

1 **Social learning by mate-choice copying increases dispersal and reduces**
2 **local adaptation**

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4 Manuel Sapage,^{1,5} Susana A. M. Varela^{1,2,3,6} & Hanna Kokko^{4,7}

5 ¹ *cE3c—Centre for Ecology, Evolution and Environmental Changes, Faculdade de Ciências,*
6 *Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal.*

7 ² *Instituto Gulbenkian de Ciência, 2780-156 Oeiras, Portugal.*

8 ³ *ISPA – Instituto Universitário, 1149-041 Lisboa, Portugal.*

9 ⁴ *Department of Evolutionary Biology and Environmental Studies, University of Zurich, Zurich,*
10 *Switzerland.*

11 ⁵ *Email: masapage@fc.ul.pt*

12 ⁶ *Email: smvarela@igc.gulbenkian.pt*

13 ⁷ *Email: hanna.kokko@ieu.uzh.ch*

14

15 **Corresponding Author**

16 **Name:** Manuel António Pinto Sapage

17 **Mailing Address:** cE3c—Centre for Ecology, Evolution and Environmental Changes, Faculdade de
18 Ciências, Universidade de Lisboa, Campo Grande, 1749-016 Lisboa, Portugal.

19 **E-mail:** masapage@fc.ul.pt

20

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33 **Statement of authorship**

34 All authors helped to conceive the problem and contributed to the design of the study. MS
35 wrote the code to the mathematical model, ran the simulations, analysed the data, and wrote the first
36 draft of the manuscript. All authors contributed substantially to the writing.

38 **Data accessibility statement**

39 Data deposited in the Dryad Digital Repository: <https://doi.org/10.5061/dryad.dncjsxkz1>, (Sapage *et.*
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42 **Abstract**

- 43 1. In heterogeneous environments, dispersal may be hampered not only by direct costs, but also
44 because immigrants may be locally maladapted. While maladaptation affects both sexes, this cost
45 may be modulated in females if they express mate preferences that are either adaptive or
46 maladaptive in the new local population.
- 47 2. Dispersal costs under local adaptation may be mitigated if it is possible to switch to expressing
48 traits of locally adapted residents. In a sexual selection context, immigrant females may learn to
49 mate with locally favoured males. Mate-choice copying is a type of social learning, where

50 individuals, usually females, update their mating preferences after observing others mate. If it
51 allows immigrant females to switch from maladapted to locally adapted preferences, their dispersal
52 costs are mitigated as mate choice helps them create locally adapted offspring.

53 3. To study if copying can promote the evolution of dispersal, we created an individual-based model
54 to simulate the coevolution of four traits: copying, dispersal, a trait relevant for local adaptation,
55 and female preference. We contrast two scenarios with copying — either unconditional, or
56 conditional such that only dispersers copy — with a control scenario that lacks any copying.

57 4. We show copying to lead to higher dispersal, especially if copying is conditionally expressed. This
58 leads to an increase in gene flow between patches and, consequently, a decrease in local adaptation
59 and trait-preference correlations.

60 5. While our study is phrased with female preference as the learned trait, one may generally expect
61 social learning to mitigate dispersal costs, with consequent feedback effects on the spatial
62 dynamics of adaptation.

63

64 **Keywords:** mate-choice copying, dispersal, sexual selection, individual-based simulations, spatial
65 dynamics, local adaptation, lek paradox

66 **Introduction**

67 Mate-choice decisions may be based on innate preferences, individual experience, or on the
68 observed choices of others. The last of these, mate-choice copying, is a type of social learning that
69 involves updating mate preferences after observing others' choices (Wade & Pruett-Jones 1990;
70 Dugatkin 1992, 1996; Pruett-Jones 1992). Females may prefer either the successful males themselves
71 (Bowers *et al.* 2012), or generalize their preferences to males with similar phenotypes (“trait copying”
72 or “mate-choice copying generalization”, (Brooks 1998; White & Galef Jr 2000; Witte & Noltemeier
73 2002; Godin *et al.* 2005; Swaddle *et al.* 2005; Drullion & Dubois 2008; Mery *et al.* 2009; Bowers *et*
74 *al.* 2012).

75 Mate-choice copying (synonymous with ‘mate copying’, Danchin *et al.* 2020) is documented
76 in many taxa (Jones & DuVal 2019; Davies *et al.* 2020), e.g. birds (Swaddle *et al.* 2005; Kniel *et al.*
77 2017), fish (Dugatkin & Godin 1992; Schlupp & Ryan 1997; Witte & Ryan 1998; Heubel *et al.* 2008),
78 mammals (Galef *et al.* 2008; Kavaliers *et al.* 2017), insects (Mery *et al.* 2009; Dagaëff *et al.* 2016;
79 Germain *et al.* 2016; Monier *et al.* 2018) and spiders (Fowler-Finn *et al.* 2015). Empirical studies
80 typically test whether copying occurs in a species or aim to evaluate conditions that make copying
81 favoured over innate preferences. Theoretical studies have complemented the picture by exploring
82 when copying is expected to invade and spread (Losey *et al.* 1986; Pruett-Jones 1992; Servedio &
83 Kirkpatrick 1996; Stöhr 1998; Dubois *et al.* 2012; Santos *et al.* 2017) and how copying affects the
84 direction and strength of sexual selection (Kirkpatrick 1982; Agrawal 2001; Santos *et al.* 2014).

85 Mate-choice copying is argued to be adaptive because it allows the female to mate with higher
86 quality mates (Gibson & Höglund 1992; Nordell & Valone 1998; Valone & Templeton 2002; Danchin
87 *et al.* 2004; Dugatkin 2005; Uehara *et al.* 2005; Wagner & Danchin 2010; reviews Vakirtzis & Roberts
88 2012, Varela *et al.* 2018). But this yields another question: why is copying needed to achieve a good
89 outcome, i.e. why should any female not already possess preferences for best traits? If temporal
90 changes are fast, i.e. the best mate for a given female varies through time (Ingleby *et al.* 2010), females

91 might need updated information regarding better adapted (Getty 2014; Wade 2014) and/or more
92 popular males (Kokko *et al.* 2007). Theoretical work that focuses on the ‘informedness’ of individuals
93 has, indeed, considered age effects. Young females are conceivably inexperienced, and although they
94 may possess innate preferences, observing and copying experienced females’ behaviour can be of
95 benefit; still, it is not always clear why informedness should increase with age, i.e. why innate
96 preferences are insufficient. Older and experienced females may also opt for mate-choice copying if,
97 for example, their previous breeding attempt failed (Amlacher & Dugatkin 2005; Hill & Ryan 2006;
98 Danchin *et al.* 2008). In both cases, the probability of copying is argued to increase with the difficulty
99 of the discrimination task (Nordell & Valone 1998).

100 Irrespective of age and experience, some individuals may be poorly informed in settings where
101 spatial variation in environmental demands combines with local adaptation and gene flow (Holman &
102 Kokko 2014). Here, immigrant females may be uninformed of locally best traits. We show that this
103 creates population-level feedback where mate-choice copying may facilitate the evolution of dispersal
104 itself.

105 The reasoning is the following. Migrants experience an additional cost of dispersal when there
106 is spatial variation in the environment (Blanquart & Gandon 2014; Berdahl *et al.* 2015), because their
107 traits are shaped by past selection in their natal environment, with unknown (and likely worse)
108 performance in the environment they disperse to. For females, an additional complication is that their
109 mate preferences — if genetically determined — may be similarly shaped by past selection. If
110 preferences (and not just traits) are locally adapted, immigrant females may mate suboptimally. This
111 problem can be minimized through copying, assuming that dispersal is not so strong that immigrants
112 swamp locally adapted females, which would lead to uninformed immigrants copying each other’s
113 choices. Copying thus allows immigrant-origin lineages gain locally adapted alleles and reduces the
114 costs of dispersal. As we show below, it also ultimately reduces the degree of local adaptation via
115 improved gene flow (reduction of genetic differentiation between different habitats).

116

117 **Material and methods**

118 We model populations of obligately sexual, haploid populations (which allows us to model one
119 allele per locus, as our focus is not on effects of genetic dominance, see Kokko 2007), initialized in a
120 locally adapted state with only short-distance dispersal (a negative exponential dispersal kernel with a
121 low mean). We thereafter allow the dispersal kernel to evolve in populations with or without a mate-
122 choice copying locus. This locus, if present, has two alleles *c* (for innate preference) and *C* (for
123 copying), only expressed in females. We contrast three scenarios. In the *unconditional* scenario,
124 females with the *C* allele copy the mate choice of others at every copying opportunity; in the
125 *conditional* scenario, they only do so if they have emigrated from their natal patch. In the *control*
126 scenario, females only express innate preferences (no mate choice copying evolves), while dispersal
127 still evolves.

128 The population inhabits a toroid world (a doughnut-shaped continuous surface, each side
129 having length 1). The benefit of using a toroid world is to avoid the need to specify what happens if
130 individuals encounter the edge of the modelled world; under toroid assumptions, they can always
131 continue moving in any direction even if the world is finite. The world is divided into 25^2 patches with
132 environmental heterogeneity that translates into a spatially varying and positively autocorrelated
133 optimum for individuals' trait values (note that we include spatial but not temporal variation of the
134 environment). Positive spatial autocorrelation ensures that neighbouring patches do not differ very
135 strongly from each other (details described in Step 1 below); in other words, it allows the scale of
136 environmental variation to be broader than a single patch. This is of benefit since broadly similar
137 conditions across several patches, combined with finite dispersal distances, allows local adaptation to
138 proceed and overcome the effects of drift — even if local patches (demes) themselves are kept small
139 for the sake of realistic mate choice (females do not evaluate very many males before mating, Roff &
140 Fairbairn 2014; see below).

141 We model genotypes with five different loci (S, T, P, C, D), some of which have sex-limited
142 expression. The S locus determines sex, with alleles 0 (for females) and 1 (for males). The T locus (T
143 stands for *trait*) has a pleiotropic effect. In both males and females, its value (real number between 0
144 and 1) relative to an environmental (spatially varying) optimum determines viability; in males, it
145 additionally codes for a phenotype directly observable to females. The P locus likewise takes allelic
146 values between 0 and 1 but is only expressed in females; it specifies a preference for specific
147 phenotypes of males. Females prefer males whose trait locus matches the female's preference locus,
148 which allows females to show local adaptation for locally adapted male traits. The C locus, with 2
149 alleles c and C, is likewise only expressed in females and controls female copying behaviour. Finally,
150 the D locus, expressed in all individuals, determines the mean of the individual's dispersal kernel, with
151 values between 0 and 1 (where 1 would imply a mean distance equal to the length of the entire world).

152 Each run of the simulation proceeds as follows: (1) creation of the patch-specific environmental
153 values, (2) population initialization, (3) survival, (4) dispersal, (5) mate choice by females, and (6)
154 reproduction. The simulation starts following steps 1 through 6, thereafter repeating steps 3 through 6
155 for each generation. Note that the order of the events dictates that viability selection is applied at the
156 natal patch. Generations are non-overlapping.

157 In step 1, to simulate environmental heterogeneity, an environmental value is attributed to each
158 patch using the algorithm described in Holman & Kokko (2014) that creates a matrix of environmental
159 values with an adjustable spatial autocorrelation. The algorithm first generates a random value between
160 0 and 1 for each patch, then, for $25^2 \times 100$ iterations (a large enough number so that each patch, on
161 average, experiences 100 impacts), it updates a randomly chosen patch p by setting its environmental
162 value E_p to $\mu_p + r(1 - \beta)$, where μ_p is the mean environmental value of the eight patches surrounding
163 patch p . These successive iterations bring the autocorrelation between neighbouring patches to a level
164 that is controlled by the parameter β ($0 \leq \beta < 1$). $\beta = 0$ implies there is no spatial autocorrelation, and
165 when $\beta \approx 1$, neighbouring patches are very similar to each other. After all iterations, the resulting

166 matrices were rescaled to have mean environmental value 0.5 and standard deviation 0.2 (see figure
167 S1 in Supporting Information for examples).

168 In step 2, we give 20000 young individuals random coordinates $0 \leq x, y < 1$. The sex of each
169 individual is randomly chosen (S locus is randomized to be 0 or 1), and we assume initial local
170 adaptation with the following procedure. Values for T and P alleles are drawn randomly from a
171 Gaussian distribution with mean E_p (where p is the patch that the individual's coordinates imply it
172 resides in) and standard deviation 0.05. Values that fall below 0 or exceed 1 are given a value of 0 or
173 1, respectively. Mate-choice copying is initially absent, i.e. all individuals are initialized with the c
174 allele at the copying locus; C alleles are introduced later via mutation (see below). For the dispersal-
175 determining D locus, individuals are initialized with random values drawn from a uniform distribution
176 ranging between 0 and 0.005.

177 Viability selection (step 3) is applied in a density-dependent manner. At most 16 individuals
178 survive in each patch. The value is chosen to allow each female to observe a low number of males and
179 females (we expect patches to contain close to 8 females and 8 males; in nature, examples of more
180 than 10 males sampled before mating appear rare, Roff & Fairbairn 2014), and also to produce a global
181 population of maximally 10000 adults. No viability selection occurs in patches containing up to 16
182 individuals. In patches with more than 16 individuals, we first compute an adaptedness value for each
183 individual i in patch p :

$$184 \quad v_{Ai} = e^{-S_N(a_{Ti} - E_p)^2}, \quad (1)$$

185 where $S_N > 0$ scales the strength of natural selection and a_{Ti} is the allele value of individual i at the T
186 locus. This expression is close to 1 when the difference between a_{Ti} and E_p is small, indicating little
187 mismatch between the phenotype and the environment, and declines at a rate controlled by S_N as the
188 mismatch increases. Actual survival probability depends on v_{Ai} relative to competitors, and to generate
189 stochasticity that allows mild differences in individual v_{Ai} to translate to different rank orders when
190 competing for the 16 survival 'slots', we compute the relative success v_{Ai}^* for individual i by drawing

191 from an exponential distribution with mean v_{Ai} . At each generation, the 16 individuals with the highest
192 v_A^* of each patch are retained, while the others die.

193 In step 4, dispersal distances are drawn for each individual from a negative exponential
194 distribution with a mean equal to the allelic value at the D locus. The direction of dispersal is random.
195 The toroid arrangement of the patches ensures that the dispersal kernel can be applied even if dispersal
196 distances exceed 1, the width of the world. More importantly (given that very long-distance dispersal
197 is unlikely), short dispersal distances may mean not leaving the natal patch; coordinates are still
198 updated, but the environmental value that the individual experiences does not change. We apply
199 dispersal mortality of 0.05 to each individual whose new coordinates bring it outside its natal patch.

200 In step 5 (mate choice), females only perceive males who reside in the same patch as potential
201 mates. Females only mate once; males may mate multiply. While we impose no restrictions on male
202 mating capacity, their realized success is limited by the fact that males can only be chosen by females
203 residing in the same patch. Within each patch, non-copier females mate first, after which copier
204 females choose mates based on observations of all non-copier females' matings. There are three
205 categories of non-copyers: (i) all females with the c allele, (ii) females with a C allele who have not left
206 their natal patch in the conditional scenario, and (iii) females who attempt to copy but their patch offers
207 no non-copier female whose behaviour they could observe. Non-copier females (of any category)
208 observe all the males in their patch and preferentially mate with a male whose value at the T locus is
209 close to the female's value at her P locus. Specifically, each non-copier female f assigns a preference
210 value v_{Pfm} for each male m according to the equation

$$211 \quad v_{Pfm} = e^{-S_S(a_{Pf} - a_{Tm})^2}, \quad (2)$$

212 where $S_S \geq 0$ scales the strength of sexual selection that female choice can impose on males, a_{Pf} is the
213 female's allelic value at the P locus, and a_{Tm} is the male's allelic value at the T locus. The expression
214 reaches its highest possible value, 1, when the male trait perfectly matches the female's preference,

215 and declines towards zero for increasing levels of mismatch. The probability that female f chooses
 216 male m^* in the presence of other competitors is

$$217 \quad \text{Prob}(f, m^*) = \frac{v_{Pfm^*}}{\sum_{m=1}^{M_p} (v_{Pfm})}, \quad (3)$$

218 where M_p is the number of males in patch p .

219 A higher value of S_s means that females are choosier, i.e. realized matings more closely match
 220 their innate preferences. Values at the P locus do not modulate the strength of preferences, but instead
 221 indicate which phenotypes of males are preferred by each female. If $S_s = 0$, mating is random, i.e.
 222 values at the P locus do not impact realized mate choice.

223 While non-copier females choose, copier females observe. We assume trait-based mate-choice
 224 copying (Danchin *et al.* 2018), i.e., copying females update their preferences for certain phenotypes
 225 rather than specific males (thus a male with zero success so far can become favoured should he be
 226 phenotypically similar to a male observed to mate). If choices made by non-copier females yield a
 227 single winner among the males, copier females replace, phenotypically, their innate preferences with
 228 a value that equals the T of this winner: $a_{Pf}^* = a_{Tm^{**}}$, where m^{**} is the identity of the winner. In case
 229 of a tie, one of the males is randomly chosen to be the winner, independently so for each of the copier
 230 females.

231 A copier female f then assigns the value v_{Pfm} to each male m analogously to the non-copier
 232 case above,

$$233 \quad v_{Pfm} = e^{-S_s(a_{Pf}^* - a_{Tm})^2}, \quad (4)$$

234 and the actual choice of a mate follows eqn. 3 above.

235 In step 6, reproduction occurs in all patches with at least one male and one female. These
 236 patches produce 32 offspring each. Each offspring has a mother and a father. The mother is chosen
 237 randomly (as we assume no fecundity differences among females), and the sire is the mother's chosen
 238 mate as determined above. Breeding is density dependent with these assumptions: a female breeding

239 in patch with a total of F_p females present will produce, on average, $32/F_p$ offspring. The expected
240 number of offspring produced by a focal male is $32/F_p$ times the number of females who chose this
241 male. Density dependence is relevant as it causes selection for dispersal to avoid competing with kin
242 (Hamilton & May 1977; Li & Kokko 2019). Offspring are initially placed at in the same coordinates
243 as their mothers.

244 For each locus, offspring inherit one allele, randomly chosen from either parent, without any
245 linkage between loci. The T, P, and D loci have a mutation probability of 0.01. Mutation is
246 implemented by adding, to the original allelic value, a random value drawn from a Gaussian
247 distribution with mean 0 and standard deviation 0.05, 0.05 or 0.005 for T, P and D loci, respectively.
248 Post-mutation allelic values below 0 or above 1 are assigned the value of 0 or 1, respectively. For the
249 biallelic mate-choice copying allele, a mutation changes the value of the allele from c to C and *vice*
250 *versa*, and the mutation probability was time-dependent: it was first set to zero for a burn-in period of
251 7500 generations (such that C individuals remain absent), and to 0.001 thereafter, except for the control
252 scenario (which never permits mate choice copying). The ‘burning in’ phase of 7500 generations
253 allows for all other loci to evolve to equilibrium values, and for dispersal specifically to show a balance
254 between avoidance of kin competition on the one hand and avoidance of dispersal costs (direct and
255 indirect) on the other.

256 After breeding, all adults die, and the offspring experience viability selection as described
257 above. Each simulation was run for 15000 generations, 20 times for each parameter value of S_S (taking
258 the values of 0, 25, 50, 75, and 100) and for each scenario (control, unconditional and conditional).
259 From generation 7500 onwards, we recorded the genotype and coordinates of all individuals every
260 2500 generations. This census was performed after the dispersal step and its associated mortality.

261 To understand the impact of mate-choice copying on local adaptation, we created a local
262 adaptation score (L) for each population. This measure quantifies the degree to which trait values, a_{Tp} ,
263 align with the environmental value in the (E_p) in the breeding patch:

264
$$L = -\frac{\sum_p (a_{Tp} - E_p)^2}{N}, \quad (5)$$

265 where N is the global number of surviving adults after dispersal. The negative sign in eqn. (5) implies
266 that high L corresponds to better local adaptation.

267 We compared mean allelic D values, C allele proportions, the local adaptation score L , and
268 trait-preference correlation coefficients across scenarios using one-way ANOVA tests (among all three
269 scenarios) or Welch two samples t-tests (between the conditional and unconditional scenarios).
270 Pairwise t -tests were used for comparisons of two different time points within populations. Significant
271 differences were followed by a post-hoc Tuckey's honest significance test. To account for multiple
272 testing, we applied Bonferroni corrections so that the corrected p-value = $\min \{n \times p, 1\}$, where p is the
273 original p-value and n the number of hypothesis being tested. This may lead to a higher number of
274 false negatives than other methods (McDonald 2014), thus our conservative approach should provide
275 a strong argument for all significant cases that we find and discuss.

276 The Shapiro-Wilk test of normality revealed that some of our data deviate significantly from
277 normality. Although the tests we employed are robust against deviations from normality, as a
278 precaution, we repeated all the analyses for the significantly non-normal data using nonparametric
279 statistical tests. Since the results were similar, we only report parametric results.

280 The code for the mathematical model (programmed in C, using the GNU Scientific Library,
281 version 2.3, Galassi *et al.* 2009) have been deposited in the Dryad Digital Repository (Sapage *et al.*
282 2020). The statistical analyses were done with R, version 3.6.1 (R Core Team 2019).

283

284 **Results**

285 **1) Presence of mate-choice copying increases dispersal**

286 Scenarios did not differ with respect to dispersal at generation 7500 (all corrected p-
287 values > 0.05 for differences in mean D allele values, table S1), an expected outcome since copying
288 was not yet present in any of the scenarios. The control scenario that continued to lack mate-choice

289 copying in subsequent generations did not show any significant difference in dispersal tendency
290 between generations 7500 and 15000 (all corrected p-values > 0.05 , table S2). In scenarios where the
291 C allele was introduced by allowing mutations to occur from generation 7500 onwards, dispersal
292 experienced a new evolutionary boost followed by reaching a new equilibrium (figure 1), as evidenced
293 by no significant difference when contrasting mean D allele values between generations 12500 and
294 15000 (all corrected p-values > 0.05 , table S2).

295 We only expect differences in dispersal across scenarios if $S_s > 0$: non-random mating is
296 required for copying to mitigate the costs of dispersal that we envisage. Indeed, $S_s = 0$ yielded no
297 differences across scenarios (corrected p-value > 0.05 , table S1) for allelic values of D at generation
298 15000, while differences emerged when $S_s > 0$: most populations with copying evolved significantly
299 higher mean values of D than control populations (figure 1). The exception, which we attribute to a
300 type II error, was the comparison between the conditional and the control scenarios at $S_s = 25$, where
301 the p-value remained marginally above significance (Tuckey HSD $p = 0.05006$).

302

303 **2) If sexual selection is strong, conditional copying increases dispersal more strongly than** 304 **unconditional copying**

305 Significant differences in the mean D allelic value at generation 15000 arose between the
306 conditional and the unconditional copying scenarios, when $S_s \geq 75$ (figure 1). Here, conditional
307 scenarios consistently produced more dispersal.

308

309 **3) Associations of the C allele and high dispersal within a population remain weak**

310 Are the above results driven by (i) C individuals (potential copiers) themselves dispersing at
311 higher rate than individuals with the allele c, or (ii) the presence of C in a population elevating dispersal
312 for everyone? At generation 15000, there was a tendency for C individuals to disperse more than c
313 individuals (in both scenarios where C alleles existed), but the difference was usually too small to be

314 significant (figure 2). Thus, any evidence for a statistical association between C and the allelic value
315 for D remains too weak to favour the first interpretation.

316

317 **4) Unconditional copying only evolves if sexual selection is suitably weak; conditional copying**
318 **does so across a range of strengths of sexual selection**

319 The frequency of the C allele remained constant (did not change significantly) between
320 generations 12500 and 15000 (all corrected p-values > 0.05, table S3), thus the proportion of copiers
321 had reached an equilibrium by generation 12500. In conditional as well as unconditional scenarios,
322 random mating ($S_s = 0$) should make the C allele neutral, and with sufficient time its frequency should
323 reach 0.5. This prediction was supported: the frequency of the C allele not differ significantly from 0.5
324 at generation 15000 (figure 3). Under non-random mating ($S_s > 0$), both scenarios deviated
325 significantly from the neutral expectation, but the effect depended on the strength of sexual selection.
326 At a low value of S_s ($S_s = 25$), the frequency of the copier allele C was elevated more in the
327 unconditional than the conditional scenario and exceeded 0.5 in both cases. This conclusion reversed
328 for $S_s \geq 50$, where unconditional copying led to a significantly lower frequency of the C allele than the
329 conditional scenario, with the former frequencies falling significantly below the neutral expectation
330 0.5 (figure 3).

331

332 **5) Mate choice copying weakens local adaptation and trait-preference correlations**

333 The local adaptation score L showed no significant differences between scenarios in generation
334 7500 (all corrected p-values > 0.05, table S4). As expected, control scenarios without copying also
335 yielded no significant differences in L between generations 7500 and 15000 (all corrected p-
336 values > 0.05, table S5), and L also did not differ between scenarios in generation 15000 under random
337 mating ($S_s = 0$, p-value > 0.05). Differences emerged when mating was non-random, and they became
338 significant once sexual selection was strong: when $S_s \geq 75$, scenarios with copying showed

339 significantly less local adaptation than the control scenario (figure 4a). Whether mate-choice copying
340 operated conditionally or unconditionally did not significantly impact the local adaptation score.

341 To understand the impact of mate-choice copying on the correlation between male traits and
342 female preferences, we calculated Pearson's correlation coefficients for the corresponding alleles.
343 They were not significantly different between scenarios in generation 7500 (all corrected p-
344 values > 0.05 , table S6), control scenarios did not show any significant difference in the correlation
345 coefficient between generations 7500 and 15000 (all corrected p-values > 0.05 , table S7), and the
346 correlation coefficient did not differ between scenarios in generation 15000 when mating was random
347 ($S_S = 0$, corrected p-value > 0.05). Introducing sexual selection ($S_S > 0$) increased these correlations,
348 but the magnitude of this response was scenario-dependent: at generation 15000, control populations
349 showed a significantly higher correlation coefficient than either scenario with mate-choice copying.
350 This was true across all positive values of S_S (figure 4b). The conditional scenario showed a
351 significantly higher correlation coefficient than the unconditional one when sexual selection was weak
352 ($S_S = 25$), but this result was reversed as S_S increased, and the reversed finding became significant for
353 $S_S = 75$ or higher (figure 4b).

354

355 **6) Sexual selection increases the effect of mate-choice copying on dispersal**

356 To investigate whether stronger sexual selection (high S_S) can amplify the effect of mate-choice
357 copying on dispersal, we created a linear model where the response variable was the mean D value at
358 generation 15000 and the predictors were S_S , the scenario, and their interaction. The control scenario
359 was used as the baseline. We also tested a linear model with the explanatory variable S_S transformed
360 to $\log(S_S + 1)$, because of the nonlinearity in eqn. (4); the model with the transformation fitted the data
361 better (AIC calculated by the 'extractAIC' function from the R statistical software (Venables & Ripley
362 2002), without transformation: -4312 ; with transformation: -4393). Diagnostic plots did not show any
363 major deviation from model assumptions. According to this model, when $\log(S_S + 1) = 0$ (i.e., $S_S = 0$),

364 mean dispersal did not differ between control populations and unconditionally copying populations
365 (allelic values for D; difference estimate: -2.40×10^{-4} ; $t = -1.12$; $p = 0.233$), but both were
366 significantly higher than dispersal in conditionally copying populations (difference estimate: $-$
367 4.24×10^{-4} ; $t = -2.11$; $p = 0.035$). Given that all populations should evolve identically under random
368 mating, and the previous results showed no significant difference between populations in this case
369 (figure 1), we regarded this particular result as an artefact of a model fit that is predominantly impacted
370 by the evolutionary responses to higher values of S_S .

371 The linear model shows S_S to increase dispersal in all scenarios. An increase of one $\log(S_S + 1)$
372 unit creates a significant increase of 1.96×10^{-4} in the mean allelic value of D in control populations
373 lacking copying ($t = 5.02$; $p < 0.001$), with an additional significant increase of 3.14×10^{-4} in the
374 unconditional copying scenario ($t = 5.677$; $p < 0.001$) and an additional significant increase of
375 5.38×10^{-4} in the conditional copying scenario ($t = 9.756$; $p < 0.001$). Overall, the dispersal-enhancing
376 effect of sexual selection is significantly strengthened by mate-choice copying, and it reaches its
377 maximum effect if copying is conditional on dispersal.

378

379 **Discussion**

380 Results show that mate-choice copying increases dispersal, especially when females are
381 choosier (sexual selection is stronger). Dispersal, in turn, has knock-on effects on gene flow and local
382 adaptation. Gene flow becomes stronger, and local adaptation becomes weaker, when immigrant
383 females can compensate for lack of local knowledge by copying the choices of others. Mate-choice
384 copying also decreased the correlation between the male trait and the female preference alleles. These
385 phenomena, taken together, counteract the depletion of male trait genetic variation by persistent innate
386 female preferences.

387 The evolution of mate-choice copying can be hampered when innate female preferences
388 coevolve with the male trait (Servedio & Kirkpatrick 1996; Santos *et al.* 2017), raising the question of

389 how sufficient variation in preferences can be maintained for a female to have any reason to switch
390 from her innate to an observed preference (in the absence of variation, a switch should never be
391 worthwhile). In their population-genetic models, Servedio & Kirkpatrick (1996) maintained the
392 polymorphism in preferences by mutation, while Santos *et al.* (2017) did so by randomly distributing
393 the preference locus each generation. In our case, environmental heterogeneity was the responsible
394 factor. Our finding that mate-choice copying can spread, but that it can also make local populations
395 less well adapted, is a novel twist on the idea that local adaptation of both traits and preferences,
396 combined with dispersal, can maintain a persistent supply of locally acting selection gradients (thus
397 helping to make the so-called lek paradox disappear, (Holman & Kokko 2014).

398 Sexual selection can be switched off in our model by assuming random mating. Dispersal
399 evolves to be low in such a setting. Complete philopatry still does not evolve as it would make
400 individuals compete for breeding resources (females) or matings (males) with close kin (Li & Kokko
401 2019), but dispersal mortality, as well as the risk of being maladapted to faraway parts of the landscape,
402 keeps dispersal rates low. Sexual selection can make this latter cost smaller, but this only works if
403 dispersing females subsequently mate with locally adapted males (and not, e.g., with males who are
404 themselves maladapted immigrants). Dispersal readily responds to this cost reduction, and evolves to
405 be higher, when the option of mate-choice copying is available. Copying allows choosy females to
406 express a different phenotype than her P locus would dictate. An immigrant female's offspring will
407 therefore, all else being equal, be better locally adapted than in the absence of mate-choice copying.
408 However, we also show that all else is not equal: when the evolutionary process with mate-choice
409 copying involves higher dispersal, this also improves gene flow and reduces local adaptation in the
410 global population as a whole.

411 Dispersal was particularly enhanced if mate-choice copying was conditionally expressed by
412 females who had dispersed, confirming the intuitive prediction that copying is best performed in
413 unfamiliar surroundings. For philopatric females, copying may lead to counterproductive updating of

414 preferences to those of immigrants, whose preferences have been shaped by selection elsewhere;
415 expressing one's own innate preferences may then be favoured. Conditional copying, then, appears the
416 superior way to alleviate the local adaptation cost of dispersal; it accordingly produces a more robust
417 feedback between copying and dispersal across different strengths of sexual selection, compared with
418 unconditional copying. This result is in line with earlier findings that indiscriminate copying can be
419 maladaptive (Dubois *et al.* 2012; see also Kendal *et al.* 2018). We are unaware of empirical studies
420 documenting differences in copying behaviour between immigrants and philopatric females; such
421 plasticity appears worth looking for.

422 Our results do not rely on assortative mating or other processes (e.g. physical linkage) creating
423 a statistical association between the C allele (copying) and the D allele (dispersal). While, in principle,
424 only high-D individuals 'need' the C allele (assuming philopatric individuals should not copy), such
425 associations remain weak at the genetic level. This does not strictly exclude any possibility for linkage
426 disequilibria: an immigrant non-copier would presumably mate non-ideally and thus high-D combined
427 with c would be selected against at the stage when her offspring viabilities are tested. But as her choices
428 are blind with respect to the dispersal status or (unexpressed) C locus of the sire, any effects here
429 remain weak. Instead, it appears that a high frequency of C in a population facilitates high D mainly
430 via (i) an overall expectation that preference updating is frequently an option for individuals in a
431 lineage (all female offspring who have inherited C from the mother or from the father can do so), and
432 (ii) a reduction of the overall importance of local adaptation. The latter is a general finding in the
433 literature on local adaptation and dispersal: once dispersal is relatively frequent, the costs of settling
434 in a new location are reduced, because recurrent gene flow prevents strong local adaptation in the first
435 place (Blanquart & Gandon 2011; Berdahl *et al.* 2015). Our contribution is to show that mate-choice
436 copying can amplify this effect quite substantially.

437 Note that the C allele in our model only experienced indirect selection, via its effects on the
438 identity of a female's chosen mate. Earlier population genetic work has investigated both direct and

439 indirect selection on copying (Servedio & Kirkpatrick 1996; Santos *et al.* 2017). Direct selection,
440 which we ignore, could either favour or disfavour copying: copying might help reduce the time and
441 energy costs of assessing male quality, or there may be mild costs inherent to the copying process itself
442 (e.g. costs of learning) or pleiotropic effects (Servedio & Kirkpatrick 1996). While our chosen focus
443 on the coevolution of copying and dispersal (via local adaptation) made us leave direct costs outside
444 our study, it is intuitively clear that copying may reach higher frequencies than reported by us if it also
445 helps to avoid direct costs.

446 Our contrasts between different scenarios were run in parallel, without the conditional strategy
447 directly competing with the unconditional one. Even so, it is still useful to reflect whether the
448 differences in the evolved frequencies of the C allele are a measure of ‘success’ of a certain kind of
449 copying strategy. Usually, high frequencies of C associate with conditional expression, but an
450 exception is found at weak sexual selection ($S_s = 25$), potentially explicable as a result of the quite
451 variable realized matings at low value of S_s (Box 1). Matings are in this case impacted by stochasticity,
452 whether the choices follow innate preferences or updated (copied) ones; the net effect is that non-
453 copier females may lose to copier females (in terms of mate quality) particularly when S_s is low (Box
454 1). Given that females with a C allele are much more likely to be copiers in the unconditional scenario
455 than in the conditional one, the situation described by Box 1 arises more often in the unconditional
456 scenario. This provides new insight into the debate (Nordell & Valone 1998; Giraldeau *et al.* 2002;
457 Vakirtzis 2011; Witte *et al.* 2015; Kendal *et al.* 2018; Varela *et al.* 2018) regarding the conditions
458 under which mate-choice copying can be adaptive.

459 Note that although the model has many parameters, it simultaneously presents a simplified
460 view of dispersal and mate-choice copying in a heterogeneous environment. For example, we modelled
461 dispersal as a simple exponential kernel, ignoring e.g. sex-biased dispersal (Li & Kokko 2019),
462 dispersal kernels with flexibilities offered by more than one variable (Chapman *et al.* 2007; Bonte *et*
463 *al.* 2010; Poethke *et al.* 2011; Nathan *et al.* 2012; Tung *et al.* 2018), or any decision-making during

464 dispersal (which can have a strong impact on the kernel in settings with two sexes, Shaw & Kokko
465 2014). Also, to avoid having to specify effects of genetic dominance on several traits, we also chose
466 to investigate haploidy. Dominance relationships between two alleles at a diploid locus can take very
467 many forms when fitness effects also depend on spatial location; we ignored these real-life
468 complications to focus on a minimal genetic setup that permits all the intended feedbacks between
469 mate-choice copying, dispersal, and local adaptation to occur. This obviously leaves avenues for
470 further study.

471 More generally, mate-choice copying is just one example of social learning, which happens to
472 be expressed in a sexual selection context (Verzijden *et al.* 2012; Kendal *et al.* 2018). If there is a need
473 to locally adapt to new conditions after dispersal, and social learning offers a way to acquire a new set
474 of behaviours (Varela *et al.* 2020), then our model's conclusions should generalize to situations where
475 behaviours other than mate choice are learned. The prediction that social learning enhances dispersal
476 appears quite generally applicable — as does its flipside, i.e. local adaptation may become less strong
477 in the long term due to homogenization of traits over the spatial range of a species when learning and
478 dispersal together promote strong gene flow (Varela *et al.* 2018). This finding, should it generalize,
479 could be of importance in cultural evolution as a whole.

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674

675 **Supporting information**

676 Additional supporting information may be found in the online version of this article.

- 677 • Figure S1 Examples of simulated environmental values landscapes for $\beta = 0.99$
- 678 • Table S1 ANOVA comparison of the mean allelic value of D between control, unconditional,
679 and conditional mate-choice copying scenarios at generations 7500 and 15000
- 680 • Table S2 Pairwise t-test comparing the mean allelic value of D between generations 7500 and
681 15000 (control) or 12500 and 15000 (unconditional and conditional)
- 682 • Table S3 Pairwise t-test comparing the proportion of individuals with the C allele between
683 generations 12 500 and 15000
- 684 • Table S4. ANOVA comparison of the local adaptation score (L) between control,
685 unconditional, and conditional scenarios at generations 7500 and 15000
- 686 • Table S5. Pairwise t-test comparing the local adaptation score (L) in the control scenario
687 between generations 7500 and 15000

- 688
- Table S6. ANOVA comparison of the Pearson correlation coefficient between the T and P
- 689 alleles between control, unconditional, and conditional mate-choice copying scenarios at
- 690 generations 7500 and 15000
- Table S7. Pairwise t-test comparing the Pearson correlation coefficient between the T and P
- 691 alleles in the control scenario between generations 7500 and 15000
- 692
- 693

694 **Figures**

695

696 **Figure 1. Mate-choice copying selects for higher dispersal.** Line plots: evolution of D for each
697 sexual selection strength (S_s) as indicated in the plot and mate-choice copying scenario (“control”,
698 “unconditional”, and “conditional” as indicated by colour). Lines depict the means (across 20
699 simulation runs) of (population-wide) D and the standard deviations of the means (shading); the
700 vertical line denotes the generation at which mutation towards copying is introduced, and the
701 coevolution with dispersal begins. Box plot: distribution of D at generation 15000. Thick lines depict
702 the medians of the distribution of each population’s mean D; box, the 25% and 75% interquartile
703 range; vertical dashed lines, the most extreme values within 1.5 of the interquartile range; opened
704 circles, extreme values outside of this range. Stars indicate pairwise differences between populations
705 within each case (Tuckey HSD test for cases where the ANOVA test with the Bonferroni correction
706 was significant, see Methods). * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Other parameters: $\beta = 0.99$, $S_N =$
707 50.

708

709

710 **Figure 2. Overall, individuals with c and C alleles show no significant differences in dispersal**
711 **across a wide range of values for the strength of sexual selection.** The distribution of the mean
712 allelic value of D at generation 15000 over 20 simulations for each set of parameters, graphed as in
713 figure 1, but separately for individuals with the c or C allele. Significance was calculated using a
714 pairwise t-test: *p < 0.05, ** p < 0.01, *** p < 0.001. Parameters as in figure 1.
715

716 **Figure 3. Unconditional copying evolves when sexual selection is weak, conditional copying**
717 **evolves across a wide range of values for the strength of sexual selection.** Box plot design follows
718 the conventions of figure 1 and 2, with data now giving the proportion of individuals with the C allele
719 at generation 15000 over 20 simulations for each set of parameters. Stars below each box represent
720 significant differences from 0.5 (one sample t-test), stars above give significance for differences
721 between populations with “unconditional” and “conditional” mate-choice copying for identical values
722 of S_s (Welch two sample t-test); for both tests, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Parameters as in
723 figure 1.
724

725 **Figure 4. Mate-choice copying (a) reduces local adaptation when sexual selection is high, and (b)**
726 **weakens trait-preference correlations.** The box plots (design as in figures 1–3) are complemented
727 with stars that indicate statistical significance (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$) of pairwise
728 differences between scenarios at generation 15000 over 20 simulations for each set of parameters
729 (Tukey HSD test, calculated for cases where the ANOVA test with the Bonferroni correction was
730 significant, see details in methods). Parameters as in figure 1.

731

732 **Box 1. Example of the effect of S_S on Mate-choice copying**

733 Consider a case where the environmental value $E_p = 0.5$, and there are three males M_A , M_B , M_C with
734 trait values 0.4, 0.5, and 0.6, respectively.

735 First, assume strong sexual selection, $S_S = 100$, and assume that there is a locally adapted
736 female with a with a value of 0.5 at the P locus. Following equations (2) and (3), she will choose a
737 male with probability $Prob(F_A, M_A) = Prob(F_A, M_C) \approx 0.212$ and $Prob(F_A, M_B) \approx 0.576$. A copier
738 female F_B ignores her innate preferences and updates her preferences to 0.4 if F_A chose M_A , to 0.5 if
739 F_A chose M_B , and to 0.6 if F_A . The actual probabilities of mating, conditional on F_A having chosen M_A ,
740 are $Prob(F_B, M_A | F_A, M_A) \approx 0.721$, $Prob(F_B, M_B | F_A, M_A) \approx 0.265$, $Prob(F_B, M_C | F_A, M_A) \approx 0.013$. The
741 probabilities are similarly calculated for all other choices of female F_A . In the end, the probability of
742 female F_B choosing a less adapted male than F_A did is approximately 0.244, the probability for her to
743 choose an equally adapted male is ≈ 0.643 , and the probability of her choosing a better adapted male
744 is ≈ 0.112 .

745 These probabilities become more ‘egalitarian’ with respect to the two females if there is more
746 randomness in the outcome. Assuming $S_S = 25$, $Prob(F_A, M_A) = Prob(F_A, M_C) \approx 0.305$ and
747 $Prob(F_A, M_B) \approx 0.391$. In this case the probability for female F_B to choose a less adapted male than F_A
748 is still considerable, approximately 0.238, but the probability to choose an equally adapted male is
749 clearly lower than before, 0.541, and the clear increase is in the probability of choosing a better adapted
750 male, ≈ 0.221 .

751

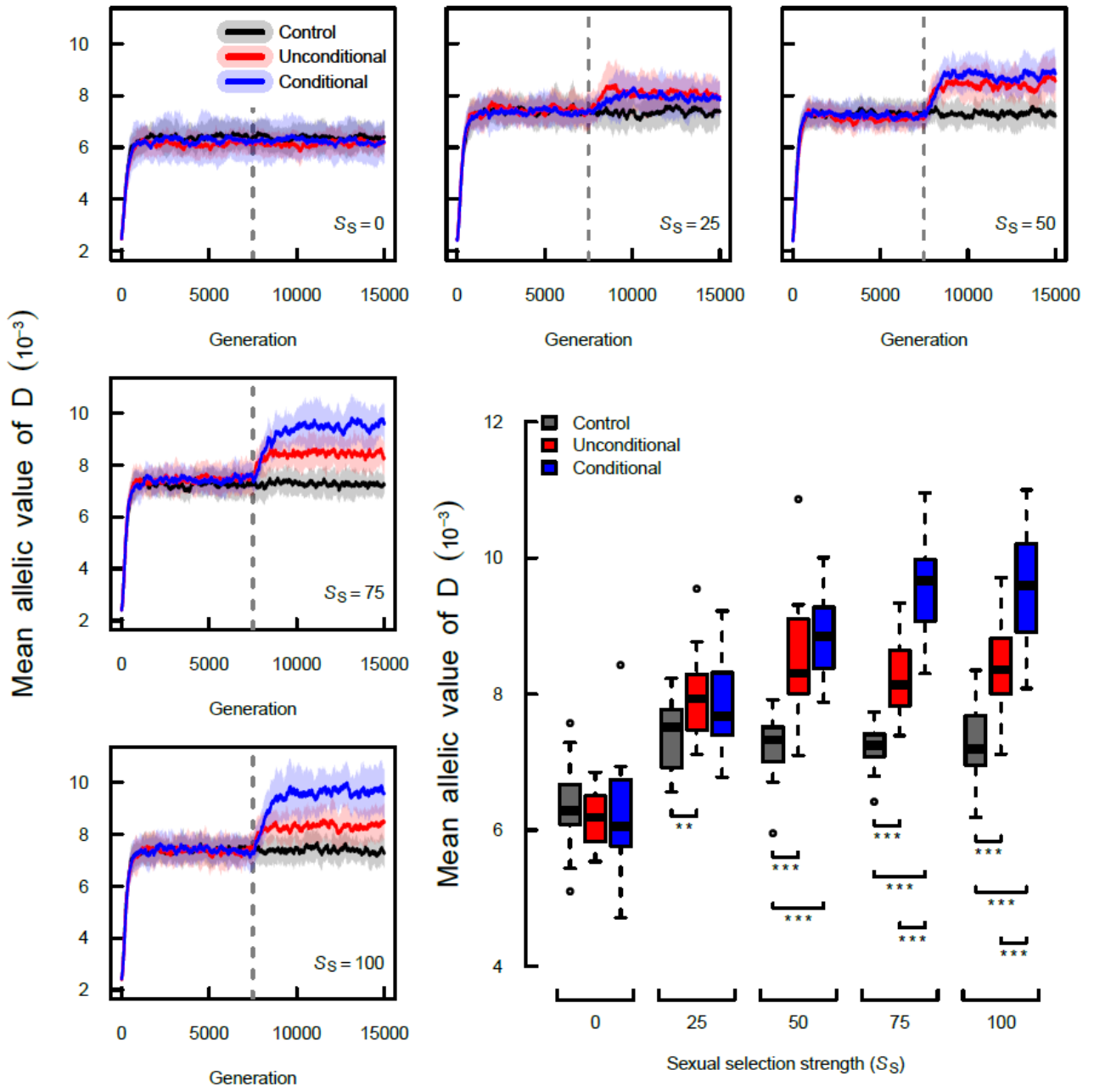


Figure 1

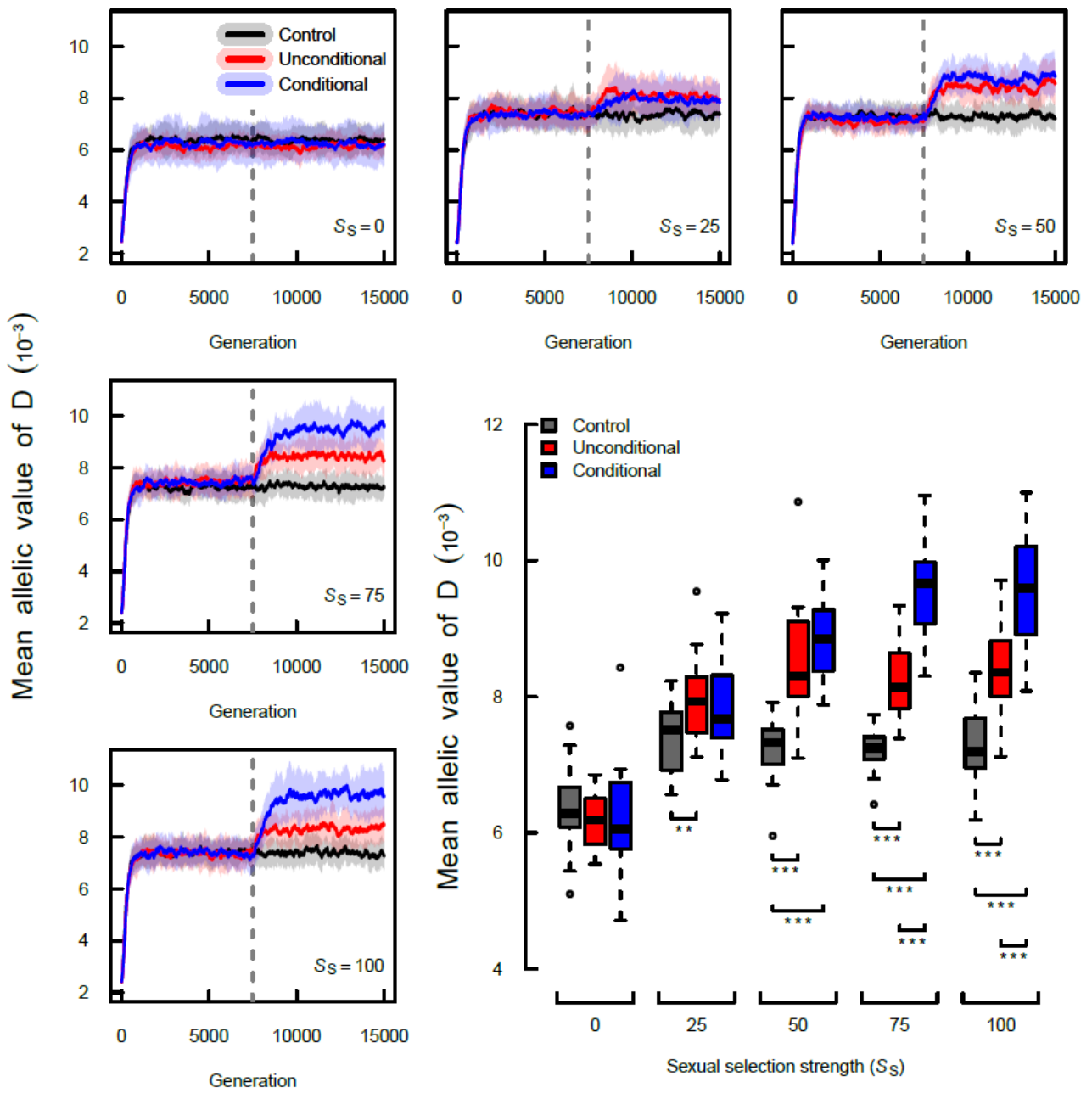
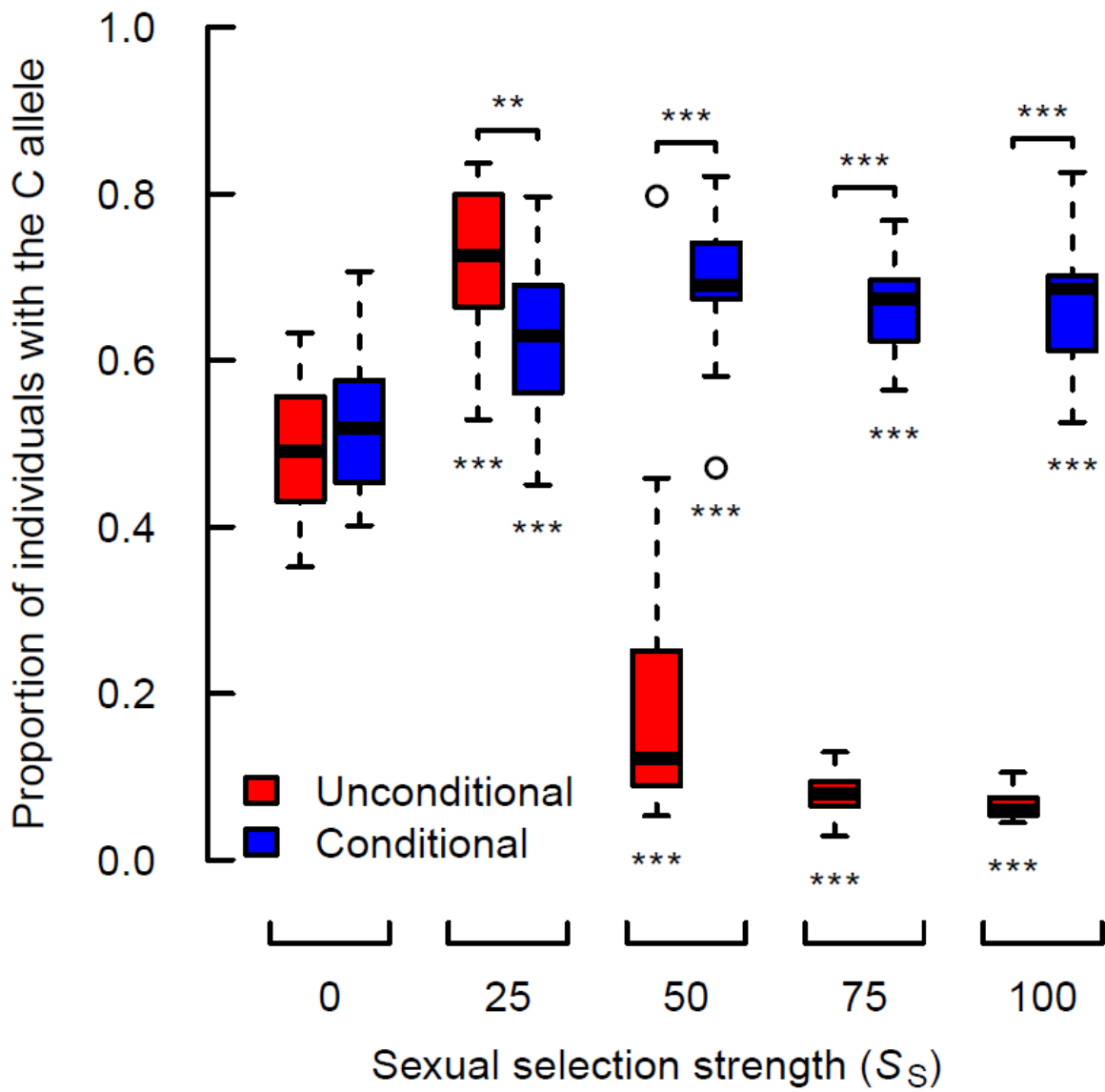
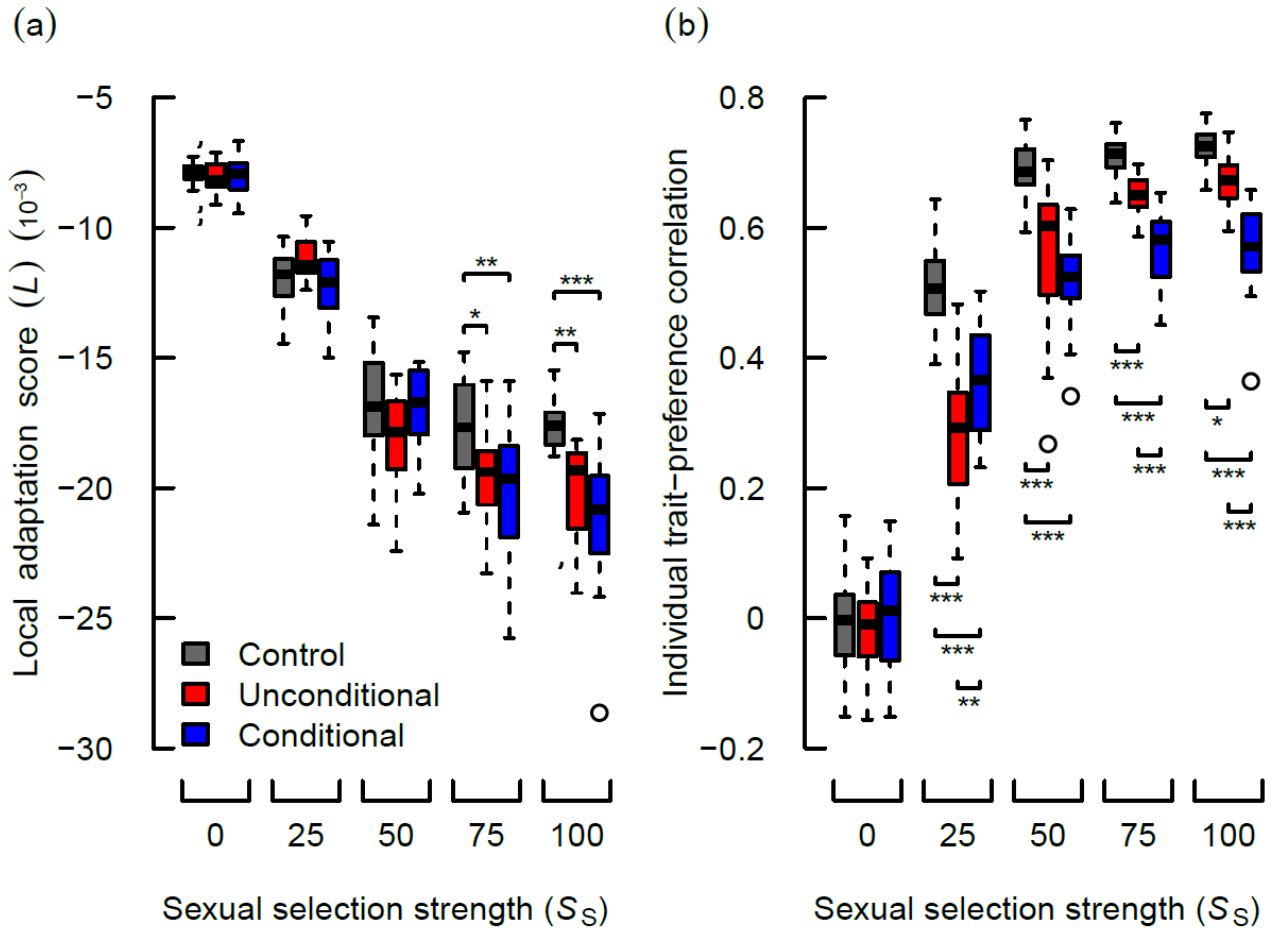


Figure 2



757
 758
 759

Figure 3



760
761

Figure 4