictions.
 425 Circles, dashed curve: $N = 500$; squares, solid curve: $N = 2000$; triangles, thick curve:
 426 $N = 5000$. Other parameter values: $L = 10$, $s = 0.05$, $h = 0.2$.



427

428 **Figure 2.** Critical inbreeding depression above which the SC mutant cannot increase
 429 in frequency in the SI population for different selection (A) and dominance (B) coeffi-
 430 cients of deleterious alleles. The points correspond to multilocus simulation results and
 431 the curves to analytical predictions. (A): circles, dashed curve: $s = 0.02$; squares, solid
 432 curve: $s = 0.05$; triangles, thick curve: $s = 0.1$. (B): Circles, dashed curve: $h = 0.1$;
 433 squares, solid curve: $h = 0.2$; triangles, thick curve: $h = 0.3$. Other parameter values:
 434 $N = 2000$, $L = 10$, $h = 0.2$ (in A), $s = 0.05$ (in B).



435

436 **Figure 3.** Critical inbreeding depression above which the SC mutant cannot increase
 437 in frequency in the SI population for different proportions λ of nearly recessive lethal
 438 mutations. The points correspond to multilocus simulation results and the curves to
 439 analytical predictions. Mildly deleterious mutations: $s = 0.05$ and $h = 0.2$. Nearly
 440 recessive lethal mutations: $s = 1$ and $h = 0.02$. Other parameter values: $N = 2000$,
 441 $L = 10$.

442 **Table 1: Parameters and default values used in simulations.**

443

| Description | Symbol | Default value |
|---|----------|---------------|
| Population size | N | 2000 |
| Mean number of cross-overs per genome per generation | L | 10 |
| Proportion of self-pollen | α | |
| 444 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} |