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► **To cite this version:**

Miguel Navascués, Solenn Stoeckel, Stephanie Mariette. Genetic diversity and fitness in small populations of partially asexual, self-incompatible plants.. *Heredity*, 2010, 104 (5), pp.482-92. 10.1038/hdy.2009.159 . hal-00505867v1

**HAL Id: hal-00505867**

**<https://hal.science/hal-00505867v1>**

Submitted on 31 Jan 2012 (v1), last revised 31 Jan 2012 (v2)

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1 **Genetic diversity and fitness in small populations of partially asexual, self-**  
2 **incompatible plants**

3

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17

18 **Keywords**

19 Self-incompatibility, asexual reproduction, number of *S*-alleles, linkage disequilibrium,  
20 inbreeding depression, mutation load

21 **Running title:** Asexuality and self-incompatibility in small populations

22 **Word count:** 5433

23

24 **Summary**

25 How self-incompatibility systems are maintained in plant populations is still a debated issue.  
26 Theoretical models predict that self-incompatibility systems break down according to the  
27 intensity of inbreeding depression and number of *S*-alleles. Other studies have explored the  
28 role of asexual reproduction in the maintenance of self-incompatibility. However, the  
29 population genetics of partially asexual, self-incompatible populations are poorly understood  
30 and previous studies have failed to consider all possible effects of asexual reproduction or  
31 could only speculate on those effects. In the present study, we investigated how partial  
32 asexuality may affect genetic diversity at the *S*-locus and fitness in small self-incompatible  
33 populations. A genetic model including an *S*-locus and a viability locus was developed to  
34 perform forward simulations of the evolution of populations of various sizes. Drift combined  
35 with partial asexuality produced a decrease in the number of alleles at the *S*-locus. In addition,  
36 an excess of heterozygotes was present in the population, causing an increase in mutation  
37 load. This heterozygote excess was enhanced by the self-incompatibility system in small  
38 populations. In addition, in highly asexual populations, individuals produced asexually had  
39 some fitness advantages over individuals produced sexually (due to the increased  
40 heterozygosity, sex produces the homozygosis of deleterious alleles). Our results suggest that  
41 future research on the role of asexuality for the maintenance of self-incompatibility will need  
42 to (1) account for whole genome fitness (mutation load generated by asexuality, self-  
43 incompatibility and drift) and (2) acknowledge that the maintenance of self-incompatibility  
44 may not be independent of the maintenance of sex itself.

45

46 **Introduction**

47 Hermaphroditic plant species reproduce with variable rates of selfing, ranging from strict  
48 selfing to strict outcrossing (Barrett, 2002). Self-incompatibility (SI) is a reproductive system  
49 that prevents self-fertilization. In the case of heteromorphic self-incompatibility, distinct  
50 morphologies result in distinct compatibility groups, whereas in the case of homomorphic  
51 self-incompatibility, compatible individuals cannot be distinguished by their morphology (de  
52 Nettancourt, 1977). Most SI systems depend on physiological mechanisms that prevent pollen  
53 germination or pollen tube growth. In sporophytic self-incompatibility (SSI) systems, the  
54 compatibility of a pollen grain depends on the diploid genotype of the plant that produced it.  
55 In gametophytic self-incompatibility (GSI) systems, the compatibility of a pollen grain  
56 depends on its haploid genotype. GSI is more widespread than SSI (Glémin *et al.*, 2001).  
57 Fisher (1941) showed that self-fertilization should have a selective advantage because a  
58 selfing genotype will transmit more copies of its genome than a non-selfing genotype (this has  
59 been termed the automatic advantage of selfing). However, numerous studies have shown that  
60 inbred offspring are less fit than outbred offspring. The relative decrease in the mean fitness  
61 of selfed versus outcrossed individuals (inbreeding depression) is generally recognized as the  
62 only main factor that counterbalances the selective advantage of selfing (Charlesworth and  
63 Charlesworth, 1987).  
64 Consequently, the level of inbreeding depression in populations should play a determining  
65 role in the evolution of SI systems. Inbreeding depression decreases as population size  
66 becomes smaller due to reduced polymorphism for selection to act on (Bataillon and  
67 Kirkpatrick, 2000). Charlesworth and Charlesworth (1979) showed that the number of *S*-  
68 alleles also plays a role in maintaining SI, since a low number of alleles will limit the number  
69 of compatible crosses in the population. A decrease in population size can also cause a  
70 reduction in the number of *S*-alleles (Brennan *et al.*, 2003), and a self-compatible mutant can

71 be positively selected for (Reinartz and Les, 1994). Thus, small populations may be  
72 particularly prone to the breakdown of SI due to weak inbreeding depression and low  
73 numbers of *S*-alleles. However, small self-incompatible populations may maintain high levels  
74 of inbreeding depression due to a sheltered load of deleterious alleles linked to the *S*-locus  
75 (Glémin *et al.*, 2001). The existence of a sheltered load has been demonstrated experimentally  
76 in *Solanum carolinense* by Stone (2004) and Mena-Alí *et al.* (2009).

77 Overall, under a wide range of conditions, SI can evolve to self-compatibility. In effect, the  
78 loss of SI systems is very frequent in plant evolution (Igic *et al.*, 2008). However, the reasons  
79 for which some species maintain a SI system while other species lose it are not completely  
80 understood. It has been suggested that asexual reproduction, “when an individual produces  
81 new individuals that are genetically identical to the ancestor at all loci in the genome, except  
82 at those sites that have experienced somatic mutations” (de Meeûs *et al.*, 2007), plays a role in  
83 the maintenance or breakdown of SI. Two studies suggest that asexuality could relieve the  
84 main selective pressures that favour the breakdown of SI. First, Chen *et al.* (1997) showed in  
85 Australian Droseraceae that all self-incompatible taxa have effective forms of asexual  
86 reproduction, whereas the obligatory sexual annual taxon, *Drosera glanduligera*, is self-  
87 compatible. Their interpretation is that self-incompatible forms accumulate recessive lethal  
88 polymorphisms, especially in association with biparental inbreeding generated by elevated  
89 levels of asexual reproduction. The hypothetical high genetic load constitutes the selective  
90 pressure that maintains the outbreeding mechanisms. Second, Vallejo-Marín and O'Brien  
91 (2007) hypothesized that asexuality could provide reproductive assurance in cross-fertilizing  
92 species subject to pollen limitation. They predicted that cross-fertilizing species subject to  
93 pollen limitation would often have some means of asexual reproduction, and they found a  
94 strong correlation between self-incompatibility and asexuality in *Solanum* (Solanaceae).  
95 Conversely, Young *et al.* (2002) developed a contrasting hypothesis for the case of *Rutidosia*

96 *leiolepis* in which they found SSI and high rates of asexual reproduction. They suggested that  
97 increased asexual reproduction causes mate limitation by reducing genotype diversity at the *S*-  
98 locus, favouring a breakdown of self-incompatibility.

99 The net effect of asexual reproduction on the maintenance or breakdown of SI systems is  
100 therefore still unknown. Moreover, it is unclear to what extent the effects of asexual  
101 reproduction discussed by the various authors are actually present in partially asexual, self-  
102 incompatible populations. Theoretical studies have described the effects of partial asexuality  
103 on the inbreeding depression of self-compatible populations (Muirhead and Lande, 1997) and  
104 the number of *S*-alleles (Vallejo-Marín and Uyenoyama, 2008). However, no model has been  
105 developed so far to study the joint effect of asexuality, self-incompatibility and drift on the  
106 evolution of diversity and fitness parameters for a hermaphroditic species. Using individual-  
107 based simulations, we investigated the effect of (i) partial asexual reproduction and drift on  
108 diversity at the *S*-locus, (ii) combined asexuality, self-incompatibility and drift on the  
109 frequency of deleterious alleles. Thus, our main goal was to characterise the dynamics of two  
110 key factors (number of *S*-alleles and inbreeding depression) for the maintenance of SI in  
111 partially asexual, self-incompatible populations. It was not the aim of this work to estimate  
112 the probability of invasion of self-compatible alleles or other modifiers of reproduction.

113

## 114 **Materials and Methods**

### 115 *Genetic model*

116 The model considered in this study was based on the model developed by Glémin *et al.*  
117 (2001). This model consists of a population of  $N$  (four population sizes evaluated: 25, 50, 100  
118 and 1000) diploid hermaphroditic individuals with a GSI system. In addition, our model also  
119 included asexual reproduction at rate  $c$  (probability that an individual is generated by asexual  
120 reproduction, seven values evaluated: 0, 0.5, 0.8, 0.9, 0.99, 0.999 and 1). We considered an

121 asexual reproduction event as the production of a new independent individual that is an exact  
122 copy of the parental individual (or only different by somatic mutation) (e.g. de Meeûs *et al.*,  
123 2007). As in Glémin *et al.* (2001), each individual genome possessed the *S*-locus, which  
124 regulated SI, and a viability locus, whose state determined individual fitness. Two neutral loci  
125 were also included for reference. The four loci were considered to be physically unlinked and  
126 were inherited independently through sexual reproduction.

127 Sexual reproduction events were controlled by the *S*-locus: crosses between individuals were  
128 only possible when the *S*-allele carried by the pollen grain was different from both *S*-alleles of  
129 the pistil (i.e. at least three different *S*-alleles were necessary in the population for sexual  
130 reproduction to occur). To focus on effects specifically attributable to asexuality on the  
131 maintenance and breakdown of SI, we assumed unlimited pollen availability and that sexual  
132 crosses were always fruitful. Thus, sexual reproduction was only limited when asexuality and  
133 genetic drift reduced the number of *S*-alleles to less than three within a population. In this  
134 case, independent of the original rate of asexual reproduction, all individuals reproduced  
135 asexually ( $c=1$ ) until mutation introduced a third *S*-allele. Then,  $c$  was reset to its original  
136 value.

137 Individual fitness,  $f$ , was determined by the viability locus, which had two alleles  $A$  and  $a$ .  
138 Strength of the dominance of allele  $A$  over deleterious allele  $a$  was regulated by the  
139 dominance coefficient  $h$ , and strength of the selection against  $a$  was regulated by the selection  
140 coefficient  $s$ . Thus, relative fitness of genotypes were:  $f_{AA}=1$ ,  $f_{Aa}=1-hs$  and  $f_{aa}=1-s$  ( $0 < s \leq 1$   
141 and  $0 < h \leq 1/2$ ). Three selection regimes at the viability locus were considered: (i) a neutral  
142 case, to be able to study the effects of the interaction between SI and asexuality without the  
143 interference of selection, where parameters  $s$  and  $h$  were set to zero; (ii) a case of mildly  
144 deleterious and partially recessive mutations, for which values assigned to  $s$  and  $h$  were

145 respectively 0.1 and 0.2; and (iii) a case of highly recessive lethal mutations, values assigned  
146 to  $s$  and  $h$  were respectively 1 and 0.02.

147 Mutations were allowed in all loci. Neutral loci mutated at rate  $\mu_N=10^{-3}$ , following a  $k$ -allele  
148 model ( $k=100$ ). Mutation at the  $S$ -locus followed an infinite-allele model (Kimura and Crow,  
149 1964) with rate  $\mu_S$ ; three values were considered for this rate ( $\mu_S=10^{-3}$ ,  $10^{-4}$  and  $10^{-5}$  as in  
150 Glémin *et al.*, 2001). Mutations at the viability locus occurred at rate  $\mu_1=10^{-3}$  from  $A$  to  $a$  and  
151 at rate  $\mu_2=10^{-4}$  from  $a$  to  $A$ .

152

### 153 *Individual-based simulations*

154 Forward-time simulations of a population of  $N$  diploid individuals with no overlapping  
155 generations were performed. Simulations started with all individuals carrying two unique  
156 alleles at the  $S$ -locus ( $2N$  different  $S$ -alleles in the whole population), alleles  $A$  or  $a$  randomly  
157 assigned (with equal probability, 0.5) to the viability locus and any of the  $k$  alleles ( $k=100$ )  
158 randomly assigned (with equal probability,  $1/k$ ) to the two neutral loci.

159 At each generation, the number of individuals generated by asexual reproduction,  $x$ , was  
160 drawn from a Poisson distribution with mean  $Nc$ , and the remaining  $N-x$  individuals were  
161 generated by sexual reproduction (parents contributing to these two types of offspring were  
162 not determined in this step). Genotypes of the  $N$  individuals were generated one by one. If a  
163 given individual originated by asexual reproduction, a genotype  $i$  was randomly drawn from  
164 all individuals of the previous generation. That genotype was assigned to the individual with a  
165 probability equal to the fitness of genotype  $i$ ; this will be called the selection step. If the  
166 genotype was not successfully assigned, the genotype draft and the selection step was  
167 repeated until a genotype passed the selection step. If the individual originated by sexual  
168 reproduction, the simulation followed a different procedure. First, an individual from previous  
169 generation was randomly drawn to act as a mother and the ovule haploid genotype was



170 randomly generated. Then, a second individual was drawn to act as a father and the pollen  
 171 haploid genotype was randomly generated. If the  $S$ -allele at the pollen grain was not different  
 172 from both  $S$ -alleles of the mother (i.e. incompatible pollen), the pollen was discarded. New  
 173 fathers and pollen grain genotypes were generated until a compatible cross was obtained (i.e.  
 174 pollen availability was unlimited). Then, a diploid genotype  $i$  was generated from the haploid  
 175 genotypes of the ovule and the pollen. The selection step was carried out on genotype  $i$  as in  
 176 the case of asexual reproduction; if the genotype was not assigned the process was repeated  
 177 by drawing two new parents until a genotype was able to pass the selection step. Once all  $N$   
 178 genotypes were selected, mutations were applied to each individual. The numbers of mutants  
 179 at the  $S$ -locus and at the two neutral loci were drawn from Poisson distributions with means  
 180  $2N\mu_S$  and  $2N\mu_N$  respectively. At the viability locus, a mutant was formed with a probability  $\mu_1$   
 181 if the allele was  $A$  and a probability  $\mu_2$  if the allele was  $a$ . The rate of asexual reproduction  
 182 was a fixed parameter of our model and did not change with the selection process.

183

#### 184 *Monitored genetic indices*

185 Simulations were run for 50 000 generations before beginning to monitor the genetic indices,  
 186 this allowed monitored indices to become stable and avoided the influence of initial  
 187 conditions in their values (Glémin *et al.*, 2001). From generation 50 000, indices were  
 188 calculated every 3 000 generations until 107 000 generations (i.e. 20 times). For the same  
 189 combination of parameters, 50 replicates of the simulations were performed providing 1 000  
 190 (indices calculated 20 times in each of the 50 replicates) evaluations of the monitored  
 191 variables for each set of parameter values. Indices were calculated from all genotypes of the  
 192 population (i.e. they were not estimates, but the true values of the population).

193 Genetic diversity indices: For each locus we calculated the number of alleles ( $n_a$ ), allele

194 frequencies, effective number of alleles ( $n_e = 1 / \sum_{i=1}^{n_a} p_i^2$ , where  $p_i$  was the frequency of allele),

195 expected heterozygosity ( $H_e = 1 - 1/n_e$ ), observed heterozygosity ( $H_o$ , proportion of  
 196 heterozygous individuals) and the inbreeding coefficient ( $F_{IS} = (H_e - H_o)/H_e$ ). Theoretical  
 197 predictions for some of these indices were obtained from the work of several authors for some  
 198 of the scenarios considered:

199 a) Vallejo-Marín and Uyenoyama (2008) studied the effects of partial asexuality in the  
 200 number of alleles of the *S*-locus using a diffusion approximation and found that the number of  
 201 common alleles ( $n_c$ , which is approximately equivalent to the effective number of *S*-alleles,  
 202  $n_e$ , Takahata, 1990) is determined by:

203 (1) 
$$\frac{M}{\theta} = \frac{1}{2} \left( \frac{1}{n_c} + \frac{1}{n_e} \right)$$

204 where  $M = N(1-c)$  and  $\theta = 2N\mu_s$ . This equation was solved numerically to obtain the  
 205 expected effective number of *S*-alleles in the simulations without selection on the viability  
 206 locus.

207 b) Glémin *et al.* (2001) obtained the expected  $F_{IS}$  for a neutral locus linked to the *S*-locus as:

208 (2) 
$$F_{IS} = \frac{(1-f_s)(1-c)}{1 + \frac{r'}{2\theta}}$$

209 where  $f_s$  is the scaling factor of the genealogy of the *S*-locus and  $r'$  is the net recombination  
 210 rate between the two loci. For the case of partial asexuality, the number of common alleles

211 was given by Equation 1 and the scaling factor was  $f_s = \frac{r'}{2\theta}$

212 (Vallejo-Marín and Uyenoyama, 2008). To correct for the reduction of recombination due to  
 213 asexuality, we used  $r' = r(1-c)$ , where  $r$  was the recombination rate during sexual  
 214 reproduction (i.e.  $r=0.5$  for unlinked loci). This approach ignored mutation on the neutral  
 215 locus.

216 c) Finally, an expression of the expected  $F_{IS}$  of a neutral locus in a self-compatible, partially  
 217 asexual population was derived following Balloux *et al.* (2003):

218 (3) 
$$F_{IS} = \frac{\gamma(1-s)}{1-\gamma(1-s)}$$

219 where  $\gamma = (1 - \mu_N)^2$  and  $s$  is the selfing rate. Selfing rate in Balloux *et al.* (2003) model is  
 220 defined as the rate of self-fertilization of individuals; thus a fertilization event between two  
 221 individuals from the same genet is considered an outcrossing event. Under random mating,  
 222  $s = 1/N$  and for negligible mutation rates,  $\gamma = 1$ .

223 Linkage disequilibrium: The linkage disequilibrium between pairs of loci ( $S$ -locus-viability  
 224 locus and the two neutral loci) was studied with the correlation coefficient between two loci,  
 225  $R_{GGD}$ , developed by Garnier-Géré and Dillmann (1992) which is particularly appropriate for  
 226 partially asexual diploids (de Meeûs and Balloux, 2004).

227 Fitness: Mean fitness of the population ( $\bar{W}$ ) was calculated from the genotype frequencies as  
 228  $\bar{W} = \sum p_{ij} w_{ij}$ , and the average fitness of individuals  
 229 potentially produced by selfing ( $W_s$ ), outcrossing ( $W_o$ ) and asexuality ( $W_a$ ) were calculated as

230 
$$W_s = \sum p_{ij} w_{ij} (1 - \mu_N),$$

231  $W_o = \sum p_{ij} w_{ij} (1 - \mu_N) (1 - \mu_N)$  (where  $p_A$  and  $p_a$  are the frequencies of alleles  
 232  $A$  and  $a$ ) and  $W_a = \bar{W}$ . Inbreeding depression ( $\delta$ ) and mutation load ( $L$ ) were calculated as

233  $\delta = 1 - (W_s / \bar{W})$  and  $L = 1 - \bar{W}$ . In addition, we compared the fitness of individuals produced

234 by asexual reproduction ( $W_a$ ) to the fitness of individuals produced sexually, using the ratio  
 235  $W_o / W_a$ .  $W_s$ ,  $W_o$  and  $W_a$  were calculated as the fitness of potential offspring if all individuals  
 236 were produced by selfing, by outcrossing and asexually, respectively. However, these modes  
 237 of reproduction might not be actually present in the different scenarios considered (e.g. in

238 self-incompatible populations, no selfing occurs, but potential  $W_s$  and inbreeding depression  
239 can be calculated).

240 Fixation probabilities: To interpret the results, we calculated the probabilities of four events:  
241 fixation of alleles  $A$  and  $a$  in the viability locus, ‘fixation’ of viability locus heterozygote ( $Aa$ )  
242 and fixation of a genotype in the  $S$ -locus (reduction of number of  $S$ -alleles to two, this was  
243 only monitored in self-incompatible populations). These fixation probabilities were estimated  
244 on 1 000 evaluations of the monitored variables as the proportion of times in which  $p_a=0$ ,  
245  $p_a=1$  and  $H_o=1$  for the viability locus, or  $n=2$  for the  $S$ -locus.

246

## 247 **Results**

### 248 *Effect of asexuality and drift on linkage disequilibrium between loci*

249 Probably the most obvious effect of partial asexual reproduction was the reduction of  
250 recombination. Asexuality generated identical genotypes in offspring, so allele associations  
251 were transmitted in the same way that they would be transmitted if they were physically  
252 linked throughout the whole genome. In fully asexual populations, maximum linkage  
253 disequilibrium was expected (equivalent to the linkage disequilibrium between fully linked  
254 loci) and in partially asexual populations, recombination was reduced proportionally to the  
255 rate of asexual reproduction. Figure 1 shows how non-random associations of alleles  
256 increased with asexual reproduction rates. Linkage disequilibrium levels also depended on  
257 population size because drift produced a departure from the expected values of frequencies of  
258 allele combinations (Figure 1). Strong drift might have even caused some combinations of  
259 alleles to be absent in the population.

260 In small populations, some generations with complete allelic association started to appear at  
261 asexual reproduction rates of 0.8 and were predominant at rates of 0.99 and higher. In larger  
262 populations, complete allelic association was only found in the fully asexual scenario. These

263 associations of alleles were observed between loci subject to selection and between neutral  
264 loci, which showed that linkage disequilibrium was not a product of selective processes  
265 (Figure 1a and Figure 1b).

266 Physical linkage between the *S*-locus and loci with deleterious alleles can decrease the  
267 number of *S*-alleles (Uyenoyama, 2003). It can also dramatically increase inbreeding  
268 depression in small populations (Glémin *et al.*, 2001). Therefore, for the present model, it was  
269 important to discern whether the linkage disequilibrium generated by asexual reproduction is  
270 sufficient for the selective forces of the *S*-locus to interact with the viability locus. The results  
271 are presented below taking this perspective into account.

272

273 *Effect of asexuality and drift on diversity parameters: number of S-alleles and heterozygote*  
274 *excess*

275 The effective number of *S*-alleles decreased with asexuality (Figure 2) as shown analytically  
276 by Vallejo-Marín and Uyenoyama (2008). Balancing selection on the *S*-locus only occurred  
277 during sexual reproduction events. Since these events were scarce at high rates of asexual  
278 reproduction, the influence of balancing selection (which promotes high allelic diversity) on  
279 the population diminished. This can temporarily stop sexual reproduction by reducing the  
280 number of *S*-alleles to two (i.e. fixation of an *S*-locus genotype, Table 1).

281 No significant differences in the number of *S*-alleles were found among the three different  
282 selection regimes for the viability locus (frequency distributions of the number of *S*-alleles  
283 among different selection regimes were undistinguishable in a Kolmogorov-Smirnov test, *P*-  
284 value>0.98). It must be noted that small populations (with high linkage disequilibrium) were  
285 fixed for the wild type allele *A* most of the time (Table 2b) and this may explain the weak  
286 influence of deleterious alleles on the *S*-locus.

287 Another general effect of partial asexual reproduction in diploids was the reduction of allele  
288 segregation. This can increase heterozygosity by the independent accumulation of mutations  
289 on the two alleles of an asexual lineage (Pamilo, 1987; Birky, 1996). To quantify this effect,  
290 we measured the inbreeding coefficient  $F_{IS}$ , which compares observed and expected  
291 heterozygosities.

292 Theoretical equilibrium values for  $F_{IS}$  at a neutral locus (unlinked to the  $S$ -locus) were very  
293 similar in self-compatible and self-incompatible populations (Figure 3), and, for large  
294 population sizes, the simulated populations followed the same pattern (Figure 3b). However,  
295 for small population sizes, drift generated strong linkage disequilibrium between the  $S$ -locus  
296 and other loci. Thus, balancing selection on the  $S$ -locus had a hitchhiking effect on other loci,  
297 increasing their heterozygosity. This explained the contrasting  $F_{IS}$  values on simulated self-  
298 compatible and self-incompatible populations (Figure 3a). Analytical predictions do not  
299 reflect this dramatic difference because they do not account for linkage disequilibrium.  $F_{IS}$   
300 decreased with asexuality and this decrease was enhanced by self-incompatibility in small  
301 populations, particularly noticeable at asexual reproduction rates higher than 0.8. This  
302 decrease in  $F_{IS}$  observed in neutral loci also occurred at the viability locus (both for the mildly  
303 deleterious and lethal recessive cases), which implied an increase in the frequency of the  
304 deleterious allele (Figure 4).

305

#### 306 *Effect of asexuality and drift on fitness*

307 For both self-compatible and self-incompatible populations, mutation load globally increased  
308 with asexuality and population size, but a greater variance among generations and populations  
309 was observed for very small populations (Figure 5). As mentioned above, the frequency of the  
310 deleterious allele increased with asexuality in small self-incompatible populations, due to a  
311 hitchhiking effect of the  $S$ -locus over the viability locus. In the self-incompatibility system,

312 when the population size was small enough, the mutation load increased with asexual  
313 reproduction rates; this load resulted from the increase of the deleterious allele frequency  
314 (Figure 5a and 5c). Under similar conditions in the self-compatible system, mutation loads  
315 were lower than the mutation load observed in the self-incompatible system (Figure 5b and  
316 5d). In contrast, inbreeding depression had similar values in self-incompatible and self-  
317 compatible populations (Figure 6), showing some increases with asexual reproduction rate for  
318 lethal recessive mutations that was more apparent in large populations.

319 The average fitness was higher in sexual populations than in asexual populations due to  
320 Mendelian segregation (e.g. Figure 5; Chasnov, 2000; Kirkpatrick and Jenkins, 1989). The  
321 relative fitness between individuals produced by sexual and asexual reproduction was  
322 influenced very little by partial asexuality in a self-compatible population (Figure 7b and 7d).  
323 However, in small self-incompatible populations, the asexual reproduction rate increased the  
324 advantage of asexual compared to sexual reproduction (Figure 7a and 7c). These populations  
325 consisted mainly of heterozygous individuals (Figure 3). Therefore, asexual reproduction  
326 produced mainly  $Aa$  individuals, with only slightly lower fitness than the fittest  $AA$  haplotype.  
327 However, sexual reproduction produced a high proportion of  $aa$  individuals, reducing the  
328 average fitness of offspring, a reduction that was not compensated by the production of the  
329 fittest  $AA$  individuals. This could potentially lead to a positive feedback effect on the asexual  
330 reproduction rate, but this was not studied in our model where the asexual reproduction rate  
331 was a fixed parameter.

332

### 333 **Discussion**

334 The number of  $S$ -alleles and inbreeding depression are considered to be the main factors that  
335 influence the maintenance or breakdown of self-incompatibility systems (Charlesworth and  
336 Charlesworth, 1979). A decrease in the number of  $S$ -alleles is expected to favour the

337 breakdown of self-incompatibility since self-compatible mutants can invade the population,  
338 whereas the maintenance of inbreeding depression within populations prevents the breakdown  
339 of self-incompatibility. In the present study, we examined how drift and partial asexuality  
340 may modify the dynamics of these two key parameters in a self-incompatible population.

341

342 *Drift, combined with partial asexuality, dramatically reduced the number of S-alleles*

343 As already predicted by Yokoyama and Hetherington (1982), we showed that the number of  
344 *S*-alleles decreases with the effective size of the population. Thus, in small populations,  
345 repeated bottlenecks or founder events may lead to the breakdown of the self-incompatibility  
346 system. However, Karron (1987) found no differences in mating systems between rare and  
347 widespread congeners across several families (but see also a study on some Brassicaceae  
348 species, Kunin and Shmida, 1997). As for the impact of asexuality, our simulation study  
349 confirmed a recent result demonstrated analytically by Vallejo-Marín and Uyenoyama (2008).  
350 The number of *S*-alleles decreased with asexuality due to the weakened influence of balancing  
351 selection in a partially asexual population (Figure 2). In contrast with other effects of  
352 asexuality that were only observed for very high rates of asexuality, intermediate asexual  
353 reproduction rates were sufficient to significantly reduce the number of *S*-alleles. High rates  
354 of asexual reproduction combined with drift produced extremely low numbers of *S*-alleles.  
355 This effect was strong enough to even reduce the number of *S*-alleles to two (i.e. fixation of  
356 an *S*-locus genotype, Table 1), which stopped all possibility of sexual reproduction until a  
357 new *S*-allele arose from mutation or migration. Therefore, in such extreme cases, this drastic  
358 effect of asexuality on the number of *S*-alleles should favour the breakdown of self-  
359 incompatibility. However, paradoxically, the number of *S*-alleles may not be very relevant in  
360 a system where asexuality serves to provide reproductive assurance.

361



362 *Drift, combined with partial asexuality and self-incompatibility, led to an increase in*  
363 *mutation load*

364 Drift influenced the level of mutation load. As population size decreased, the frequency of the  
365 deleterious allele decreased and mutation load decreased, due to more effective purging. We  
366 also observed a much greater variance in mutation load in very small populations (Table 2  
367 and Figure 5,  $N=25$ ). In this case, selection was overwhelmed by drift and this caused a higher  
368 probability of fixation of the deleterious allele, and an increase in mutation load. Similar  
369 results have been described by Bataillon and Kirkpatrick (2000), Glémin (2003) and Haag and  
370 Roze (2007).

371 Drift is also a key component of mutation load in asexual populations (Haag and Roze, 2007).  
372 Indeed, large asexual and sexual populations showed comparable frequencies of the  
373 deleterious allele and comparable mutation loads (Figure 5; see also Haag and Roze, 2007).  
374 However, mutation load was greater in small asexual populations than in small sexual ones.  
375 This could be explained by the absence of segregation in asexual populations, in which  
376 heterozygous individuals are present in high frequencies (Table 2 and Figure 5; see also Haag  
377 and Roze, 2007).

378 In this study, we additionally showed that self-incompatibility played a role in increasing  
379 mutation load in partially asexual, self-incompatible populations. Partial asexual reproduction  
380 and small population sizes produced strong associations (i.e. linkage disequilibrium) between  
381 deleterious alleles (on any locus of the genome) and *S*-alleles. Glémin *et al.* (2001) have  
382 already shown that deleterious mutations on loci linked to the *S*-locus may be sheltered by  
383 balancing selection acting on rare *S*-alleles. Asexuality and self-incompatibility both favoured  
384 the increase of the heterozygote genotype *Aa* within the population, leading to an increase of  
385 mutation load in small self-incompatible, partially asexual populations.

386

387 *Inbreeding depression remained low in small, partially asexual, self-incompatible*  
388 *populations*

389 Inbreeding depression followed different patterns than the ones observed for mutation load.  
390 For very small populations, inbreeding depression is expected to decrease (Bataillon and  
391 Kirkpatrick, 2000), due to the absence of polymorphism at the viability locus. This was  
392 observed in small self-compatible and self-incompatible populations (Glémin *et al.*, 2001, and  
393 our own simulations, Figure 6). As for the impact of asexuality, our results showed no large  
394 differences between the self-compatible and the self-incompatible cases for small populations.  
395 The effect of strong drift, in the presence of strong asexuality, was to reduce genotype  
396 diversity. In most cases, populations were fixed at one allele, but sometimes the population  
397 was fixed at the heterozygote genotype *Aa*. This mainly occurred in self-incompatible  
398 populations (see Table 2). With no or very low genotype diversity, inbreeding depression had  
399 very low values, even if deleterious alleles were present at high frequencies in the population.  
400 Chen *et al.* (1997) proposed that asexuality would favour the maintenance of SI. Their  
401 reasoning was that asexual reproduction would increase a population's genetic load due to  
402 lethal recessive mutations, which was confirmed by our simulation results. However,  
403 mutation load and inbreeding depression did not show parallel trends, and the high level of  
404 mutation load due to the combination of drift, asexuality and SI was accompanied by low  
405 levels of inbreeding depression. Nevertheless, inbreeding depression generally tended to  
406 increase with asexuality due to the accumulation of deleterious alleles and this should favour  
407 the maintenance of SI.

408

409 *Evolution of partially asexual, self-incompatible populations: a third possible outcome*

410 Until now, the evolutionary interest of partially asexual, self-incompatible populations has  
411 been focused on two possible outcomes: (1) the system is stable and SI is maintained or (2)

412 the system is unstable and SI disappears (Vallejo-Marín, 2007; Vallejo-Marín and O'Brien,  
413 2007; Chen *et al.*, 1997; Young *et al.*, 2002). However, a third possible outcome should be  
414 considered: being the unstable system, sexual reproduction completely disappears. This type  
415 of event was observed in our simulations due to a reduction in the number of *S*-alleles to two  
416 (see above). However, we also studied how selection on the viability locus could contribute to  
417 the potential loss of sexuality. Our results showed that the fitness of individuals produced by  
418 asexual reproduction ( $W_a$ ) was greater than that of individuals produced by random sexual  
419 mating ( $W_o$ ) in small populations (Figure 7). Fitness of individuals (potentially) produced by  
420 selfing ( $W_s$ ) was also lower than  $W_a$  in small self-incompatible populations, suggesting that  
421 asexuality may have an immediate advantage over selfing under such circumstances.

422 Therefore, we speculate that asexual reproduction could take over sexual reproduction more  
423 easily than self-compatibility over self-incompatibility when low numbers of *S*-alleles reduce  
424 mate availability. Despite the effect of asexuality on inbreeding depression and *S*-locus  
425 diversity, asexual reproduction may offer an alternative means of reproduction under these  
426 adverse conditions and self-incompatibility may be temporarily dormant instead of breaking  
427 down. Asexual populations could subsequently recover a sexual self-incompatible  
428 reproductive system when new *S*-alleles are introduced in the population (for instance, by  
429 migration). However, prolonged periods of asexual reproduction may facilitate the  
430 accumulation of mutations affecting sexual traits, including self-incompatibility, since  
431 selective pressures are ineffective for these traits (Eckert, 2001). Thus, alternative periods of  
432 sexual and asexual reproduction may be necessary for such dynamics, which is probably the  
433 case for plants combining asexual and sexual reproduction (Bengtsson and Cephitis, 2000).  
434 Nevertheless, the scenarios described here need to be confirmed by further and more complex  
435 simulations and other factors may favour self-compatible sexual reproduction, such as the  
436 more effective purging of deleterious mutations.

437

438 *Perspectives*

439 In this study, we used a model with physically unlinked loci and a single viability locus.  
440 However, because the linkage disequilibrium produced by asexuality affected the whole  
441 genome, population genomic models may be necessary to fully study the effect of deleterious  
442 alleles on the *S*-locus for small, partially asexual populations. In addition, physically linked  
443 loci with deleterious alleles (which were not studied here) may reduce the number of *S*-alleles  
444 (Uyenoyama, 2003) and the strength of that effect may be influenced by the rate of asexuality  
445 as discussed by Vallejo-Marín and Uyenoyama (2008). Moreover, in the present study, it was  
446 not possible to investigate the evolutionary dynamics of mating system and asexuality  
447 modifiers since these were assumed to be fixed parameters. It would be then interesting to  
448 develop a model to test the invasion propensity of self-compatible or asexual mutants. Finally,  
449 models incorporating migration or population structure are necessary to study more realistic  
450 dynamics of partially asexual, self-incompatible populations. Population structure is expected  
451 to affect the genetic diversity of viability and the *S*-locus, for instance by introducing a third  
452 allele via migration within subpopulations fixed at two *S*-alleles. These models should also  
453 take into account the specificities of the different types of asexual reproduction where, for  
454 instance, the asexual propagules may have a lower dispersal capacity (e.g. vegetative  
455 reproduction) and may create spatial clusters of individuals with the same genotype.

456 Recent theoretical work (Vallejo-Marín and Uyenoyama, 2008) and our own model lead to  
457 several predictions about *S*-locus diversity, mutation load and inbreeding depression within  
458 partially asexual self-incompatible populations. However, we need more experimental  
459 observations to test and validate these theoretical advances. First, as outlined by Vallejo-  
460 Marín and O'Brien (2007), if asexuality relieves selective pressures favouring the breakdown  
461 of SI, the co-occurrence of asexuality and self-incompatibility should be frequent. Association

462 of self-incompatibility and asexuality has been studied in only a few monospecific studies  
463 (*Rutidosia leiolepis*, Young *et al.*, 2002; *Eucalyptus morrisbyi*, Jones *et al.*, 2005; *Prunus*  
464 *avium*, Stoeckel *et al.*, 2006). The association was found at a multispecific level by Chen *et*  
465 *al.* (1997) in Australian Droseraceae and by Vallejo-Marín and O'Brien (2007) in Solanaceae.  
466 More reports on species combining self-incompatibility and asexuality would enhance our  
467 understanding of pressures explaining their maintenance. Second, experimental measurements  
468 of asexual reproduction rates and number of *S*-alleles in species showing various levels of  
469 asexual reproduction would be useful to test predictions from our simulations. Although  
470 experimental measurements of inbreeding depression in self-incompatible species are  
471 available (Mena-Alí *et al.*, 2008), studies comparing inbreeding depression from different  
472 populations with contrasting sizes and rates of asexual reproduction are lacking.

473

#### 474 *Conclusions*

475 This study investigated for the first time the effect of partial asexual reproduction on the  
476 fitness of self-incompatible populations. For loci unlinked to the *S*-locus and large  
477 populations, fitness values were similar to those of a self-compatible population. However, in  
478 small populations, the combination of drift, asexuality and SI increased mutation load due to  
479 the accumulation of deleterious alleles. This increase in the mutation load was accompanied  
480 by a selective advantage of asexually produced offspring compared to sexually produced  
481 offspring. Therefore, future studies addressing the maintenance of SI in partially asexual  
482 populations (by studying the invasibility of self-compatible genotypes) will need to (1)  
483 account for whole genome fitness and (2) acknowledge that the process may not be  
484 independent of the maintenance of sex itself (i.e. will need to establish whether modifiers of  
485 asexual reproduction rates invade more easily than self-compatible alleles).

486

487 **Acknowledgements**

488 Collaboration between MN and SM was promoted through the implementation of the  
489 REPROFOR project, financed by the Spanish Ministry for Education and Science. We would  
490 like to thank Santiago C. González-Martínez and Ricardo Alía for helping to develop this  
491 collaboration. E. Porcher is acknowledged for helpful discussions on self-incompatibility  
492 evolution. We are also very thankful to P. Garnier-Géré for a detailed discussion on linkage  
493 disequilibrium estimators.

494

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- 579

580 **Figure legends**

581 **Figure 1** Linkage disequilibrium ( $R_{GDD}$  index, Garnier-Géré & Dillmann 1992) at increasing  
582 rates of asexual reproduction. Box-plots represent median (black line), first and third quartiles  
583 (box) and 5% and 95% percentiles (whiskers) of 1 000 observations from simulations  
584 performed at seven rates of asexual reproduction ( $c=0, 0.5, 0.8, 0.9, 0.99, 0.999$  and  $1$ ) and  
585 four population sizes ( $N=25, 50, 100$  and  $1000$ ). (a)  $R_{GDD}$  index between  $S$ -locus and viability  
586 locus ( $s=0.1, h=0.2$ ); (b)  $R_{GDD}$  index between two neutral loci.

587 **Figure 2** Effective number of  $S$ -alleles at increasing rates of asexual reproduction. Box-plots  
588 represent median (black line), first and third quartiles (grey box) and 5% and 95% percentiles  
589 (whiskers) of 1 000 observations from the simulations performed at six rates of asexuality  
590 ( $c=0, 0.5, 0.8, 0.9, 0.99$  and  $1$ ), population size  $N=25$  (a) and  $N=100$  (b), mutation rate  $\mu_S=10^{-5}$ ,  
591  $s=0$  and  $h=0$  for the viability locus. Grey line represents the theoretical expected number of  
592 common  $S$ -alleles obtained numerically from Equation 1 (Equation 3.7 in Vallejo-Marín &  
593 Uyenoyama, 2008).

594 **Figure 3** Inbreeding coefficient  $F_{IS}$  at a neutral locus at increasing rates of asexual  
595 reproduction. Box-plots represent median (black line), first and third quartiles (white and grey  
596 boxes, for self-compatible and self-incompatible populations respectively) and 5% and 95%  
597 percentiles (whiskers) of 1 000 observations from the simulations performed at six rates of  
598 asexuality ( $c=0, 0.5, 0.8, 0.9, 0.99$  and  $1$ ), mutation rates  $\mu_S=10^{-5}$  and  $\mu_N=10^{-3}$ , and population  
599 size (a)  $N=25$  and (b)  $N=100$ . Theoretical equilibrium values for  $F_{IS}$  at a neutral locus in a  
600 self-compatible, random-mating population (dotted black line, from Equation 3, neglecting  
601 mutation) and in a self-incompatible population (continuous grey line, from Equation 2) are  
602 also represented.

603 **Figure 4** Frequency of deleterious alleles at increasing rates of asexual reproduction under  
604 two selection regimes. Box-plots represent median (black line), first and third quartiles (white

605 and grey boxes, for self-compatible and self-incompatible populations respectively) and 5%  
606 and 95% percentiles (whiskers) of 1000 observations from the simulations performed at seven  
607 rates of asexuality ( $c=0, 0.5, 0.8, 0.9, 0.99, 0.999$  and  $1$ ), mutation rates  $\mu_S=10^{-5}$  and  $\mu_N=10^{-3}$ .  
608 Population size and viability locus coefficients: (a)  $N=25, s=0.1, h=0.2$ , (b)  $N=25, s=1,$   
609  $h=0.02$ , (c)  $N=100, s=0.1, h=0.2$ , and (d)  $N=100, s=1, h=0.02$ .

610 **Figure 5** Mutation load at increasing rates of asexual reproduction under two different  
611 selection regimes according to reproductive system. Box-plots represent median (black line),  
612 first and third quartiles (box) and 5% and 95% percentiles (whiskers) of 1 000 observations  
613 from simulations performed at seven rates of asexual reproduction ( $c=0, 0.5, 0.8, 0.9, 0.99,$   
614  $0.999$  and  $1$ ) and four population sizes ( $N=25, 50, 100$  and  $1000$ ). (a) Self-incompatible  
615 population with a viability locus with mildly deleterious allele ( $s=0.1, h=0.2$ ), (b) self-  
616 compatible population with a viability locus with mildly deleterious allele ( $s=0.1, h=0.2$ ), (c)  
617 self-incompatible population with a viability locus with highly recessive lethal allele ( $s=1,$   
618  $h=0.02$ ), and (d) self-compatible population with a viability locus with highly recessive lethal  
619 allele ( $s=1, h=0.02$ ).

620 **Figure 6** Inbreeding depression at increasing rates of asexual reproduction and under two  
621 different selection regimes according to reproductive system. Box-plots represent median  
622 (black line), first and third quartiles (box) and 5% and 95% percentiles (whiskers) of 1000  
623 observations from simulations performed at seven rates of asexual reproduction ( $c=0, 0.5, 0.8,$   
624  $0.9, 0.99, 0.999$  and  $1$ ) and four population sizes ( $N=25, 50, 100$  and  $1000$ ). (a) Self-  
625 incompatible population with a viability locus with mildly deleterious allele ( $s=0.1, h=0.2$ ),  
626 (b) self-compatible population with a viability locus with mildly deleterious allele ( $s=0.1,$   
627  $h=0.2$ ), (c) self-incompatible population with a viability locus with highly recessive lethal  
628 allele ( $s=1, h=0.02$ ), and (d) self-compatible population with a viability locus with highly  
629 recessive lethal allele ( $s=1, h=0.02$ ).

630 **Figure 7** Fitness ratio between sexually and asexually produced individuals at increasing rates  
631 of asexual reproduction under two different selection regimes according to reproductive  
632 system. Box-plots represent median (black line), first and third quartiles (box) and 5% and  
633 95% percentiles (whiskers) of 1 000 observations from simulations performed at seven rates  
634 of asexual reproduction ( $c=0, 0.5, 0.8, 0.9, 0.99, 0.999$  and  $1$ ) and four population sizes  
635 ( $N=25, 50, 100$  and  $1000$ ). (a) Self-incompatible population with a viability locus with mildly  
636 deleterious allele ( $s=0.1, h=0.2$ ), (b) self-compatible population with a viability locus with  
637 mildly deleterious allele ( $s=0.1, h=0.2$ ), (c) self-incompatible population with a viability locus  
638 with highly recessive lethal allele ( $s=1, h=0.02$ ), and (d) self-compatible population with a  
639 viability locus with highly recessive lethal allele ( $s=1, h=0.02$ ).  
640

641 **Table 1** Genotype fixation probability at the *S*-locus under two different selection regimes at  
 642 the viability locus

Population size	Selection regime	Rate of asexual reproduction						
		<i>c</i> =0	<i>c</i> =0.5	<i>c</i> =0.8	<i>c</i> =0.9	<i>c</i> =0.99	<i>c</i> =0.999	<i>c</i> =1
<i>N</i> =25	Mildly deleterious <sup>1</sup>	0.000	0.000	0.036	0.325	0.784	0.807	0.997
<i>N</i> =25	Lethal recessive <sup>2</sup>	0.000	0.000	0.018	0.315	0.790	0.805	0.994
<i>N</i> =50	Mildly deleterious	0.000	0.000	0.000	0.002	0.072	0.117	0.990
<i>N</i> =50	Lethal recessive	0.000	0.000	0.000	0.001	0.075	0.090	0.989
<i>N</i> =100	Mildly deleterious	0.000	0.000	0.000	0.000	0.001	0.001	0.983

643 The probability of genotype fixation at the *S*-locus (only two alleles in the population) was  
 644 estimated as the proportion of observations in which this event was recorded. Results in this  
 645 table are for populations with a mutation rate of  $\mu_S=10^{-5}$  at the *S*-locus.

646 <sup>1</sup> Viability locus selection and dominance coefficients:  $s=0.1$  and  $h=0.2$

647 <sup>2</sup> Viability locus selection and dominance coefficients:  $s=1$  and  $h=0.02$

648

649 **Table 2** Fixation probabilities at the viability locus in a self-incompatible population under  
 650 two different selection regimes.

Population size	Selection regime	Rate of asexual reproduction						
		$c=0$	$c=0.5$	$c=0.8$	$c=0.9$	$c=0.99$	$c=0.999$	$c=1$
(a) Fixation of deleterious allele $a$								
$N=25$	Mildly deleterious <sup>1</sup>	0.066	0.049	0.056	0.050	0.085	0.081	0.067
$N=50$	Mildly deleterious	0.000	0.000	0.001	0.000	0.001	0.001	0.001
$N=100$	Mildly deleterious	0.000	0.000	0.000	0.000	0.000	0.000	0.000
(b) Fixation of allele $A$								
$N=25$	Mildly deleterious	0.670	0.714	0.663	0.519	0.264	0.279	0.082
$N=25$	Lethal recessive <sup>2</sup>	0.831	0.783	0.767	0.581	0.293	0.317	0.085
$N=50$	Mildly deleterious	0.583	0.541	0.574	0.507	0.474	0.466	0.139
$N=50$	Lethal recessive	0.661	0.635	0.596	0.564	0.518	0.493	0.150
$N=100$	Mildly deleterious	0.314	0.306	0.320	0.294	0.274	0.290	0.187
$N=100$	Lethal recessive	0.437	0.361	0.318	0.313	0.269	0.296	0.189
(c) Fixation of genotype $Aa$								
$N=25$	Mildly deleterious	0.000	0.000	0.023	0.184	0.472	0.467	0.723
$N=25$	Lethal recessive	0.000	0.000	0.013	0.212	0.551	0.569	0.879
$N=50$	Mildly deleterious	0.000	0.000	0.000	0.000	0.026	0.050	0.585
$N=50$	Lethal recessive	0.000	0.000	0.000	0.000	0.032	0.041	0.721
$N=100$	Mildly deleterious	0.000	0.000	0.000	0.000	0.000	0.000	0.230
$N=100$	Lethal recessive	0.000	0.000	0.000	0.000	0.000	0.000	0.317

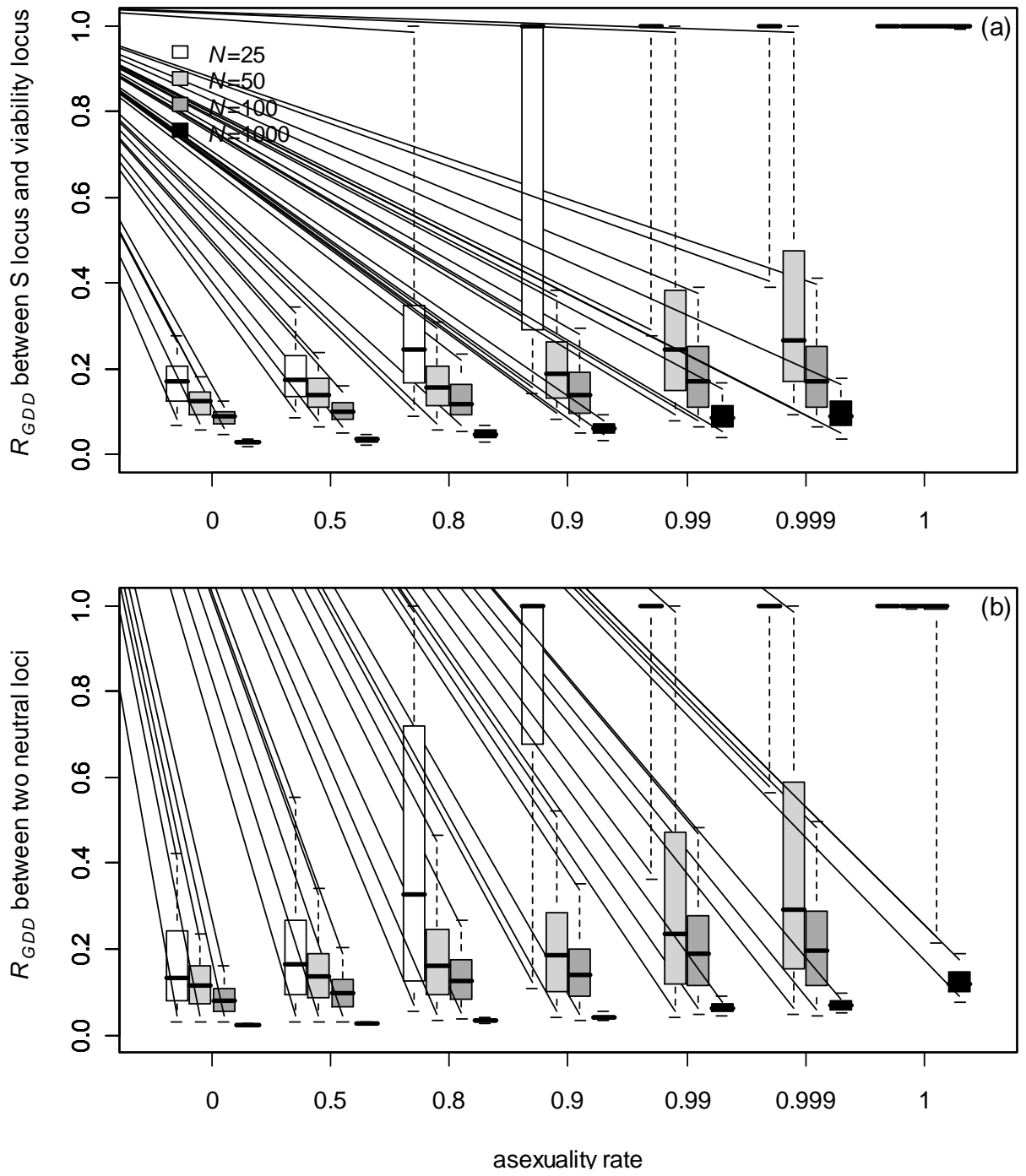
651 The probability of fixation at the viability locus (fixation of genotypes,  $AA$ ,  $aa$  or  $Aa$ ) was  
 652 estimated as the proportion of observations in which fixation was recorded.

653 <sup>1</sup> Viability locus selection and dominance coefficients:  $s=0.1$  and  $h=0.2$

654 <sup>2</sup> Viability locus selection and dominance coefficients:  $s=1$  and  $h=0.02$

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656 **Figure 1**

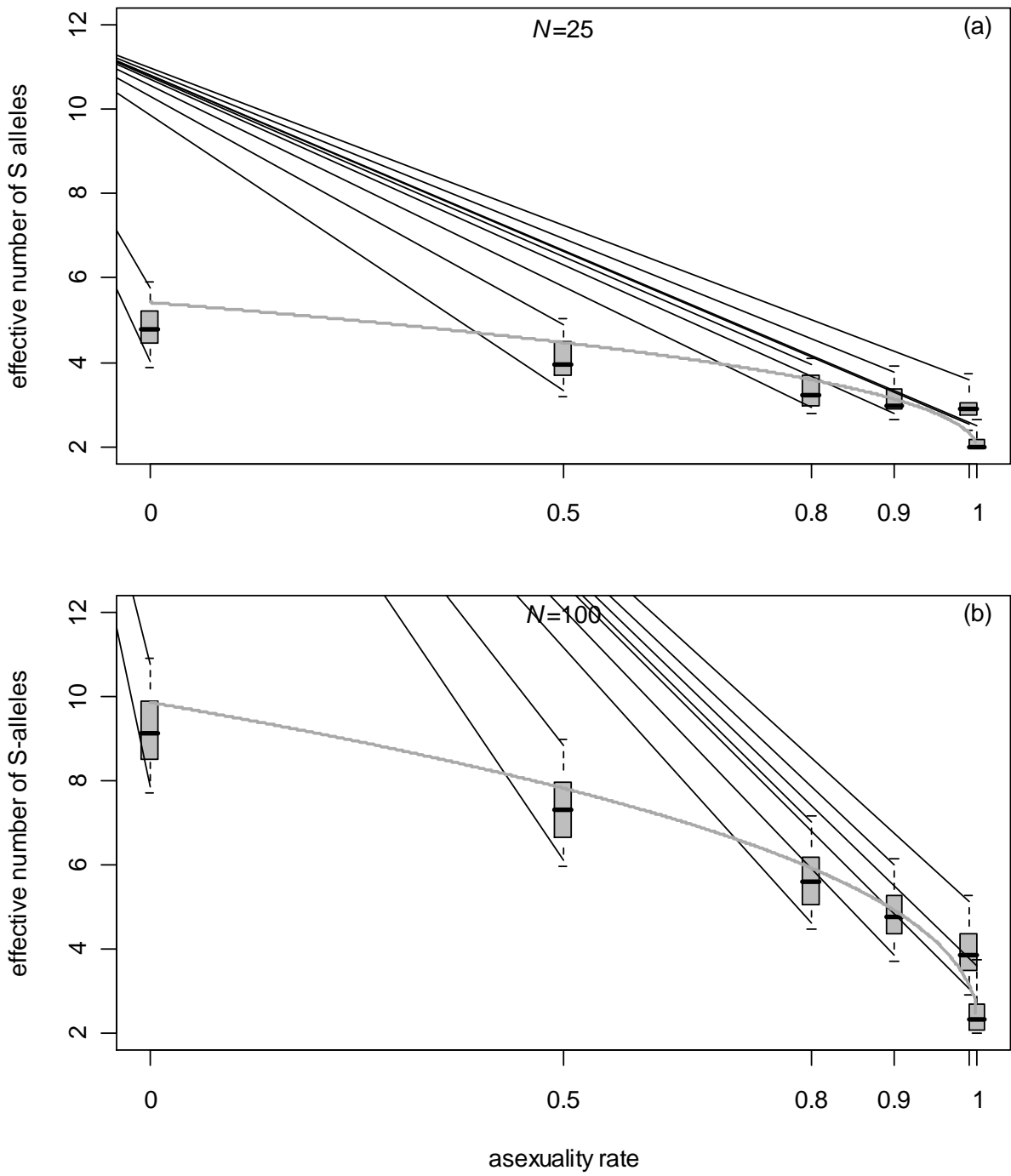


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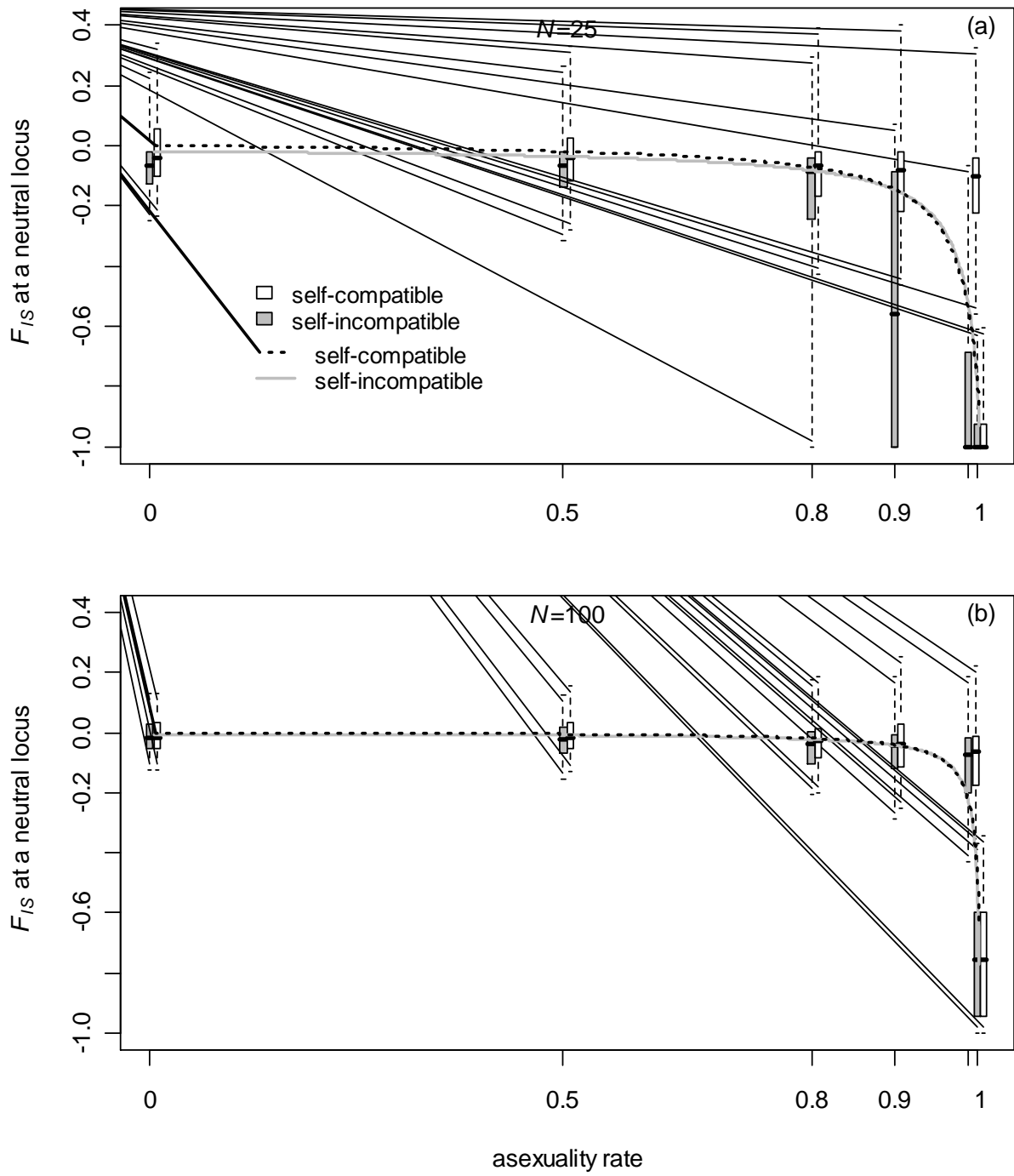
659 **Figure 2**



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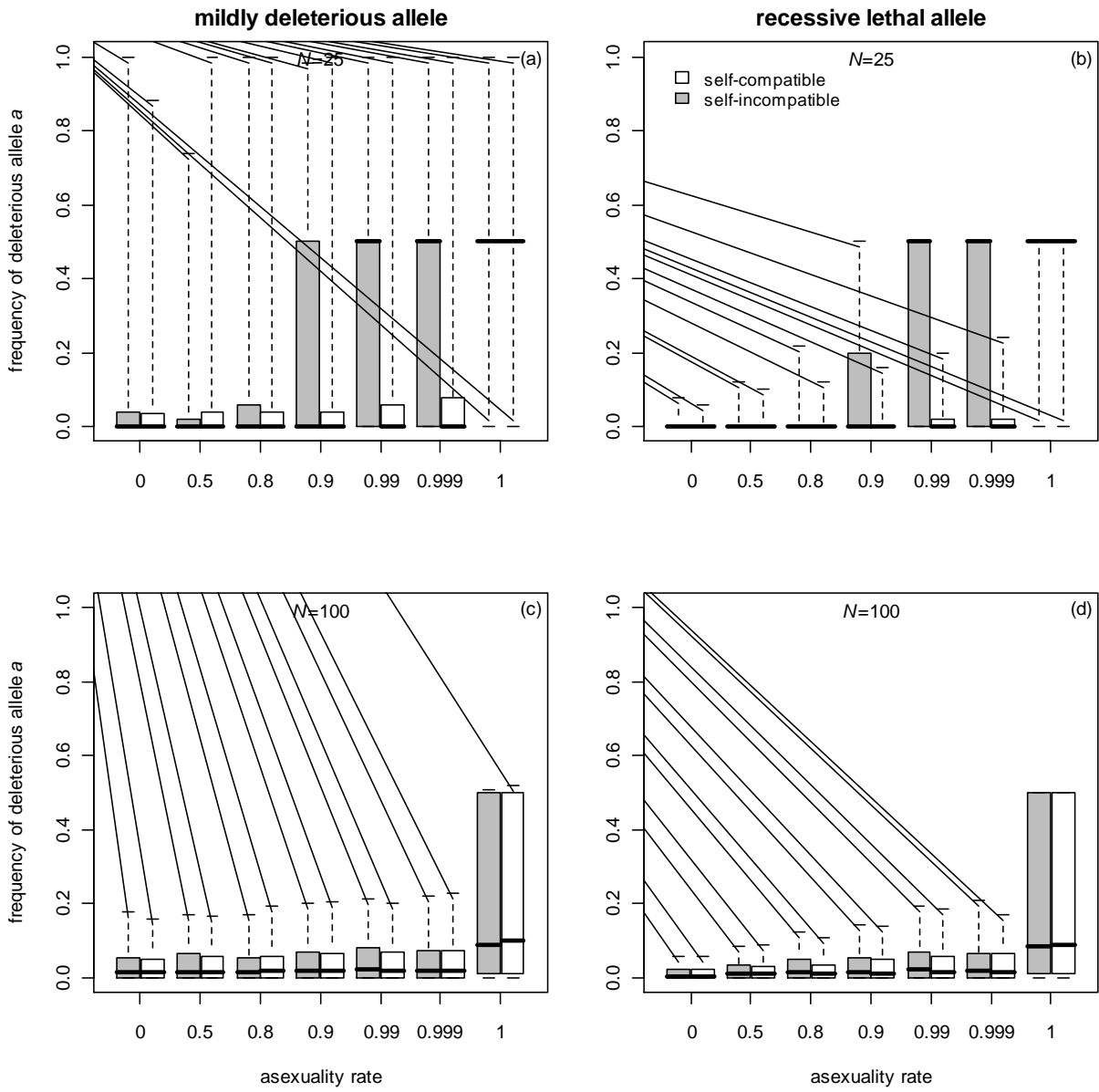
662 **Figure 3**



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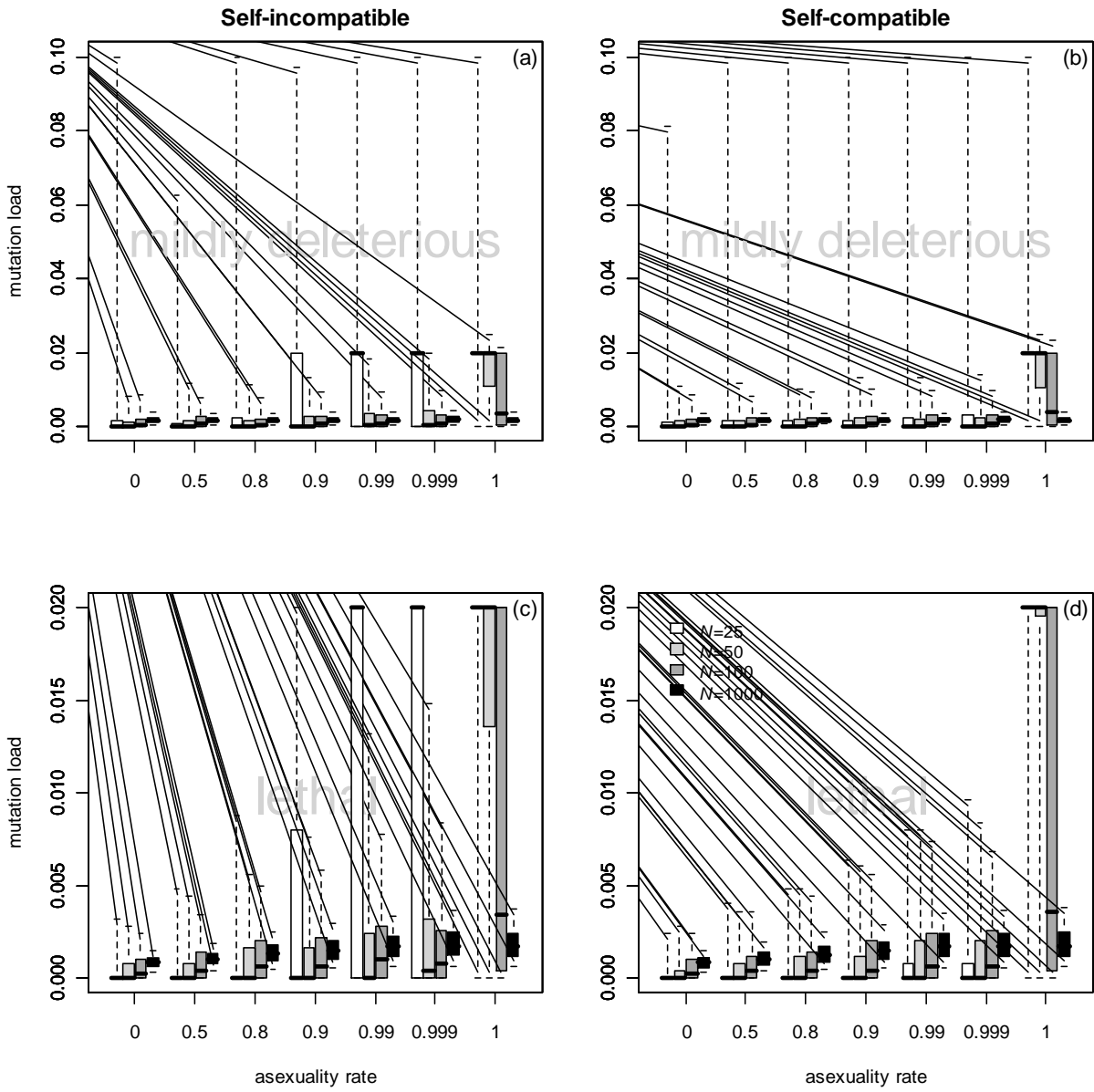
665 **Figure 4**



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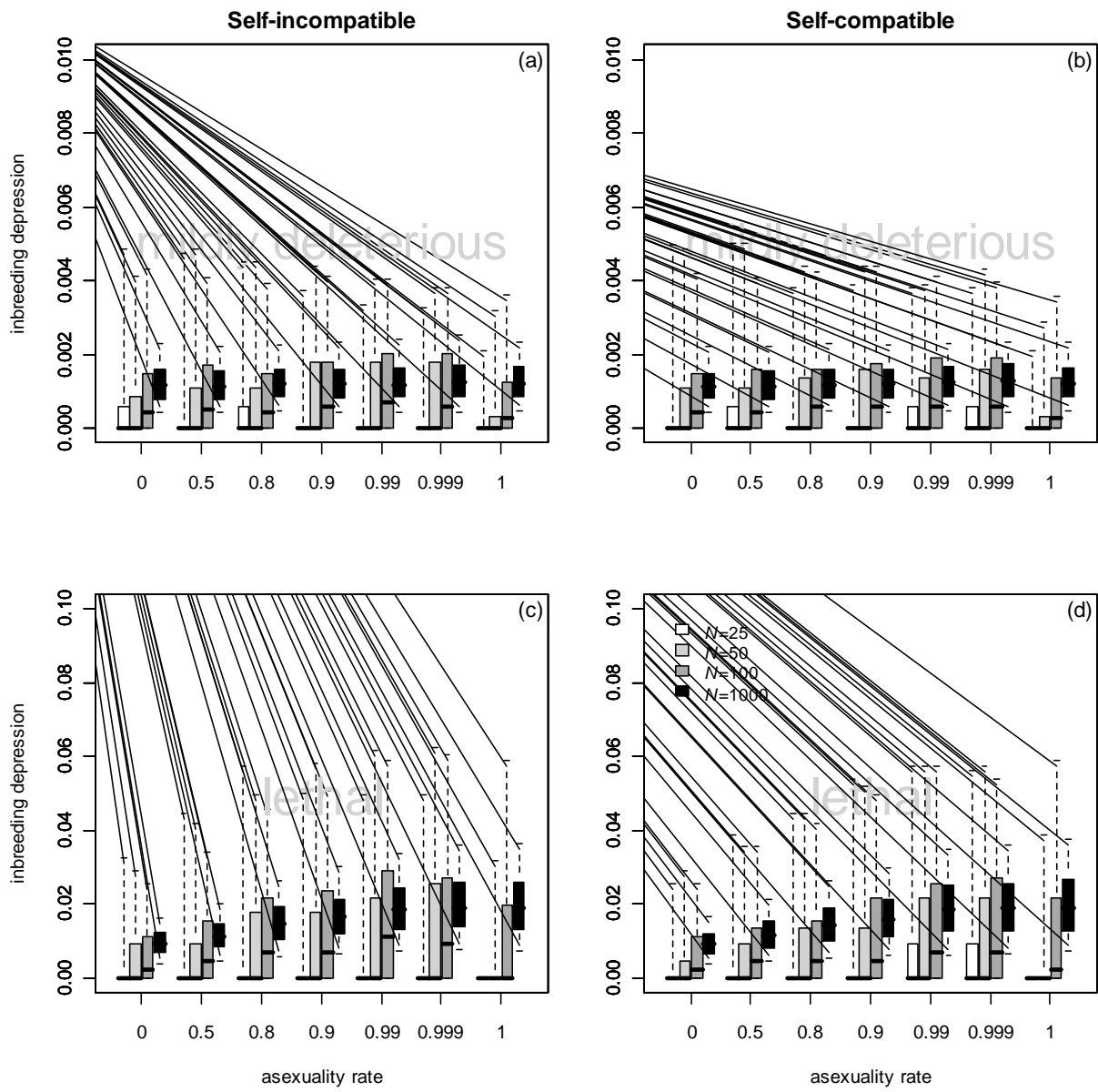
668 **Figure 5**



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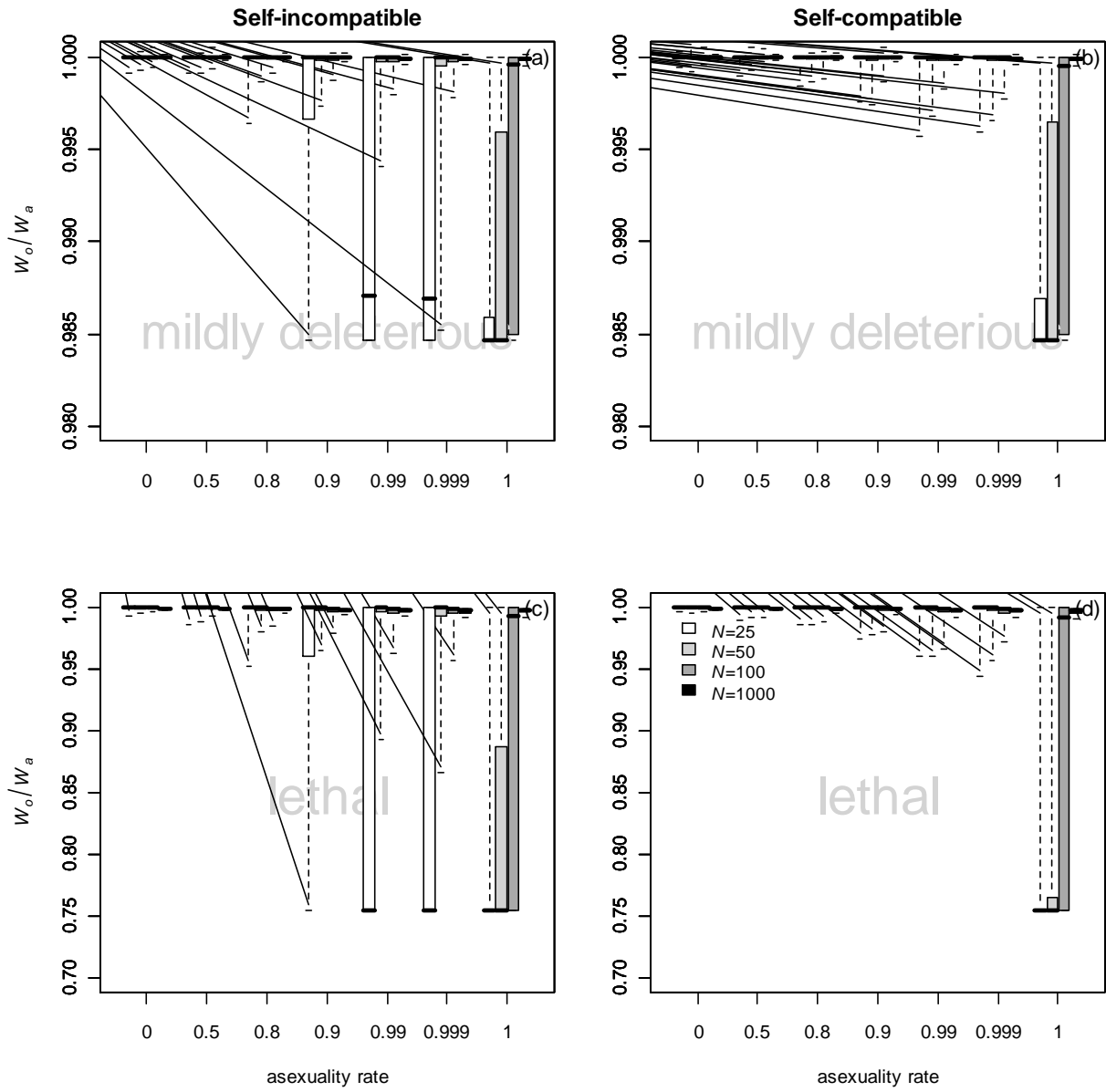
671 **Figure 6**



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674 **Figure 7**



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