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Interplay between extreme drift and selection intensities favors the fixation of beneficial mutations in selfing maize populations

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ABSTRACT Population and quantitative genetic models provide useful approximations to predict long-term selection responses sustaining phenotypic shifts, and underlying multilocus adaptive dynamics. Valid across a broad range of parameters, their use for understanding the adaptive dynamics of small selfing populations undergoing strong selection intensity (thereafter High Drift-High selection regime, HDHS) remains to be explored. Saclay Divergent Selection Experiments (DSEs) on maize flowering time provide an interesting example of populations evolving under HDHS, with significant selection responses over 20 generations in two directions. We combined experimental data from Saclay DSEs, forward individual-based simulations, and theoretical predictions to dissect the evolutionary mechanisms at play in the observed selection responses. We asked two main questions: How do mutations arise, spread, and reach fixation in populations evolving under HDHS? How does the interplay between drift and selection influence observed phenotypic shifts? We showed that the long-lasting response to selection in small populations is due to the rapid fixation of mutations occurring during the generations of selection. Among fixed mutations, we also found a clear signal of enrichment for beneficial mutations revealing a limited cost of selection. Both environmental stochasticity and variation in selection coefficients likely contributed to exacerbate mutational effects, thereby facilitating selection grasp and fixation of small-effect mutations. Together our results highlight that despite a small number of polymorphic loci expected under HDHS, adaptive variation is continuously fueled by a vast mutational target. We discuss our results in the context of breeding and long-term survival of small selfing populations.

KEYWORDS Truncation selection, Experimental evolution, Adaptive dynamics, Distribution of fitness effects, Selection cost, Effective population size, Environmental stochasticity

Understanding the evolutionary processes sustaining phenotypic shifts is at the core of quantitative genetic models. Empirical description of such shifts takes its roots in the breeding literature where truncation selection generates significant and sustainable responses (Hill and Caballero 1992; Walsh and Lynch 2018). Truncation selection is known to be the most effective form of directional selection (Crow and Kimura 1979). Under truncation selection, limits to the evolution of phenotypes are rarely reached as heritable variation persists through time (Odhambo and Compton 1987; Moose *et al.* 2004; Weber and Diggins

1990; Caballero *et al.* 1991; Mackay 2010; Lillie *et al.* 2019). Such observations fit well with the breeder equation and its derivatives (Lush 1943; Lande 1979; Lande and Arnold 1983) which accurately predict selection response after one generation. With the additional hypothesis of constant genetic variance provided by the Fisher's infinitesimal model (Fisher 1930), theoretical models predict a continuous and linear response with no finite limits. However, the rate of response is expected to decline with selection-induced linkage disequilibrium (Bulmer 1971; Hospital and Chevalet 1996). Furthermore under finite population size, selection response is predicted to reach an asymptotic finite limit (Robertson 1960) as exemplified in mice (Roberts 1967; Falconer 1971). Results from other species are more equivocal (e.g. drosophila (Weber 1990; Weber and Diggins 1990; Weber 1996),

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1 or maize (Odhambo and Compton 1987; Moose *et al.* 2004; Dud- 63
2 ley and Lambert 2010; De Leon and Coors 2002; Lamkey 1992). 64
3 Incorporation of *de novo* mutations indeed predicts a slower rate 65
4 of response instead of a hard limit (Hill 1982b,a; Weber and Dig- 66
5 gins 1990; Wei *et al.* 1996; Walsh and Lynch 2018). A sub-optimal 67
6 average selection response is expected in two situations: when 68
7 population size, N is below 10^4 reducing the genetic variance 69
8 (\widehat{V}_G) at mutation-drift equilibrium (Hill 1982b; Houle 1989); and 70
9 when \widehat{V}_G is reduced due to strong selection (Houle 1989). Over- 71
10 all, quantitative genetic models that include selection, drift and 72
11 mutation (Houle 1989) are well-suited for predicting observed 73
12 selection responses in a broad range of parameters (Hill and Ras- 74
13 bash 1986) — providing appropriate corrections, *e.g.* deviations 75
14 from low drift and low selection intensity (Walsh and Lynch 76
15 2018). Most of these models, however, make the assumptions of 77
16 random mating and of a probability of fixation of new mutations 78
17 — determined by the product of population size by their selection 79
18 coefficient, Ns — to be either $\ll 1$ or $\gg 1$. Mathematical models 80
19 for the intermediate regime $Ns \approx 1$ and non-random mating still 81
20 remain unsatisfactory. Furthermore, the description of mecha- 82
21 nisms of long-term selection response — and whether it can be 83
22 understood and predicted by existing equations — has yet to 84
23 be explored for polygenic traits evolving in small selfing popu- 85
24 lations under high selection intensity, a regime subsequently 86
25 called HDHS (High-Drift High-Selection).

26 Both the Distribution of mutational Fitness Effects (DFE) and 87
27 the mutation rate are central to long-term predictions of selec- 88
28 tion responses. Selection makes the DFE of fixed mutations 89
29 different from that of incoming *de novo* mutations (Kassen and 90
30 Bataillon 2006). In large populations, a high proportion of in- 91
31 coming *de novo* beneficial mutations are predicted to reach fixa- 92
32 tion, together with vanishing small effect deleterious mutations 93
33 (Crow and Kimura 1971; Kimura 1983). In small populations 94
34 and/or at small selection intensity, frequent loss of beneficial 95
35 mutations due to drift together with the fixation of moderately 96
36 strong deleterious mutations is expected. Hence Kimura’s equa-
37 tion that links the fixation probability (P_{fix}) of a mutation to its
38 frequency (p), the population size (N) and selective coefficient
39 (s) — $P_{fix}(s, p, N) = (1 - e^{-4spN}) / (1 - e^{-4sN})$ — applies to a
40 vast range of parameters including s values as high as 0.1 and
41 N as small as 10 individuals (Carr and Nassar 1970). An addi-
42 tional layer of complexity to DFE prediction comes from the
43 mating system. Adaptation of very large asexual populations
44 (such as microbes) is indeed affected by competition between
45 alternative beneficial mutations occurring in different genetic
46 background, a process referred to as clonal interference (Gerrish
47 and Lenski 1998). Here the absence of recombination favors
48 enrichment of the DFE in large beneficial mutational effects (Ger-
49 rish and Lenski 1998). However, if selection overpowers drift,
50 *i.e.* $Ns \gtrsim 1$, or if the rate of beneficial mutation (μ_B) is small
51 enough, the expected time lag between two successive muta-
52 tions is sufficiently large for the first beneficial mutation to fix
53 without interference of the second. While such behavior is ex-
54 pected when $N\mu_B \ll 1/\ln(Ns)$, for $N\mu_B \gtrsim 1/\ln(Ns)$ beneficial
55 mutations evolve under clonal interference (Desai and Fisher
56 2007). Altogether these results highlight how the interplay of
57 key parameters - N , s , μ , effective recombination — determine
58 the DFE and in turn, the long-term selection response.

59 Genomic footprints of selection have considerably enriched 120
60 our vision of allele trajectories sustaining selection responses. On 121
61 the one hand, one can observe genomic footprints such as hard 122
62 and/or soft selective sweeps. A hard sweep is characterized by

a strong decrease in genomic diversity at the selected locus and 63
its surrounding region through genetic hitchhiking (Hermisson 64
and Pennings 2017); while a soft sweep is associated with a weak 65
genomic signature either because recombination on standing 66
variation occurs so that a given advantageous mutation is asso- 67
ciated with multiple haplotypes, or because recurrent *de novo* 68
mutations are associated with multiple haplotypes. Together 69
these footprints indicate that adaptation proceeds through a 70
succession of sweeps at loci encoding the trait. On the other 71
hand, absence of selection footprints is expected under the so- 72
called polygenic selection model (Berg and Coop 2014; Wellen- 73
reuther and Hansson 2016; Walsh and Lynch 2018), that rather 74
posits a collective response at many loci translating into simul- 75
taneous subtle shifts in allele frequencies, in compliance with 76
the infinitesimal model. Whether adaptation proceeds through 77
hard/soft sweeps or polygenic model primarily depends on the 78
population-scaled mutation rate (θ) as well as the number of re- 79
dundant loci that offer alternative ways for adaptation (L) — the 80
mutational target. Adaptation proceeds through hard sweeps 81
for small $\theta \times L (\leq 0.1)$ while polygenic adaptation requires large 82
 $\theta \times L (\geq 100)$ with partial/soft sweeps in between (Messer and 83
Petrov 2013; Höllinger *et al.* 2019). Extension of the hitchhiking 84
model to a locus affecting a quantitative trait with an infinitesi- 85
mal genetic background predicts that, under the hypothesis of a 86
Gaussian fitness function, the fixation of a favorable mutation 87
critically depends on the initial mutation frequency and the dis- 88
tance to the optimum (Chevin and Hospital 2008). Interestingly, 89
while demographic parameters— population size, bottleneck 90
strength — play a relatively small role in the speed of adaptation 91
compared to standing and mutational variance, they change 92
its qualitative outcome. Population bottlenecks diminish the 93
number of segregating beneficial alleles, favoring hard sweeps 94
from *de novo* mutations over soft sweeps from standing variation 95
(Stetter *et al.* 2018). 96

By exploring short-term temporal dynamics of adaptation, 97
experimental evolution has provided further hints into allele 98
frequency changes, and into the extent of polymorphism 99
and competition among beneficial mutations under various 100
drift/selection/recombination regimes. Temporal dynamics are 101
obtained either through pedigree information or time series sam- 102
ples. This last approach, widely used in microorganisms has 103
revealed complex patterns of mutation spreading during the 104
course of adaptation. These include clonal interference, the re- 105
duction of the relative advantage of a beneficial mutation in 106
fit *versus* less fit genotypes (diminishing-return epistasis), and 107
evidence for the same favorable mutation being selected in mul- 108
tiple independent evolved clones (genetic parallelism) (Good 109
et al. 2017; Spor *et al.* 2014; Neher 2013; Good *et al.* 2012; Desai 110
and Fisher 2007; Gerrish and Lenski 1998). However, in asexu- 111
ally reproducing microbes, adaptation proceeds through *de* 112
nov mutations, which may reveal specific patterns not found 113
in sexually-reproducing eukaryotes. In yeast, for instance, most 114
adaptive changes correspond to the fixation of initial standing 115
variation (Burke *et al.* 2014; Burke 2012). Patterns of allele fre- 116
quency changes depend crucially on both N_e and the frequency 117
of sex, that are themselves intimately linked (see Hartfield *et al.* 118
(2017)). Considering a single locus, fixation time decreases cor- 119
relatively with the level of self-fertilization (Haldane 1927). At 120
the same time, multilocus simulations have shown that self- 121
ing reduces effective population size through background se- 122
lection and in turn, beneficial mutations are less likely to fix 123
(Kamran-Disfani and Agrawal 2014; Roze 2016). In addition, 124

1 as selection interference reduces the efficiency of selection in
 2 low-recombining regions, high selfing rates also increase the
 3 fixation of deleterious mutations through genetic hitchhiking
 4 (Hartfield and Glémin 2014). These insights are together in line
 5 with the low selection approximation that posits that reduction
 6 in effective recombination decreases selection efficiency.

7 In the current paper, we aimed at investigating the dynamics
 8 of the response to selection in small selfing populations evolu-
 9 ing under high selection intensity. Situated at the parameters
 10 boundaries of current models, this regime is of particular interest
 11 to understand the limits of adaptation and long-term survival
 12 of small selfing populations undergoing strong selection. We
 13 relied here on two Divergent Selection Experiment (DSEs) con-
 14 ducted for 18 generations on Saclay’s plateau (Saclay DSEs),
 15 south of Paris (France). These Saclay DSEs are ideal settings
 16 to address those issues: selection-by-truncation has been ap-
 17 plied in a higher organism (maize), on a highly polygenic and
 18 integrated trait (flowering time, (Buckler et al. 2009; Tenaillon
 19 et al. 2018)) that directly affects fitness. Previous results in-
 20 dicate continuous phenotypic responses sustained by a constant
 21 mutational input (Durand et al. 2010, 2012, 2015) — values of
 22 mutational heritability ranged from 0.013 to 0.025. We asked
 23 two main questions: How do mutations arise, spread, and reach
 24 fixation in populations where both drift and selection are ex-
 25 tremely intense? How does the interplay between drift and
 26 selection influence the response to selection? To answer those
 27 questions, we confronted the observed phenotypic responses
 28 in Saclay DSEs to forward individual-based simulations that
 29 explicitly modeled the same selection and demographic scheme,
 30 and used theoretical predictions to measure deviations from
 31 expectations.

32 Materials and Methods

33 Saclay Divergent selection experiments

34 We have conducted two independent divergent selection exper-
 35 iments (Saclay DSEs) for flowering time from two commercial
 36 maize inbred lines, F252 and MBS847 (thereafter MBS). These
 37 experiments were held in the field at Université Paris-Saclay
 38 (Gif-sur-Yvette, France). The selection procedure is detailed in
 39 Fig. S1 and Durand et al. (2010). Briefly, within each Saclay DSE,
 40 the ten earliest/ten latest flowering individuals were selfed at
 41 each generation to produce 100 offspring used for the next gen-
 42 eration of selection within the Early/Late populations, so that
 43 1000 plants were evaluated in each population. Following Du-
 44 rand et al. (2015), we designated as *progenitor*, a selected plant
 45 represented by its progenies produced by selfing and evaluated
 46 in the experimental design at the next generation. Seeds from
 47 progenitors from all generations were stored in cold chambers.

48 Within each population, we evaluated offspring of a given
 49 progenitor in four rows of 25 plants randomly distributed in a
 50 four-block design. Each block contained 10 rows representing
 51 the 10 progenitors. We applied a multi-stage pedigree selec-
 52 tion. First the three earliest (latest) flowering plants within each
 53 row were selfed and their flowering time was recorded. This
 54 corresponded to 12 plants per progenitor, *i.e.* 120 plants per
 55 population. The second stage consisted in choosing 10 plants
 56 among the 120 on an index based on three criteria: flowering
 57 time, total kernel weight and pedigree. When two plants had the
 58 same flowering date, we chose the one with the highest kernel
 59 weight. In addition, we maintained two independent *families*
 60 within each population, *i.e.* two sub-pedigrees derived from
 61 two different progenitors in the ancestral G_0 population, and

62 we never selected more than three plants from the same G_{n-1}
 63 progenitor. Practically, each family was composed of three to
 64 seven progenitors at each generation. Altogether, we selected in
 65 each population 10 plants out of 1000 which corresponded to a
 66 selection intensity of 1%.

67 We traced back the F252 and MBS pedigrees from generation
 68 20 (G_{20}) to the start of the divergent selection experiments, G_0 .
 69 The initial MBS pedigrees encompassed four families: ME1 and
 70 ME2 for the MBS Early (ME) population, and ML1 and ML2
 71 for the MBS Late (ML) population (Fig. S2a). F252 Early (FE)
 72 population was composed of FE1 and FE2 families (Fig. S2b).
 73 F252 Late populations genealogies were more complex: FVL
 74 families (F252 Very Late in Durand et al. (2015)) ended at gener-
 75 ation 14 with the fixation of a strong effect allele at the *elf-4A*
 76 gene (Durand et al. 2015). To maintain two families in F252 Late
 77 population, two families FL2.1 and FL2.2 were further derived
 78 from the initial FL2. These two families pedigrees are rooted in
 79 FL2 from a single G_3 progenitor (Fig. S2b).

80 Phenotypic data collection and empirical selection responses

81 The same approach as Durand et al. (2015) was applied. Briefly,
 82 progenitor flowering dates, measured here as the number of
 83 days to flowering after sowing equivalent to 20°C days of devel-
 84 opment (Parent et al. 2010), were recorded as the 12 earliest
 85 or latest plants in their progeny at each generation of the Saclay
 86 DSEs. We used these records to investigate the response to
 87 selection treating each family independently. After correction
 88 of the phenotypic values Z_{ijklmn} for block effects, and year ef-
 89 fects according to equation (1) of Durand et al. (2015) (so that
 90 $Y_{ijklm} = Z_{ijklmn} - \widehat{\text{Year}}_i - \widehat{\text{Block}}_{in}$, *in* corresponding to the block
 91 effect n in selection year i), the linear component b_{jk} of the within-
 92 family response to selection was estimated using the following
 93 linear model:

$$94 Y_{ijklm} = \mu_0 + b_{jk} \times \text{gener}_i + \varepsilon_{ijklm} \quad (1)$$

95 where i stands for the year and corresponding generation of
 96 selection (so that gener_i takes values between 0 to 20) j for the
 97 population (Late or Early), k for the family within population (*e.g.*
 98 ME1 or ME2), l for progenitor within family, and m for the plant
 99 measurements within progenitor (so that ε_{ijklm} corresponds to
 100 the residual variance due to differences between progenitor of
 101 the same generation, and family and plant effect). Finally, μ_0
 102 is the intercept corresponding to the average flowering time at
 103 generation G_0 .

104 Family means and standard errors were also computed at
 105 each generation to represent families selection responses pre-
 106 sented Fig. 1 (a). All the values were centered around 100 for
 107 comparison purposes with the simulated responses.

108 Model framework

109 We used forward individual-based simulations that explicitly
 110 modeled the same selection — proportion of selected individ-
 111 uals=1% of the most extreme) — and demographic scheme —
 112 variations in population size — as Saclay DSEs. This regime is
 113 referred to High-Drift High Selection intensity (HDHS). **Initial G_0**
 114 **simulation:** We obtained our initial population by mimicking a
 115 classical selection scheme used to produce fixed maize inbred
 116 lines in industry. To do so, we started from an heterozygous
 117 individual that was selfed for eight generations in a single-seed
 118 descent design. An additional generation of selfing produced
 119 60 offspring that were reproduced in panmixia for two genera-
 120 tions to constitute the 60 individuals of the G_0 initial population.

1 Therefore, we started our simulations with a small initial residual heterozygosity ($\leq 0.5\%$). **G₁ simulation:** Considering one
2 Saclay DSE, we selected from the initial population (60 individuals), the two earliest and the two latest flowering parents on the
3 basis of their average phenotypic value. Each of these individuals constituted the ancestor of each of the four families. They
4 were selfed to produce 100 offspring. **Subsequent generations**
5 **n:** From there, we simulated the exact same selection scheme that included a two-steps procedure (Fig. S1). First, we selected
6 the 12 earliest (within each early family) and the 12 latest individuals (within each late family) from the 100 offspring of each
7 progenitor. We next selected the five earliest (within each early family) and five latest (within each late family). In other words,
8 at each step we retained 5 out of 500 (5/500) individuals within each of the four families. Note that we imposed that the five
9 selected individuals did not share the same parent.

17 Simulated genetic and phenotypic values

18 Maize flowering time is a highly polygenic trait (Buckler *et al.*
19 2009; Tenaillon *et al.* 2018). Over 1000 genes have been shown to
20 be involved in its control in a diverse set of landraces (Romero
21 Navarro *et al.* 2017). We therefore set the number of loci to
22 $L = 1000$. As in maize, the genome of one individual was composed
23 of 10 chromosomes. In each simulation: (i) we randomly assigned
24 each locus to a chromosome so that genome composition varied from
25 one simulation to another; (ii) the position of each locus within
26 each chromosome was uniformly drawn between 0 and 1.5, 1.5 Morgan
27 being the total genetic length of each chromosome; (iii) the crossing-
28 over positions along chromosomes were drawn in an exponential law
29 of parameter 1, which corresponded to an effective crossing-over
30 every Morgan. The initial population (G_0) consisted of 60 individuals
31 polymorphic for a small fraction of loci (residual heterozygosity).
32 Let G_g^i be the genotype of the individual i of the generation g . Let
33 $a_l^{f(i,g)}$ the allelic value at the locus l of the paternal chromosome
34 f of the individual i at the generation g and $a_l^{m(i,g)}$ the allelic
35 value at locus l of maternal chromosome m of individual i at
36 generation g . This allows us to model the genotype of an individual
37 as :

$$G_g^i = [(a_1^{f(i,g)}, a_2^{f(i,g)}, \dots, a_l^{f(i,g)}, \dots, a_L^{f(i,g)}), (a_1^{m(i,g)}, a_2^{m(i,g)}, \dots, a_l^{m(i,g)}, \dots, a_L^{m(i,g)})] \quad (2)$$

38 We expect the distribution of allele effects to follow a leptokurtic
39 Gamma distribution (e.g. Kimura (1979); Hill (1982a); Keightley
40 (1994); Shaw *et al.* (2002); Piganeau and Eyre-Walker (2003)).
41 We made the simplifying assumption that the unknown shape
42 parameter of the Gamma distribution α was equal to 1, corresponding
43 to an exponential distribution. Overall, the initial allelic values were
44 drawn in an reflected exponential distribution, that is to say:

$$\forall l \wedge \forall (f(i,g) \vee m(i,g)), a_l \sim \text{Reflected exp}(\lambda) \quad (3)$$

46 Hence the probability density:

$$f(a_l, \lambda) = \frac{1}{2} \lambda e^{-|\lambda a_l|} \quad (4)$$

47 which implied that:

$$\mathbb{E}[a_l] = 0 \text{ and } \mathbb{V}[a_l] = \frac{2}{\lambda^2} \quad (5)$$

48 Starting from a hybrid heterozygote at all L loci, we computed
49 the expectation of the genic variance $\mathbb{E}(\sigma_{g+2}^2)$ after g generations
50 of selfing and two generations of bulk. Selfing reduces the genic
51 variance by 1/2 each generation. In the absence of linkage disequilibrium,
52 panmixia does not change allelic frequencies:

$$\mathbb{E}(\sigma_{g+2}^2) = \frac{1}{2^g} \times L \times \mathbb{V}[a_l] = \frac{1}{2^g} \times L \times \frac{2}{\lambda^2} \quad (6)$$

53 Therefore, to match the field estimate $\widehat{\sigma_{A_0}^2} = \mathbb{E}(\sigma_{g+2}^2)$, one
54 could let

$$\lambda = \sqrt{2L \frac{1}{2^g} \frac{1}{\sigma_{A_0}^2}}. \quad (7)$$

55 However, drift, linkage disequilibrium and mutation can lead to
56 deviations from the expected value of the initial genetic variance.
57 We therefore recalibrated all the allelic values at generation 0 to
58 match the initial $\widehat{\sigma_{A_0}^2}$ additive variance. To do so, we multiplied
59 all the allelic values by a corrective factor $k = \sqrt{\widehat{\sigma_{A_0}^2} / \mathbb{V}(A_0)}$, where
60 $\mathbb{V}(A_0)$ was the additive variance of our population G_0 , calculated
61 in multiallelic as $2 \times \sum_{l=1}^L \sum_{i=1}^n p_{il} \alpha_{il}^2$ with n the number of
62 alleles at locus l , p_{il} the frequency of the allele i at locus l .
63 α_{il} , its additive effect, is defined as in Lynch *et al.* (1998)
64 (Chapter 4), so that after dropping subscript l , $\alpha_i = \mathbb{E}(G_{ij}|i) - \mu_G$,
65 with μ_G the population genotypic mean, $\mathbb{E}(G_{ij}|i)$ the conditional
66 expectation of the genotypic value of genotype G_{ij} knowing i .
67 So at G_0 , $\mathbb{V}(A_0) = \widehat{\sigma_{A_0}^2}$.

68 Mutations occurred at each reproduction event. We drew the
69 number of mutations per haplotype in a Poisson distribution of mean
70 $L \times \mu$ where μ was the mutation rate per locus. Following
71 Kimura (1979); Hill (1982a); Keightley (1994); Shaw *et al.*
72 (2002); Piganeau and Eyre-Walker (2003), we drew the value of a
73 mutation at a locus in a reflected exponential distribution of
74 parameter $\lambda_{mut} = 2\sqrt{(L\mu)/\sigma_M^2}$. We computed phenotypic values
75 as the sum of all allelic values a_{il} ($L \times 2$) plus an environmental
76 effect randomly drawn in a normal distribution of mean 0 and
77 variance σ_E^2 .

78 Selection and drift regimes

79 As control, we considered a model without selection (the No
80 Selection regime, NS) where neutral evolution occurred in a
81 population with the same census size and the same number of
82 progenitors as in the selection model. At each generation, we
83 randomly drew 1% of the individuals to form the next generation,
84 instead of choosing them from their phenotypic values.

85 In addition, we considered an alternative drift regime, where
86 we increased the census population size by a factor 10, all other
87 parameters remaining unchanged. This regime is referred to as
88 the Low Drift regime (LD) where 50/5000 instead of 5/500
89 individuals were selected. Both Low Drift-High Selection (LDHS)
90 and Low Drift-No selection (LDNS) were considered.

91 We performed 2000 independent simulations for each of the
92 four families in each of the four regimes. All downstream analyses
93 were carried out over all simulations, except when specified.

94 Parameter calibration

95 Our model encompassed three key parameters: the initial additive
96 variance $\sigma_{A_0}^2$, the mutational variance, σ_M^2 , and the environmental
97 variance σ_E^2 . We chose to sample parameter values in an

inverse-gamma distribution with parameters (shape and scale) chosen such as (i) the expected means of the two inverse-gamma for $\mathbb{E}(\sigma_{A_0}^2)$ and $\mathbb{E}(\sigma_M^2)$ were roughly equal to the estimate provided by (Durand *et al.* 2010) for MBS-DSE, (ii) 95% of the values of the two inverse-gamma fell within the range of observed values for the DSEs (Durand *et al.* 2010), (iii) mean and variance for σ_E^2 corresponded to the values measured for maize experiments in Saclay's Plateau. Parameters values are summarized Tab. 1.

Table 1 Initial variances parameters

Parameter	Expectation	Variance	shape	rate
$\sigma_{A_0}^2$	2.25	3.28	3.540	5.715
σ_M^2	3.38×10^{-2}	7.27×10^{-5}	17.67	0.5626125
σ_E^2	2.25	0.32	17.67	37.50075

Genomic parameters were taken from the literature. In maize, Clark *et al.* (2005) estimated the nucleotidic substitution rate to 30×10^{-9} . We relied on the maize reference genome V4 (Jiao *et al.* 2017) to estimate an average mRNA length of 6000 (median=5197, mean=7314). Based on both estimates, we therefore considered a mutation rate per locus of: $\mu = 6000 \times 30 \times 10^{-9} = 1.8 \times 10^{-4}$.

Expected response, effective population size and time to the most recent common ancestor

We computed the expected cumulative response after t generations for haploid population as (Hill 1982b; Wei *et al.* 1996; Weber and Diggins 1990; Walsh and Lynch 2018):

$$R(t) \approx N_e \frac{i}{\sigma_p} \left[t\sigma_m^2 + \left(1 - e^{-\frac{t}{N_e}}\right) \left(\sigma_A^2(0) - N_e\sigma_m^2\right) \right] \quad (8)$$

The effective population was the only parameter not explicitly defined in our simulations and is of crucial importance in the response to selection. We estimated N_e following two approaches. First using the Time to the Most Recent Common Ancestor (TMRCA) from the standard coalescence theory for a haploid sample of size k at generation g (Walsh and Lynch 2018):

$$\mathbb{E}(\text{TMRCA}_g) = 2N_{e(g)}^{\text{Coal}} \times \left(1 - \frac{1}{k}\right) \quad (9)$$

Second, from the variance in offspring number (Crow and Kimura 1971; Durand *et al.* 2010), where N_e can be computed as

$$N_{e(g)}^{\text{Var}(o)} = \frac{N - 1}{\text{Var}_{(g)}(\text{OffspringNumber})} \quad (10)$$

In the simulations, $N_{e(g)}^{\text{Coal}}$ and $N_{e(g)}^{\text{Var}(o)}$ were computed at generation G_{20} . We also computed the harmonic means between generations G_1 and G_{20} and computed the whole distribution (in $2N_e$ generations) of the Kingman coalescent TMRCA as (Tavaré 1984):

$$f_{\text{TMRCA}}(t) = \sum_{i=2}^n \frac{(2i-1)(-1)^i(n(n-1)\dots(n-i+1))}{n(n+1)\dots(n+i-1)} \binom{i}{2} e^{-\binom{i}{2}t} \quad (11)$$

Fitness function and Kimura's expected fixed mutational DFE

Using diffusion equations, Kimura (Kimura 1962) predicts the fixation probability of a mutation of selective value $s(a)$ — with a its allelic value — and initial frequency p :

$$P_{\text{fix}}(s(a), p, N_e) = \frac{1 - e^{-4s(a)pN_e}}{1 - e^{-4s(a)N_e}}. \quad (12)$$

When occurring, a new mutation arises during meiosis in one plant among the 500 of a family observed at a given generation. Hence, its effect on the phenotypic variance is negligible. Therefore, the plant carrying this newly arisen mutation was selected essentially independently of the new mutation. Consequently, the 5 individuals selected in one family comprised one heterozygote (Aa) bearing the mutation, and 4 homozygotes (aa). Each selected individual produced 100 progenies, so that the fitness effect of the mutation was evaluated at the next generation in a population of 500 plants where the frequency of the mutant allele was $p = 1/10$ (Table 2).

Table 2 Fitness model

Genotype	AA	Aa	aa
Genotypic frequency	1/20	2/20	17/20
Fitness value	w_{AA}	w_{Aa}	w_{aa}
Mutational effect	$a_{AA} = 2a$	$a_{Aa} = a$	$a_{aa} = 0$

In this population, the distribution of flowering time resulted from a mixture of Gaussian distributions.

$$f(x) = \sum_k \Pi_k f_k(x) \quad (13)$$

where $f_k(x)$ is the flowering time distribution for plants with genotype $k \in AA, Aa, aa$. As we selected 1% of the latest/earliest flowering plants, all selected plants did flower after the date z , computed as the 1% quantile of the mixture distribution. The selection effect $s(a)$ depended on the effect a of the mutation on flowering time (Table 2). Indeed, the relative weight of homozygous mutants AA among selected individuals was computed as:

$$w_{AA} = \frac{1 - F_{AA}(z)}{\sum_k 1 - F_k(z)} \quad (14)$$

Which leads to:

$$s(a) = \frac{F_{aa}(z) - F_{AA}(z)}{1 - F_{aa}(z)} \quad (15)$$

The fixation probability $P_{\text{fix}}(s(a), p, N_e)$ was computed as in (Eq. 12) using $s(a)$ (Eq. 15), $p = 1/10$, and $N_{e(g)}^{\text{Coal}}$ for N_e . The mutational effect a was drawn in a reflected exponential distribution of parameter λ_{mut} and density function $g_{\lambda_{\text{mut}}}(a)$. Hence, the density of fixed mutations $h(a)$ was computed as:

$$h(a) = \frac{g_{\lambda_{\text{mut}}}(a)P_{\text{fix}}(s(a), p, N_e)}{\int g_{\lambda_{\text{mut}}}(x)P_{\text{fix}}(s(x), p, N_e)dx}. \quad (16)$$

Moreover, we recorded the simulated values a_{sim} of each fixed mutation and computed the realized distribution $h_{\text{obs}}(a)$ using kernel estimate methods.

1 Results

2 In order to examine the evolution and fate of small selfing popula- 62
3 tions submitted to strong selection intensity, we investigated 63
4 the dynamics of the response to selection under a High Drift- 64
5 High Selection intensity (HDHS) regime imposed on two diver- 65
6 gent artificial selection experiments for flowering time in maize 66
7 (Saclay DSEs). We compared experimental data to results of 67
8 a simulation model specifically devised to mimic our experi- 68
9 ments; and further computed when possible expectations from 69
10 population and quantitative genetics theory. 70

11 **Empirical response after 20 generations of selection** In line with 69
12 previous observations for the first 16 generations, we observed 70
13 significant responses (Fig. 1 a, Tab. 3a, 3b) to selection after 71
14 20 generations in all families. Marked differences among fam- 72
15 ilies nevertheless characterized these responses. This is well 73
16 exemplified in the Late F252 families where one family (FVL) 74
17 responded very strongly with a mean shift of 11.32 Days to 75
18 Flowering (DTF) after 13 generations, corresponding to a linear 76
19 regression coefficient of 0.86 DTF/generation (Tab. 3a). This 77
20 family fixed a deleterious allele at G_{13} and could not be main- 78
21 tained further (Durand *et al.* 2012). We examined two derived 79
22 families from G_3 (Fig. S2b), the FL2.1 and FL2.2. These families 80
23 were shifted by 3.19 DTF and 2.60 DTF from the G_0 FL2 mean 81
24 value for FL2.1 and FL2.2, respectively. These corresponded to 82
25 a linear regression coefficient of 0.11 DTF/generation for FL2.1 83
26 and 0.12 DTF/generation for FL2.2 (Tab. 3a). The selection 84
27 response were more consistent for the two Early F252 families, 85
28 with a shift after 20 generations of -4.27 DTF for FE1, and a shift 86
29 of -5.34 DTF for FE2 (Tab. 3a). Considering MBS genetic back- 87
30 ground, the late/early MBS families were shifted by 8.64 DTF 88
31 for ML1, and 11.05 DTF for ML2 (respectively -9.34 DTF for 89
32 ME1 and -11.72 DTF for ME2), with linear regression coeffi- 90
33 cient of 0.24 DTF/generation for ML1, and 0.46 DTF/generation 91
34 for ML2 (respectively -0.41 DTF/generation for ME1 and - 92
35 0.42 DTF/generation for ME2) DTF (Tab. 3b). 93

36 **Simulation model validation** To parameterize our simulation 87
37 model, we used priors: variance components were described 88
38 by inverse-gamma distributions whose parameters were chosen 89
39 following previously reported values for Saclay's DSEs Durand 90
40 *et al.* (2010), mutation rate was taken from the maize literature 91
41 (Clark *et al.* 2005), and the number of loci was set to $L = 1000$ 92
42 according to the large mutational target described for maize flow- 93
43 ering time (Romero Navarro *et al.* 2017). In order to validate the 94
44 parametrization of our model, we compared the observed MBS 95
45 responses in all families to the simulated selection responses 96
46 under HDHS regime. Because of the symmetry in the model 97
47 construction and for simplicity, simulated results are described 98
48 for late populations only. We recovered a simulated response 99
49 with a mean genetic gain of 0.49 DTF/generation (Fig. 1, Tab. 3c). 100
50 Starting from a mean genotypic value of 100 DTF, the mean 101
51 genotypic value was shifted by 13.0 DTF (SD: 5.2) after 20 gen- 102
52 erations. Our simulated response therefore closely matched the 103
53 observed response (p-value not significant, Tab. 3b) indicating 104
54 an accurate parametrization of our simulation model (Fig. 1), 105
55 that captured the average selection response per generation of 106
56 MBS. Note however, that inter-generational fluctuations were 107
57 higher in the observations than in the simulations (Fig. 1). 108

58 We used simulations both to validate our model and to ex- 109
59 plore two drift intensities, High and Low. We used correspond- 110
60 ing negative controls with No Selection (NS) which lead to four 111
61 regimes: High Drift-High Selection intensity (HDHS, the default 112

regime), High Drift-No Selection (HDNS), Low Drift-High Selec- 62
tion intensity (LDHS) and Low Drift-No Selection (LDNS). We 63
formally tested the significance of our simulated response by 64
comparing the linear response under HDHS to that obtained 65
under HDNS. We were able to reject the null hypothesis of no 66
selection response in 96.4% of the simulations under HDHS 67
(P-value<0.05). 68

To investigate the impact of a ten-fold increase of the 69
census population size on selection response, we contrasted 70
HDHS to LDHS. Just like for HDHS, we obtained a signif- 71
icant response under LDHS with a mean genetic gain of 72
1.10 DTF/generation (Fig. 1, Tab. 3c). This gain was greater 73
than the +0.035 DTF/generation (SD: 0.035) obtained for the 74
LDNS control model, and we were able to reject the null hypoth- 75
esis of no selection response in 100% of the simulations. The 76
gain under LDHS corresponded to a shift of +24 DTF (SD: 6.2), 77
which was substantially higher than that observed under HDHS. 78
Hence multiplying the census population size of HDHS by 10 79
(LDHS) resulted in roughly doubling the selection response. 80

In sum, we validated the accuracy of our model by showing 81
that the simulated response closely matched the observed re- 82
sponse. We further demonstrated that selection triggered the 83
response in all populations under both Low and High Drift. Fi- 84
nally, we confirmed our expectation that the selection response 85
was higher in a Low Drift than in a High Drift regime. 86

Effective population size: We estimated coalescent effective 87
population sizes N_e from the standard coalescence theory 88
(Eq: (9)) using a Wright-Fisher population of size 5 (HD) and 50 89
(LD) individuals. With 5 individuals, we expected a theoretical 90
coalescence time around 8 generations, and with 50 individuals, 91
around 98 generations (i.e. more than the number of simulated 92
generations). Focusing on the last generation, our simulations 93
provided estimates of the mean G_{20} TMRCA of 7.6 generations 94
under neutrality (NS) for HD, closely matching the theoretical 95
expectation of 8 (Tab. 3c). Considering the LDNS simulations, 96
theoretical expectations (98) largely exceeded the number of gen- 97
erations (20). In contrary, we found a mean G_{20} TMRCA of 3.9 98
under HDHS, and 6.4 under LDHS. Fig. 2 shows the distribution 99
of the TMRCA estimated at G_{20} in the three regimes. Under 100
HDNS, the distribution fits the expectation from Eq: (11). As 101
compared to the neutral case, Fig. 2 also shows that both the high 102
drift (HDHS) and low drift (LDHS) selection regimes display 103
reduced TMRCA. 104

We next assessed the impact of selection on N_e and compared 105
different estimates, either based on TMRCA (Eq: (9)), or on the 106
variance in offspring number (Eq: (10)), or on the cumulated 107
response to selection (Eq: (8)). Values obtained are summarized 108
in Tab. 3c. We found that in the absence of selection, N_e esti- 109
mated from the mean TMRCA were close to the actual number 110
of reproducing individuals (4.8 for HDNS and >10 for LDNS), 111
while they were much smaller under both selection regimes (2.5 112
for HDHS and 3.3 for LDHS). The observed differences between 113
 $N_{e(20)}^{Coal}$ and the harmonic mean of $N_{e(G1-20)}^{Coal}$ revealed a strong in- 114
fluence of the first generation on the adaptive dynamics. When 115
 N_e was computed from the variance in offspring number, esti- 116
mates without selection (4.1 under HDNS and 42 under LDNS) 117
were close to the actual number of reproducing individuals. Fi- 118
nally, N_e estimates from the cumulated response to selection 119
fell within the same range as the ones from the variance in off- 120
spring number in both selection regimes. In summary, most N_e 121
estimates were close to the actual number of reproducing indi- 122
viduals in the absence of selection but high selection intensity 123

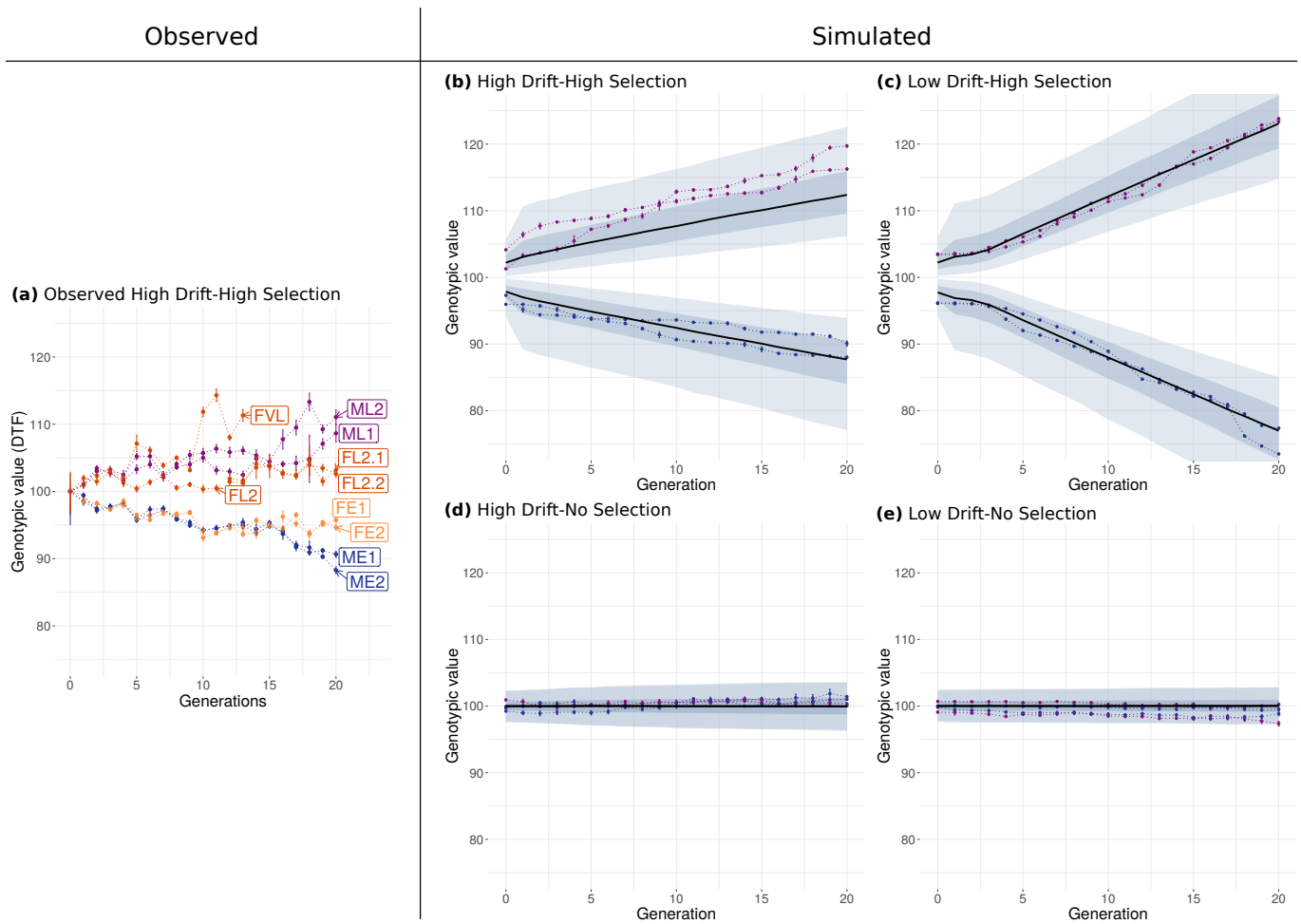


Figure 1 Observed and simulated selection response. Selection response is visualized by the evolution of the mean genotypic values of the selected progenitors per family (expressed in Days To Flowering, DTF) across generations in observed (a) and simulated (b-e) data. Observed genotypic values correspond to mean phenotypic values corrected for environmental effects. In (a), red/orange corresponds to late/early flowering F252 families, while violet/blue corresponds to late/early flowering MBS families. All families were centered around 100, and Vertical bars correspond to ± 1 genotypic standard error around the mean. We simulated four regimes with the parameters calibrated from the MBS observed response: High Drift-High Selection intensity (b), Low Drift-High Selection (c), High Drift-No Selection (d), Low Drift-No Selection (e). Violet/blue color identifies late/early population. In each population, the black line represents the evolution of the median value over 2000 simulations of the family genotypic mean. The shaded area corresponds to the 5th-95th percentiles (light blue) and to the 25th-75th percentiles (dark blue). In addition, two randomly chosen simulations are shown with dotted lines

1 strongly reduced N_e estimates.

2 **Stochasticity in the response to selection:** We addressed the qual-
 3 itative nature of selection response focusing on its linearity. To
 4 do so, we measured in each family the average genetic gain per
 5 generation over 2000 simulations by fitting a linear regression
 6 model. The average genetic gain was 0.49 DTF/generation under
 7 HDHS, and 1.1 DTF/generation under LDHS (Tab. 3c). Associ-
 8 ated $R^2 > 0.95$ indicated an accurate fit of the data to the linear
 9 model. Yet, large standard deviations around these estimates
 10 (0.2 and 0.27 for HDHS and LDHS, respectively) pointed either
 11 to high stochasticity or a non-linear response. Single simulations
 12 indicated non-linear response (Fig. S3). Noteworthy, a strong
 13 response was observed between G_0 and G_1 (G_0G_1 Fig. S3) with
 14 similar values in HDHS and LDHS, around 1.6 DTF/generation
 15 (Tab. 3c). Subsequently, simulations displayed discontinuities
 16 with abrupt changes of slopes at some generations, a signal com-

patible with the fixation of new mutations (Fig. S3). In order to
 17 characterize such discontinuities, we fitted a linear segmentation
 18 regression on individual simulations from G_1 and onwards. We
 19 estimated the number of breakpoints (i.e. slope changes), the
 20 corresponding slopes, and the first and greatest slope based on
 21 AIC minimization (Durand *et al.* 2010). The first slope described
 22 an average gain of 0.59 DTF/generation in the HDHS regime,
 23 and almost twice (0.96 DTF/generation) in the LDHS regime
 24 (Tab. 3c). These values were lower than those observed in G_0G_1 .
 25

Those results are consistent with a G_0G_1 response resulting
 26 from the recruitment of initial genetic variance, independently
 27 of the population size, and a later response based on mutational
 28 variance being less effective in small than in large populations.
 29 To confirm those results, we performed a principal component
 30 analysis (PCA) and explored correlations between input param-
 31 eters: initial additive genetic variance $\sigma_{A_0}^2$, mutational variance
 32

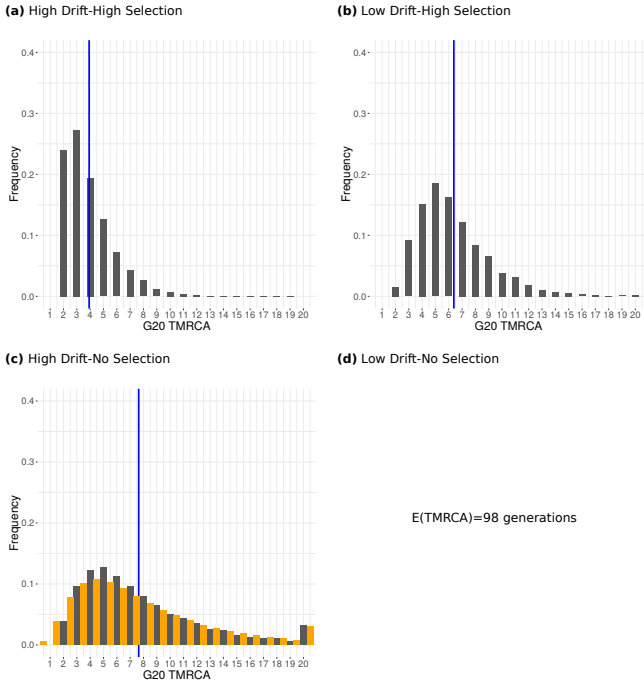


Figure 2 Frequency distribution of the Time to the Most Common Ancestor of progenitors constituting the last simulated generation. G_{20} TMCA distribution (in grey) was obtained under HDHS (a), LDHS (b), HDNS (c) with mean TMCA indicated as a blue vertical line. In (c), we plotted in gold the theoretical expectation of TMCA distribution following Eq. (11). Note that under LDNS, theoretical expectations for TMCA reached 98 generations, while our simulations were run for 20 generations. We therefore discarded the corresponding graph.

1 σ_M^2 and residual variance $\sigma_{E'}^2$, and descriptors of the response to
 2 selection : G_0G_1 response, number of breakpoints, first slope and
 3 greatest slope. In line with our interpretation, irrespective of the
 4 selection regime, $\sigma_{A_0}^2$ positively correlated with G_0G_1 , and σ_M^2
 5 positively correlated with the first (after G_1) and greatest slope
 6 (Fig. S4). Note that this stochastic process of mutation occur-
 7 rence and fixation resulted in large differences among replicates,
 8 as illustrated by the breadth of the response (shaded areas in
 9 Fig. 1).

10 **Evolution of genetic diversity:** Because of the well-established
 11 role of standing variation in selection response, we focused on its
 12 temporal dynamics. Standing variation in our experiment con-
 13 sisted in residual heterozygosity found in the initial inbred lines.
 14 Starting with a mean residual heterozygosity of 3.0×10^{-3} at G_0
 15 (Tab. 3c), we observed a consistent decrease throughout selfing
 16 generations until the mutation-drift-equilibrium was reached
 17 (Fig. S5). The mean values reached $\approx 7.0 \times 10^{-4}$ at G_{20} without
 18 selection, and $\approx 8.0 \times 10^{-4}$ with selection (Tab. 3c) irrespective
 19 of the census population size.

20 Concerning the number of polymorphic loci, a mutation-
 21 drift-equilibrium was reached in all cases except for the LDNS
 22 selection regime (Fig. S6). The equilibrium value depended on
 23 the census population size: around 6 polymorphic loci with high
 24 drift (HDHS and HDNS), 40 polymorphic loci under LDHS, and
 25 > 66 polymorphic loci after 20 generations under LDNS (Tab. 3c

(c) and Fig. S6). Altogether, our results show that the mean
 heterozygosity was affected neither by drift, nor by selection,
 but instead by the mutation rate. On the contrary, the number of
 polymorphic loci depended on the census population size.

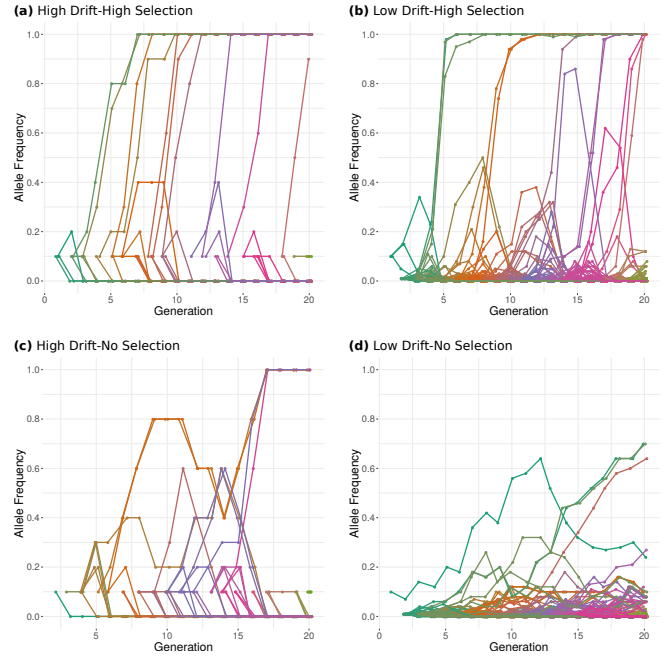
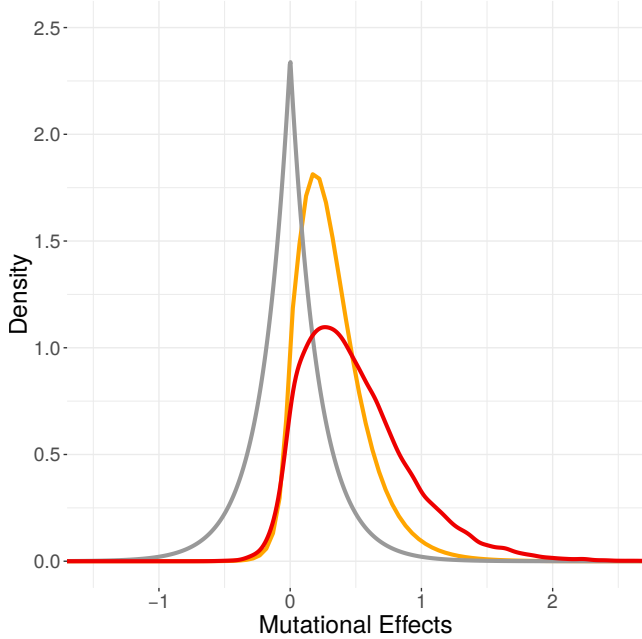


Figure 3 Evolution of allele frequencies within families under four simulated regimes. Examples of mutational fates are given for HDHS (a), LDHS (b), HDNS (c), LDNS (d). Mutations are recorded only when occurring in one of the selected progenitors, and corresponding frequencies are computed over all selected individuals. For example under High Drift regimes, the initial frequency of a mutation occurring in any given progenitor within a family is $1 \div (2 \times 5)$ as 5 diploid individuals are selected at each generation. Under Lower Drift regimes, the mutation initial frequency equals $1 \div (2 \times 50)$.

30 **The dynamics of *de novo* mutations:** Evolution of frequencies
 31 of new mutations revealed three fates: fixation, loss, and rare
 32 replacement by *de novo* mutation at the same locus. The four
 33 regimes strikingly differed in their mutational dynamics (Fig. 3).
 34 Under HDHS, most mutations quickly reached fixation (3.8 gener-
 35 ations), with an average of 7.7 fixed mutations/population in
 36 20 generations (Tab. 3c). The corresponding Low Drift regime
 37 (LDHS) displayed longer fixation time 5.9 generations, and an
 38 average of 10 fixed mutations/family (Tab. 3c). Regimes without
 39 selection tended to exhibit a depleted number of fixed muta-
 40 tions, with no fixation under LDNS after 20 generations. Vari-
 41 ation around the mean fixation time was substantial across all
 42 regimes (Fig. S7). In sum, HDHS was characterized by the fast
 43 fixation of new mutations whose direction corresponded to the
 44 direction of selection: 53% were fixed within 2 to 3 generations
 45 which contrasted to 15% under LDHS or 17% under HDNS. Se-
 46 lection therefore increased the number of fixed mutations while
 47 decreasing their fixation time.

48 **Effects of mutations:** Beyond fixation time, a key aspect of our
 49 work was to investigate the impact of drift and selection on the
 50 type of fixed mutations, best summarized by their genotypic

(a) High Drift-High Selection



(b) Low Drift-High Selection

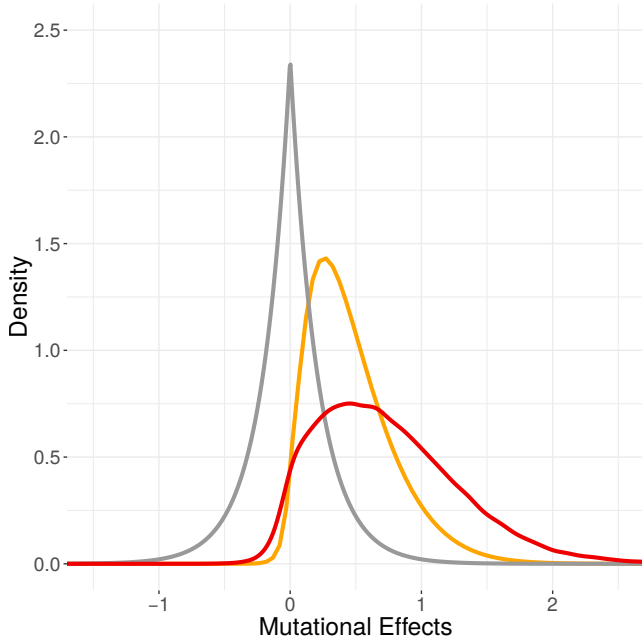


Figure 4 Distribution of effects of *de novo* and fixed mutations under High Selection intensity regimes. Density distributions for the HDHS (a) and the LDHS (b) regime are shown for all *de novo* mutational effects in grey — reflected exponential distribution —, and fixed mutations over 2000 simulations in red. Theoretical expectations from (Eq: 16) are plotted in gold.

quantile=1.3) and LDHS (quantile 5%=0.011, median value=0.66, 95% quantile=1.7) (Fig: 4). We also derived a theoretical expectation from Kimura's allele fixation probability using the selection coefficient computed in the case of truncation selection (Eq: 16). Accounting for the specificities of our selection procedure we found under both selection regimes, a slight excess of detrimental mutations, and a large excess of beneficial mutations as compared to Kimura's predictions. Note however that, comparatively, the excess of detrimental mutations in the simulations compared to theoretical expectations was more reduced under HDHS than under LDHS (Fig: 4).

As expected, selection generated a relation between the average size of a mutation and its time to fixation: the higher the effect of the mutation, the lower the time to fixation (Fig. 5 (a) and Fig. 5 (b)). Comparison between HDHS and LDHS revealed interesting features: under high drift, the average effect of mutations fixed was lower and variance around mutational effects tended to decrease correlatively with fixation time so that large size mutations were all fixed during the first generation while they persisted at subsequent generations under Low Drift (Fig. 5 (a) and Fig. 5 (b)).

In sum, our two selection regimes lead to an enrichment of beneficial mutations. Compared with LDHS, HDHS regime fixed fewer detrimental mutations but the average effect of fixed beneficial mutations was smaller.

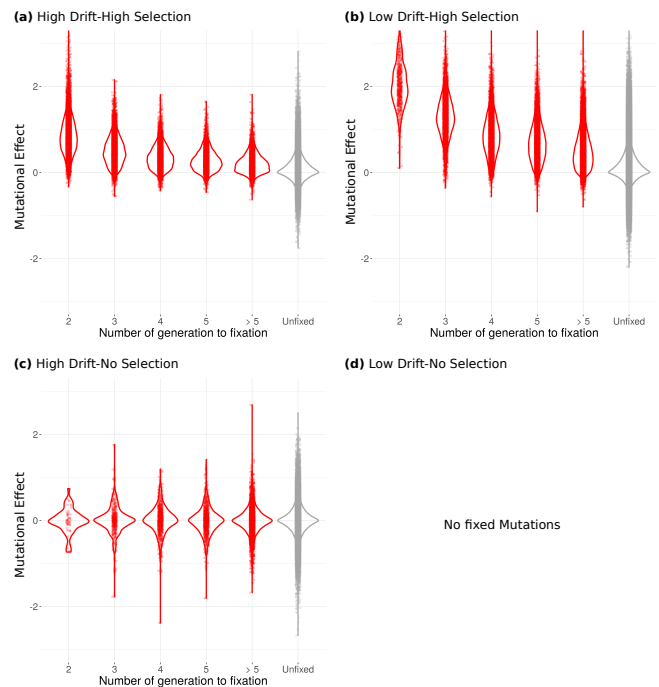


Figure 5 Violin plots of raw mutational effects according to fixation time under three simulated regimes. Plots are indicated for fixed (red) and lost (grey) mutations under HDHS (a), LDHS (b) and HDNS (c). Note that under LDNS, we obtained very few fixed mutations so that we were unable to draw the corresponding distribution.

1 effects. In order to do so, we compared the distribution of incoming
2 *de novo* mutations to that of fixed mutations. We observed a
3 strong depletion of deleterious mutations together with a striking
4 enrichment of beneficial mutations under the two Selection
5 regimes, HDHS (quantile 5%=-0.02, median value=0.43, 95%

Covariation between mutational and environmental effects: A puzzling
observation was that normalizing raw mutational effects by the environmental
standard deviation of selected individuals translated into a distortion of the
distribution so that the median

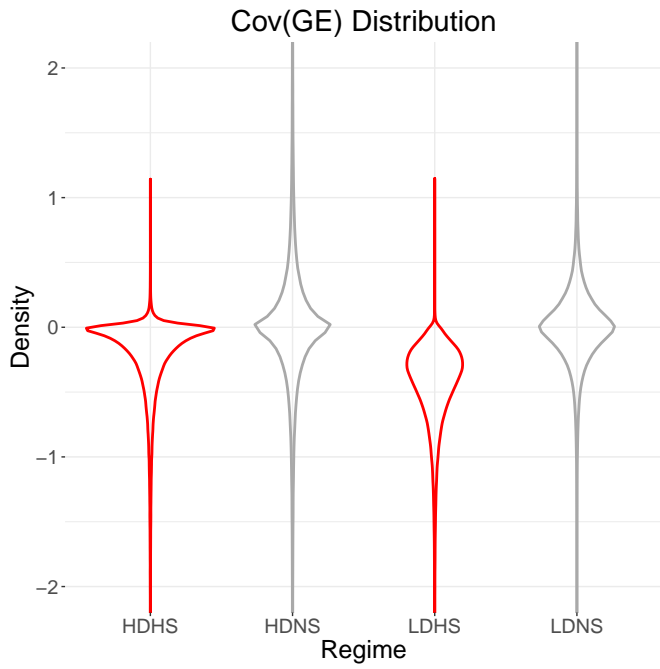


Figure 6 Violin plots of $\text{Cov}(G_{|\text{selected}}, E_{|\text{selected}})$ under four simulated regimes. Violin plots were computed over 2000 simulations and 4 families, four families and across all generations under regimes with High Selection intensity in red (HDHS, LDHS), and regimes with No Selection in grey (HDNS, LDNS).

1 value of fixed effects increased by 0.29 (from 0.43 to 0.72) under
 2 HDHS and by 0.2 under LDHS (Tab. 3 and Fig. S8). Similarly,
 3 95% quantile increased by 1.2 (from 1.3 to 2.5) under HDHS and
 4 0.66 (from 1.7 to 2.4) under LDHS. Hence, normalization distortion
 5 resulted in much more similar fixed mutations effects distribution
 6 under HDHS and HDNS. This was due to a non-zero
 7 negative genetic-environment covariance in selected individuals.
 8 Indeed, conditioning on the subset of selected individual,
 9 we obtained negative estimate of $\text{Cov}(G_{|\text{selected}}, E_{|\text{selected}})$ both
 10 under HDHS and LDHS, with a median value (respectively 5%
 11 and 95% quantile) of -0.11 (respectively -0.88 and 0.029) under
 12 HDHS and -0.37 (respectively -1.1 and -0.072) under LDHS. In
 13 contrast, with no selection, values of randomly chosen individual
 14 $\text{Cov}(G_{|\text{random}}, E_{|\text{random}})$ were centered around 0 as expected.
 15 The evolution of $\text{Cov}(G_{|\text{selected}}, E_{|\text{selected}})$ through time (Fig. S9)
 16 evidenced a high stochasticity among generations but no temporal
 17 autocorrelation (Fig. S9). In other words, because of the negative
 18 correlation between residual environmental effects and genetic effects
 19 induced by selection, mutational effects tightly depended on their
 20 environment of selection.

21 Discussion

22 Population and quantitative genetics provide theoretical frame-
 23 works to investigate selection responses and underlying multilocus
 24 adaptive dynamics. Here, we focused on Saclay DSEs which
 25 were specifically designed to depict the evolutionary mechanisms
 26 behind the response to selection of a highly complex trait
 27 — with a high mutational target — in small populations evolving
 28 under truncation selection (1% of selected individual), limited
 29 recombination (complete selfing) and limited standing variation.

30 Our main motivation was to explore how such a combination
 31 of unusual conditions, at the limits of parameters boundaries of
 32 classic models, can sustain the long-term maintenance of addi-
 33 tive genetic variation and a significant selection response with
 34 no observed load (annual field observations). In this purpose
 35 we (1) devised forward individual-based simulations that explic-
 36 itly modeled our Saclay DSEs and were calibrated on observed
 37 values of initial, mutational and environmental variances, and
 38 (2) relied on theoretical predictions to investigate the interplay
 39 of evolutionary forces and patterns associated with fixation of
 40 mutations.

41 The broadness of the mutational target sustains long-term mutational input

42 The three determinants of the observed selection response
 43 were best summarized by three variance components
 44 namely, the initial additive variance $\sigma_{A_0}^2$, the mutational variance
 45 σ_M^2 , and the environmental variance σ_E^2 (Fig. S4). Quanti-
 46 tatively, we demonstrated the importance of both initial stand-
 47 ing variation and the necessity of a constant mutational input
 48 to explain the significant selection response in the two Saclay
 49 DSEs (Fig. 1 & S4). This result was consistent with previous
 50 reports (Durand *et al.* 2010, 2015) and showed that the first
 51 selection response between G_0 and G_1 was correlated with $\sigma_{A_0}^2$,
 52 while response in subsequent generations was mainly deter-
 53 mined by σ_M^2 (Fig. S4). In our simulations, we chose initial
 54 values for variance components that closely matched previous
 55 estimates in the Saclay DSE derived from the MBS inbred line
 56 (Durand *et al.* 2010). The small value for initial additive vari-
 57 ance came from the use of commercial inbred lines in our ex-
 58 perimental evolution setting. It sharply contrasted with more
 59 traditional settings where distant genetic material and crosses
 60 are often performed to form an initial panmictic population
 61 on which selection is applied (Kawecki *et al.* 2012). While cru-
 62 cial in the first generation (Fig. S4), $\sigma_{A_0}^2$ was quickly exhausted.
 63 Hence, we showed that the long-term selection response was
 64 sustained by a strong mutational variance. The chosen variance
 65 $\mathbb{E}(\sigma_M^2) = 3.38 \times 10^{-2}$, corresponded to an expected mutational
 66 heritability of $\mathbb{E}(\sigma_M^2/\sigma_E^2) \approx \mathbb{E}(\sigma_M^2)/\mathbb{E}(\sigma_E^2) = 1.5 \times 10^{-2}$ (in
 67 units of residual variance per generation). This value, observed
 68 in our setting for flowering time, stands as a higher bound to
 69 what was previously described in other species/complex traits
 70 (Keightley 2010; Walsh and Lynch 2018).

71 σ_M^2 is intimately linked to the broadness of the mutational
 72 target, a key parameter of our setting. While decreasing the
 73 genomic mutation rate (U) - either by modifying the number of
 74 loci or by the per-base mutation rate - we observed at first sight a
 75 stronger average response to selection (Fig. S10). This is because
 76 incoming *de novo* mutational effects increase correlatively with
 77 decreasing U, to maintain σ_M^2 constant. Note that stochasticity
 78 of the response is boosted by scarcity of strong effect mutations
 79 that are preferentially fixed (Fig. S10). If instead of condition-
 80 ing on σ_M^2 , we conditioned on the distribution of incoming *de*
 81 *novi* mutational effects, responses under low values of U were
 82 drastically reduced (Fig. S10). These results further highlight
 83 that adaptive evolution results from a subtle balance between
 84 mutation, drift and selection.

85 We implemented an additive incremental mutation model
 86 (Clayton and Robertson 1955; Kimura 1965; Walsh and Lynch
 87 2018). This model assumed non-limiting mutational inputs, and
 88 has been shown to be particularly relevant in systems where,
 89 just like ours, effective recombination is limited (Charlesworth
 90 1993; Walsh and Lynch 2018). Alternative model such as the
 91 House Of Cards (HoC) that sets random allelic effect upon oc-

Table 3 Descriptive statistics of the selection response dynamics in observed F252 genetic background (a), observed MBS genetic background (b) and the 4 simulated regimes (c).

(a) HDHS observed in F252 genetic background

F252 families:	FE1	FE2	FVL (G13)	FL2.1	FL2.2
Cumul. Resp. in DTF	-4.27	-5.34	11.32	3.19	2.60
Linear Regression Coefficient (SD)	-0.21 (0.048)	-0.22 (0.037)	0.86 (0.17)	0.11 (0.04)	0.12 (0.035)
Adjusted R-squared	0.49	0.63	0.65	0.23	0.34
Linear regression p-value	0.000269	1.074 e-05	0.000305	0.016	0.00353

(b) HDHS observed in MBS genetic background

MBS families:	ME1	ME2	ML1	ML2
Cumul. Resp. in DTF (p-val ^a)	-9.34 (0.24 ^a)	-11.72 (0.45 ^a)	8.64 (0.19 ^a)	11.05 (0.39 ^a)
Linear Regression Coefficient (SD)	-0.41 (0.03)	-0.42 (0.04)	0.24 (0.05)	0.46 (0.06)
Adjusted R-squared	0.89	0.84	0.57	0.76
Linear regression p-value	1.01 e-10	3.52 e-09	4.46 e-05	1.56 e-07

(c) Simulated regimes^b

Simulated regimes:	HDHS	HDNS	LDHS	LDNS
Cumul. Resp. in DTF (SD)	13 (5.2)	1.7 (1.7)	24 (6.2)	1.3 (1.3)
Linear Regression Coefficient (SD)	0.49 (0.2)	0.067 (0.066)	1.1 (0.27)	0.035 (0.035)
R2 Linear Response	0.95	0.47	0.99	0.44
G ₀ G ₁ Response (SD)	1.6 (1.9)	0.26 (0.38)	1.7 (2.1)	0.3 (0.42)
First Slope (SD)	0.59 (0.52)	0.2 (0.3)	0.96 (0.46)	0.067 (0.091)
Greatest Slope (SD)	0.56 (0.49)	0.16 (0.24)	1 (0.46)	0.08 (0.098)
G ₂₀ TMRCA (SD)	3.9 (1.9)	7.6 (4.3)	6.4 (2.8)	> 20 (0.098) ^c
N _e ^{Coal} _{e(G₂₀)} (Ne from G ₂₀ TMRCA) (SD)	2.5 (1.2)	4.8 (2.7)	3.3 (1.4)	> 10 (0.05) ^c
N _e ^{Coal} _{e(G₁₋₂₀)} Ne (Harmonic Ne from all TMRCA) (SD)	1.8 (0.22)	2.5 (0.37)	2 (0.22)	2.8 (0.00096)
N _e ^{Var(o)} _{e(G₁₋₂₀)} (Harmonic Ne from Var Off) (SD)	3 (0.44)	4.1 (0.6)	16 (3)	42 (4.6)
Ne required for the Simulated Cumul. Resp. (SD)	3.3 (2.0)	0.4 (0.4)	9.0 (21.1)	0.3 (0.3)
Heterozygosity at G ₀ (SD)	0.003 (0.003)	0.003 (0.004)	0.003 (0.003)	0.003 (0.004)
Heterozygosity at G ₂₀ (SD)	0.00083 (0.00047)	0.00073 (0.00043)	0.00087 (0.00021)	0.00072 (0.00014)
Number Of Polymorphism at G ₀ (SD)	3 (3)	3.2 (4.1)	3.1 (3.3)	3.3 (4.1)
Number Of Polymorphism at G ₂₀ (SD)	5.1 (2.5)	6 (3.1)	40 (8.8)	66 (9.2)
Simulation Fraction Without Any Fixed Mutation	0	0.0025	0	0.999 ^d
Fixation Time in generations (SD)	3.8 (1.7)	7.2 (3)	5.9 (2.3)	NA ^d
Number Of Fixed Mutation Per Family (SD)	7.7 (2.6)	2.3 (1.4)	10 (3)	NA ^d
Q5 Fixed Mut. effect (Non Normalized)	-0.019	-0.5	0.011	NA ^d
Q50 Fixed Mut. effect (Non Normalized)	0.43	-0.00086	0.66	NA ^d
Q95 Fixed Mut. effect (Non Normalized)	1.3	0.5	1.7	NA ^d
Q5 Fixed Mut. effect (Normalized)	-0.034	-0.44	0.015	NA ^d
Q50 Fixed Mut. effect (Normalized)	0.72	-0.00054	0.86	NA ^d
Q95 Fixed Mut. effect (Normalized)	2.5	0.42	2.4	NA ^d
CovGE (SD)	-0.23 (0.35)	-0.0035 (0.68)	-0.45 (0.34)	-0.0011 (0.36)
Q5 CovGE	-0.88	-0.87	-1.1	-0.5
Q50 CovGE	-0.11	0	-0.37	-0.00017
Q95 CovGE	0.029	0.86	-0.072	0.49

^a P-values are computed from the distribution of cumulative response under simulated HDHS.

^b All values are computed as the mean (SD or quantile respectively, when specified) over 2000 simulations.

^c Under LDNS, we expected a neutral coalescent time around 98 generations well beyond the 20 simulated generations, which provided highly biased G₂₀ TMRCA and N_e estimators.

^d Under LDNS, we obtained very few fixed mutation so that we were unable to compute the corresponding statistics.

currence of a new allele (Kingman 1978; Turelli 1984) — rather than adding effects incrementally — would have likely resulted in smaller estimate of σ_M^2 (Hodgins-Davis *et al.* 2015). Whether the incremental model or the HoC or a combination of both such as the regression mutation model (Zeng and Cockerham 1993) was better suited to mimic our Saclay DSEs is an open question. However several lines of evidence argue in favour of a non-limiting mutational input in our setting. First, the architecture of maize flowering time is dominated by a myriad of QTLs of small additive effects (Buckler *et al.* 2009). Over 100 QTLs have been detected across maize lines (Buckler *et al.* 2009), and over 1000 genes have been shown to be involved in its control in a diverse set of landraces (Romero Navarro *et al.* 2017). Second, in Saclay DSEs alone, transcriptomic analysis of apical meristem tissues has detected 2,451 genes putatively involved in the response to selection between early and late genotypes, some of which being interconnected within the complex gene network that determines the timing of floral transition (Tenaillon *et al.* 2018). This suggests that not only the number of loci is considerable, but also that their connection within a network further enhances the number of genetic combinations, and in turn, the associated phenotypic landscape.

The breadth of the mutational target is a key parameter for adaptation (Höllinger *et al.* 2019). Altogether, our results suggest that despite a small number of segregating loci (Tab. 3c and Fig. S6) expected under HDHS, adaptive variation was continuously fueled by a large mutational target which translated into a long-term selection response. In other words, the large mutational target compensates for the small population sizes, and triggers the long-term maintenance of adaptive diversity at the population level after the selection-drift-mutation equilibrium is reached, i.e. after three to five generations. Noteworthy the expected level of heterozygosity in our controls (No Selection models, NS) corresponded to neutral predictions (Crow and Maruyama 1971; Kimura 1969).

Quick fixation of *de novo* mutations drive Saclay DSEs selection response The observed fixation time of mutations without selection is expected under standard neutral theory. The Kingman coalescent indeed predicts a TMRCA around 8 generations for a population size of 5 which matched closely our observed value of 7.6 obtained under HDNS. With selection, instead, we observed a quick fixation of mutations in three to four generations under HDHS. Likewise, the number of fixed mutation increased from 2.3 in HDNS to 7.7 in HDHS (Tab. 3). Note that while one would expect emerging patterns of hard sweeps following such rapid mutation fixation, our selfing regime which translated into small effective recombination likely limits considerably genetic hitchhiking footprints, so that such patterns may be hardly detectable.

Short fixation times made the estimate of effective population sizes challenging. We used two estimates of N_e to shed light on different processes entailed in HDHS stochastic regime. These estimates were based on expected TMRCA and on the variance in the number of offspring (Crow and Kimura 1971), respectively. We found the latter to be greater than the former. This can be explained by the fact that selection is known to substantially decrease effective population size on quantitative trait submitted to continuous selection, because of the increase in covariance between individuals due to selection (Santiago and Caballero 1995), and because selection on the phenotypic value acts in parts on non-heritable variance (i.e., on the environmental variance component of V_P (Chantepie and Chevin 2020)). Note that

our estimates of N_e — based on coalescence times computed from the known genealogical structure — allow to account for these effects. However, this is not without drawback: TMRCA estimates were much shorter than expected, a result consistent with the occurrence of multiple merging along pedigrees, i.e. multiple individuals coalescing into a single progenitor. In fact, multiple merger coalescence models may be better suited to describe rapid adaptation than the Kingman coalescent (Neher 2013).

Both fixation time and probability depend on the selection coefficient s and the initial frequency of the mutation in the population. In our setting, conditioning on its appearance in the subset of selected individuals, the initial frequency of a mutation was 0.10, which was unusually high and translated into selection and drift exerting greater control over mutations. In contrast, in more traditional drift regimes, even when an allele is strongly selected ($2N_e s \gg 1$), drift dominates at mutation occurrence, i.e. with two absorbing states for allele frequency near zero and one (Walsh and Lynch 2018). Under HDHS regime, selection induces repeated population bottlenecks that change the structure of the pedigrees and translate into a decrease in effective population size compared to the HDNS regime. Drift and selection can therefore not be decoupled, and they do not act additively.

High stochasticity promotes the fixation of small effect mutations

Interplay between drift and selection promoted stochasticity in our setting, which manifested itself in various ways : (i) through the selection response, with different families exhibiting contrasting behaviors, some responding very strongly and others not (Fig. 1); (ii) through the dynamics of allele fixation (Fig. 2 & 3); and (iii) through the distribution of $Cov(GE)$ (Fig. 6). Stochasticity tightly depends on census population size (Hill 1982a,b). Unexpectedly, however, we found a bias towards the fixation of advantageous mutations compared with the expectation (Fig. 4). Comparison of the distributions of the mutational raw effects indicated that, among advantageous mutations, a greater proportion of those with small effects were fixed under the High Drift than under the Low Drift regime (Fig. 4 (a) versus (b)). This result echoes those of Silander *et al.* (2007), who showed — using experimental evolution with bacteriophage — that fitness declines down to a plateau in populations where drift overpowers selection. The authors note: "If all mutations were of small effect, they should be immune to selection in small populations. This was not observed; both deleterious and beneficial mutations were subject to selective forces, even in the smallest of the populations."

What are the underlying mechanisms behind this fixation bias? We found a negative covariance between selected genotypes and their corresponding micro-environmental values, that modified the mutational effect to an apparent mutational effect perceived in the particular micro-environment. The negative $Cov(GE)$ arose mechanically from selection of two independent random variables, whatever the sampling size as illustrated in Fig. S11 and Fig. S12. This effect evokes the so-called Bulmer effect (Bulmer 1971), that causes a reduction of genetic variance due to the effect of selection on the covariance between unlinked loci. Interestingly, under the High Drift regime, we observed a less negative $Cov(GE)$ on average than with a 10 times higher census size (Low Drift). This translated, after dividing by the environmental standard deviation of selected individuals, to a greater apparent effect of small mutations under the High Drift regime. In other words, High Drift-High Selection intensity tends to magnify mutational effects from an environmental per-

spective. In support of this explanation, normalization by the environmental standard deviation actually erased the difference between the two distributions of mutational effect (under low and High Drift, Fig. S8). Unlike the Bulmer effect however, this one was restricted to the generation of mutation occurrence, but favored long-term fixation of slightly advantageous mutations by a transient increase of their frequency. Because of a significant variance of $\text{Cov}(GE)$, this effect on small effect mutation fixation was mostly stochastic. Therefore, we interpreted the fixation of a high proportion of slightly beneficial mutations, and their significant contribution to selection response, by the less efficient exploration of the initial distribution per simulation (increasing their prevalence) but the stochastic "help" of a lesser negative $\text{Cov}(GE)$.

Just like $\text{Cov}(GE)$, epistatic interactions may further exacerbate stochasticity Dillmann and Foulley (1998). While we showed that *de novo* mutations are fixed sequentially and therefore rarely interact, additive effects of new mutations tightly depend on the genetic background in which they occur (Plucain *et al.* 2014), and mutational history modulates the amount of additive genetic variance (Hill *et al.* 2008). While we have not accounted for them, epistatic interactions may hence result in a distortion of the distribution of mutation effects. Epistasis can also generate asymmetrical selection responses (Lynch *et al.* 1998; Keightley 1996). Because the two initial inbred lines, F252 and MBS, have been intensively selected for earliness (Camus-Kulandaivelu *et al.* 2006; Rebourg *et al.* 2003), we expect in our setting a diminishing return of mutational effects in the Early populations and, conversely, mutations of high effect in the Late populations (Durand *et al.* 2010). Any new mutant occurring within these 'early' genetic backgrounds, can either constrain or accentuate phenotypic effects, depending on direction of selection. Altogether, epistasis could explain some discrepancies between observations and simulations, such as the high stochasticity in Saclay DSEs.

Deficit of fixation of deleterious mutations suggests a limited cost of selection As expected, we observed that selection decreased the number of segregating polymorphic loci at equilibrium compared to regimes without selection (Tab. 3). Interestingly however, this effect was reduced for small population size. Under High Drift, selection induced an average loss of a single polymorphism at equilibrium (HDHS vs. HDNS, Tab. 3) while under the Low Drift regime over 20 polymorphisms were lost (LDHS vs. LDNS, Tab. 3). A similar trend was recovered at the mutation fixation level where on average 7.7 mutations were fixed under the High Drift-High Selection intensity and only 10 under Low Drift-High Selection intensity. In other words, the 10-fold population increase did not translate into a corresponding increase in the number of segregating and fixed mutations, as if there was a diminishing cost with decreasing population size. Under High Drift (/Low Drift), at each generation 500 (/5000) offspring of 2×1000 loci were produced. Considering a mutation rate per locus of $6000 \times 30 \times 10^{-9}$, (*i.e.* (Clark *et al.* 2005)), it translated into 180 mutations events (/1800 mutations events). However most mutations are lost as only mutations occurring in the subset of selected individuals survive. The initial frequency of a mutation in this subset, *i.e.* of size 5 or 50, is 1/10 under High Drift and 1/100 under Low Drift. In the former, the interplay between the initial frequency and selection intensity allows a better retention of beneficial mutations of small effect (Fig. 4) than in the latter. Interestingly at equilibrium, we also observed a higher level of residual heterozygosity with selection than without, irrespective

of population size, suggesting a small impact of selection in the long-term heterozygosity maintenance. Overall, our High Drift-High Selection intensity regime maintains a small, but sufficient number of polymorphisms for the selection response to be significant.

Our selection response evidenced a deficit of fixation of deleterious mutations and hence a modest genetic load (Fig. 4 and S8). We identified three reasons behind this observation. Firstly, in our design, the selection intensity of 1% was applied on the trait. Hence, in contrast to the infinitesimal model for which a high number of polymorphic loci are expected to individually experience a small selection intensity, selection intensity was "concentrated" here on a restricted number of loci, *i.e.* those for which polymorphisms were segregating. Secondly, we applied truncation selection whose efficiency has been demonstrated (Crow and Kimura 1979). The authors noted: "It is shown, for mutations affecting viability in *Drosophila*, that truncation selection or reasonable departures therefrom can reduce the mutation load greatly. This may be one way to reconcile the very high mutation rate of such genes with a small mutation load." Thirdly, the lack of interference between selected loci in our selection regime may further diminish the selection cost (Hill and Robertson 1966). Reduced interference in our system is indeed expected from reduced initial diversity and quick fixation of *de novo* mutations. Whether natural selection proceeds through truncation selection or Gaussian selection is still a matter of debate (Crow and Kimura 1979). Measuring the impact of these two types of selection on the genealogical structure of small populations including on the prevalence of multiple merging branches will be of great interest to better predict their fate.

This under-representation of deleterious variants echoes with empirical evidence that in crops, elite lines are impoverished in deleterious variants compared to landraces owing to a recent strong selection for yield increase (Gaut *et al.* 2015). Likewise, no difference in terms of deleterious variant composition was found between sunflower landraces and elite lines (Renaut and Rieseberg 2015). Hence, while the dominant consensus is that the domestication was accompanied by a genetic cost linked to the combined effects of bottlenecks, limited effective recombination reducing selection efficiency, and deleterious allele surfing by rapid population expansion (Moyers *et al.* 2018), recent breeding highlights a different pattern. We argue that our results may help to understand this difference because under High Drift-High Selection intensity, a regime likely prevalent in modern breeding, genetic load is reduced. Moreover, our results may provide useful hints to explain the evolutionary potential of selfing populations located at the range margins. Just like ours, such populations are generally small, display both, inbreeding and reduced standing variation (Pujol and Pannell 2008) and are subjected to environmental and demographic stochasticity.

Conclusion In conclusion, our High Drift-High Selection intensity regime with non-limiting mutation highlights an interesting interplay between drift and selection that promotes the quick fixation of adaptive *de novo* mutations fueling a significant but stochastic selection response. Interestingly, such selection response is not impeded by the fixation of deleterious mutations so that adaptation in HDHS proceeds with limited genetic load. Our results provide an explanation for patterns highlighted during recent breeding as well as the high colonization ability of small selfing populations located at species range margins. They also call for a better mathematical description of the multilocus adaptive process sustaining the evolution of small populations

1 under intense selection.

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18 **Data availability**

19 The complete R script for performing the simulations as well
20 as the summary data for flowering time (2 DSEs and 20
21 generations) are available at INRAe dataverse (data.inrae.fr):
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23 **Conflicts of Interest**

24 The authors declare that there is no conflict of interest.

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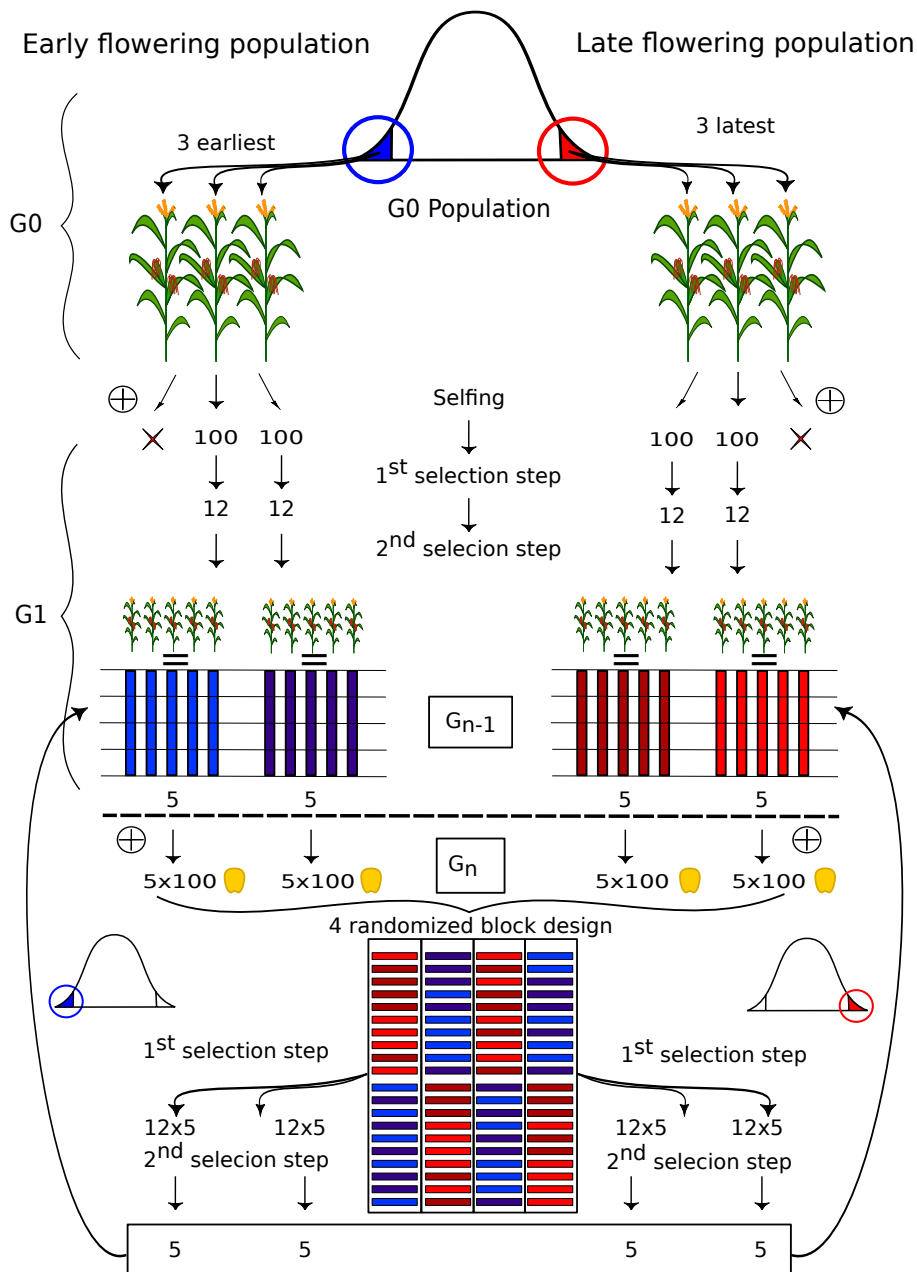


Figure S1 Experimental scheme of Saclay DSEs. For clarity a single scheme is shown but was replicated for the two DSEs. Starting from an inbred G_0 population with little standing variation ($< 1\%$ residual heterozygosity (Durand *et al.* 2015)), the three earliest/latest flowering individuals represented in blue/ red were chosen based on their offspring phenotypic values as the founders of two families forming the early/ late population. For the subsequent generations, 10 (≈ 5 per family) extreme progenitors were selected in a two step selection scheme among 1000 plants. More specifically, 100 seeds per progenitor were evaluated in a four randomized-block design, *i.e.* 25 seeds per block in a single row. In a first selection step, the $3 \times 4 = 12$ earliest/ latest flowering plants among the 100 plants per progenitor were selected in a first step. Then in a second selection step, 10 (≈ 5 per family) individuals were selected within each population based on both flowering time and kernel weight and the additional condition of preserving two progenitors per family from the previous generation.

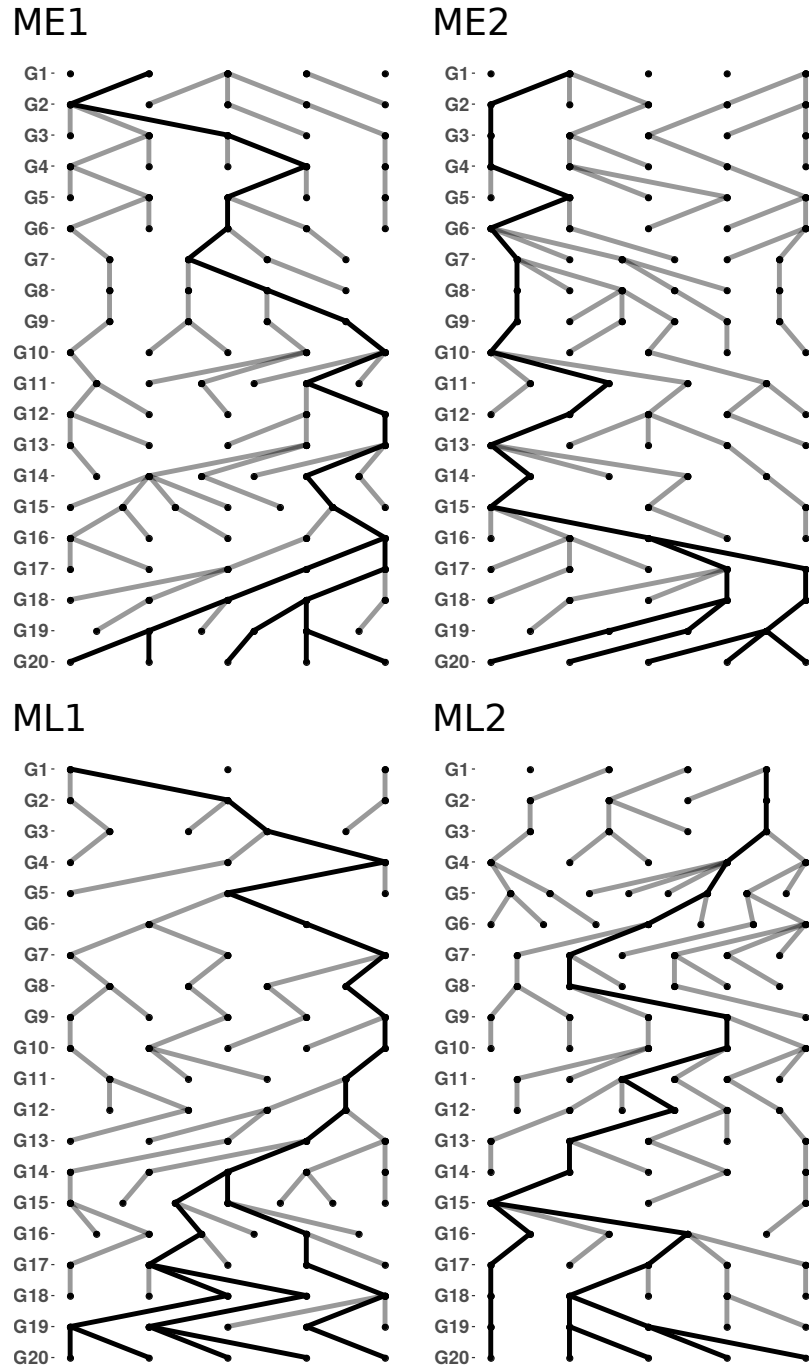


Figure S2a MBS family pedigrees from G1 to G₂₀. The two early families ME1 (a) and ME2 (b), and the two late families ML1 (c) and ML2 (d) are presented. Each node corresponds to a progenitor selected at a given generation. Each edge corresponds to a filial relationship between a progenitor and its offspring. Thick black lines indicate the ancestral path of the last generation (G₂₀).

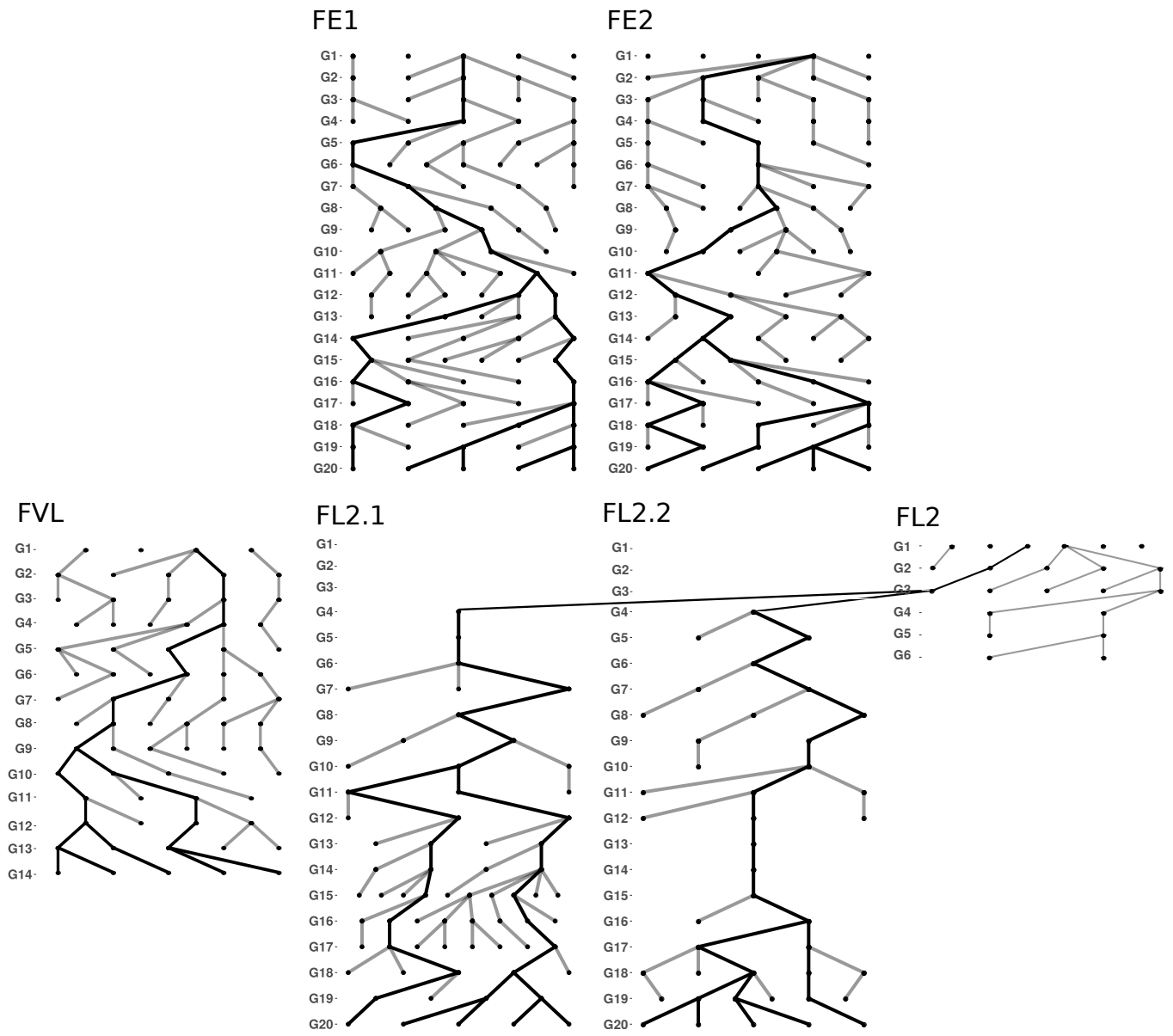


Figure S2b F252 family pedigrees from G1 to G20. Two early families FE1 (a), FE2 (b) and two late families FVL (c) & FL2 (f), are represented. FVL (c) could not be maintained after G14 as flowering occurred too late in the season for seed production. Both FL2.1 (d) and FL2.2 (e) were derived from a same individual from FL2 (f) at G3, after FVL was discarded. Each node corresponds to a progenitor selected at a given generation. Each edge corresponds to a filial relationship between a progenitor and its offspring. Thick black lines indicate the ancestral path of the last generation. (G₂₀)

1 Selection response and input - output variables relationship description

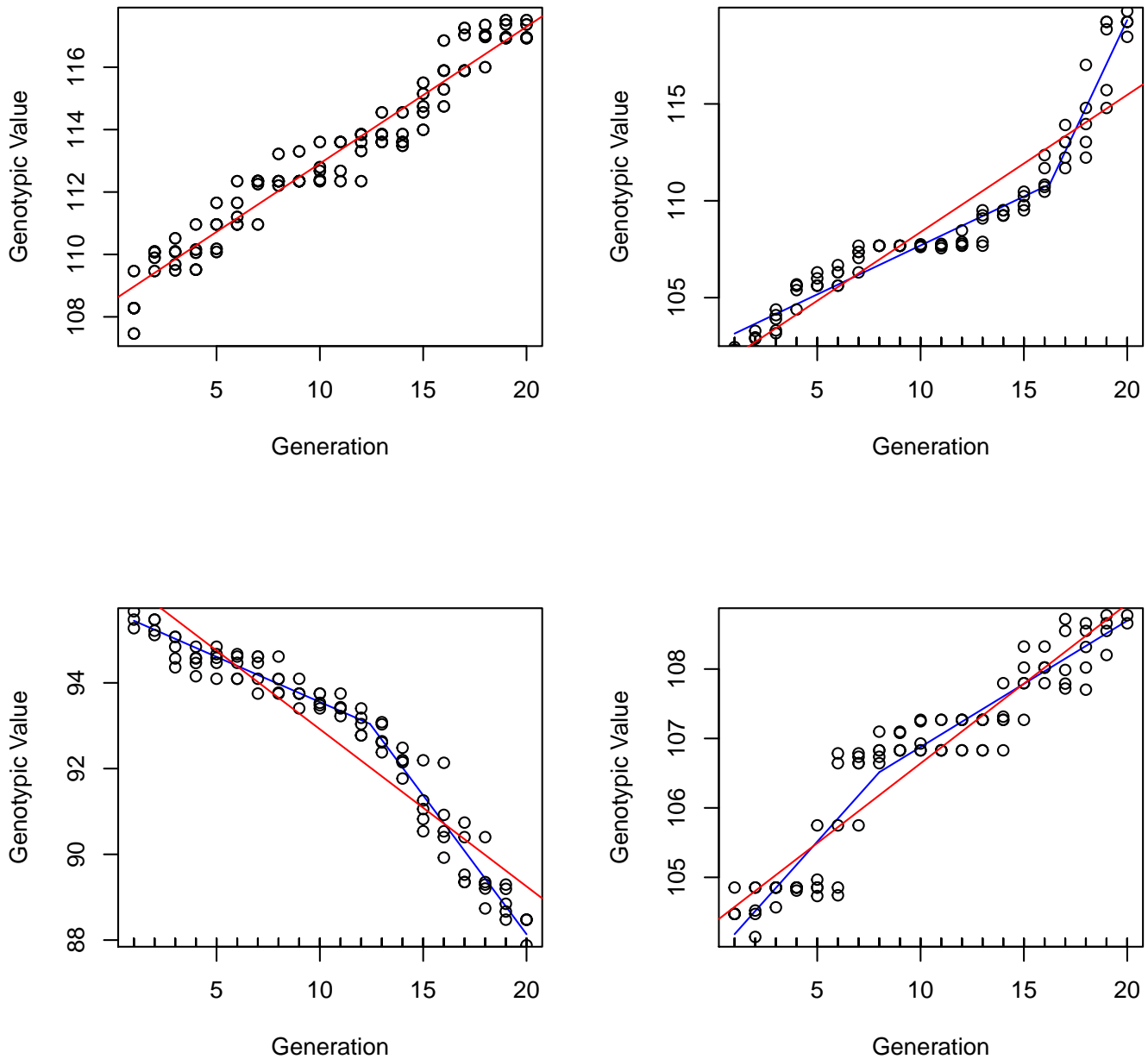


Figure S3 Illustration of simulated non-linear selection response in MBS. Each panel presents the evolution through time (x axis) of the genotypic value (y axis) of the 5 selected individual per family (empty dots). The red lines shows the linear regression of the selected genotypic values through times, while blue lines correspond to the best (AIC criterion) segmented linear model. The top left panel is an example for which a simple linear model fitted best the selection response, while the three others show a diversity of non-linear behaviors.



Figure S4 Correlation between model input variables (σ_{A0}^2 , σ_M^2 and σ_E^2) and output variables (G_0G_1 Response, # Breakpoints, First Slope and Greatest Slope). We obtained the output variables by fitting a segmented linear regression to the selection response from G_1 to G_{20} in individual. We estimated the number of breakpoints, the corresponding slopes, as well as the first & greatest slope by AIC maximization. In addition we determined the G_0G_1 response. A Principle Component Analysis was carried out on a subset of 200 independent simulations per regime (HDHS, LDHS, HDNS, LDNS). The darker the arrow representing a variable, the higher the intensity of its correlation to the axes.

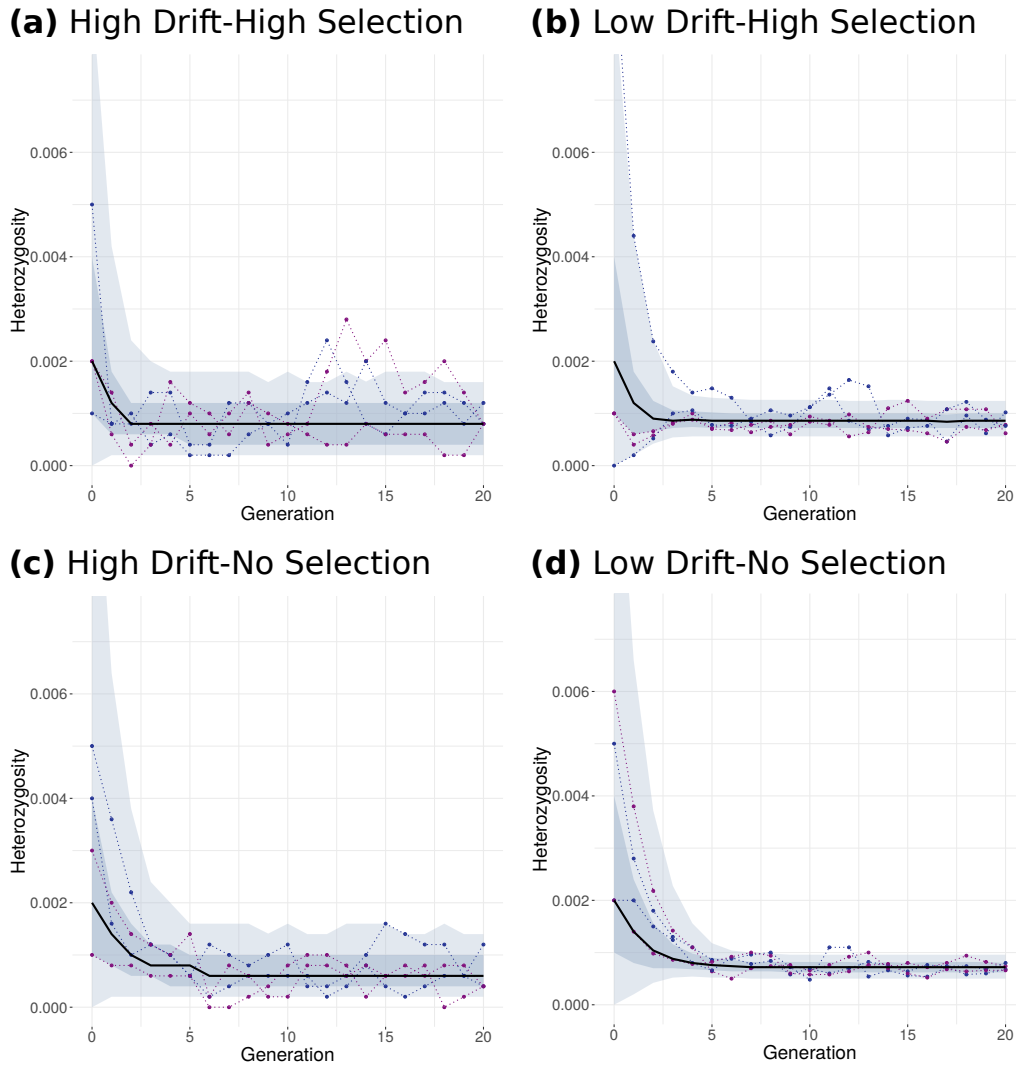
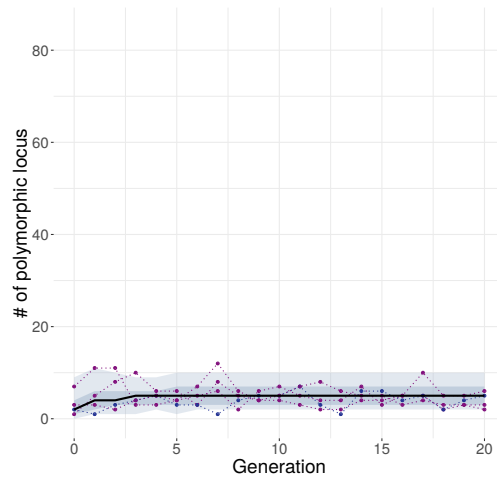
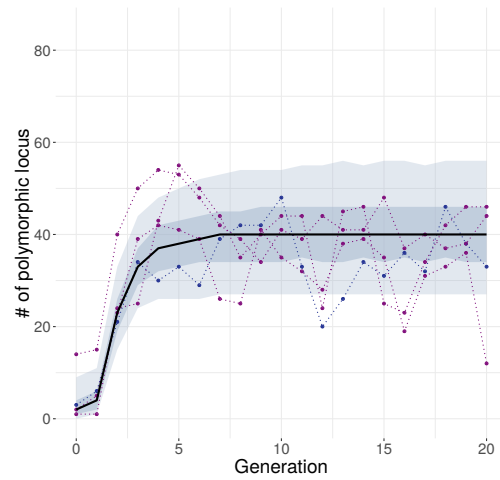


Figure S5 Evolution through time of the per-family mean heterozygosity over all loci, under HDHS (a), LDHS (b), HDNS (c), LDNS (d). The black line represents the median value of the per-family mean heterozygosity. The shaded area corresponds to the 5th-95th percentile (light blue) and to the 25th-75th percentile (dark blue). Four randomly chosen simulated families are represented with dotted line.

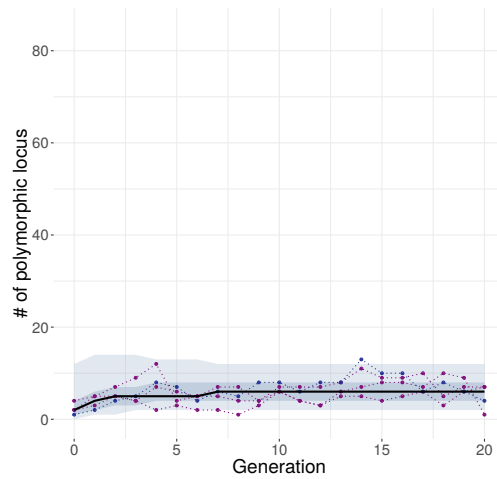
(a) High Drift-High Selection



(b) Low Drift-High Selection



(c) High Drift-No Selection



(d) Low Drift-No Selection

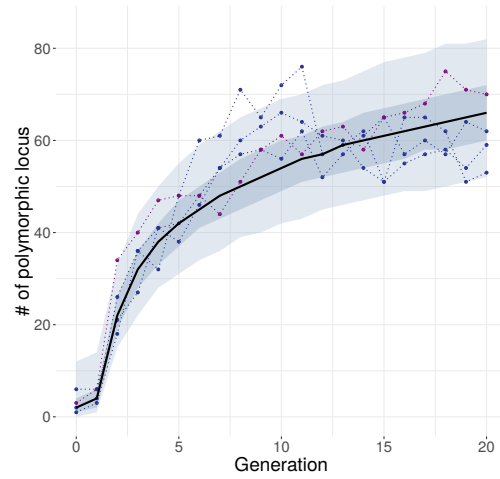
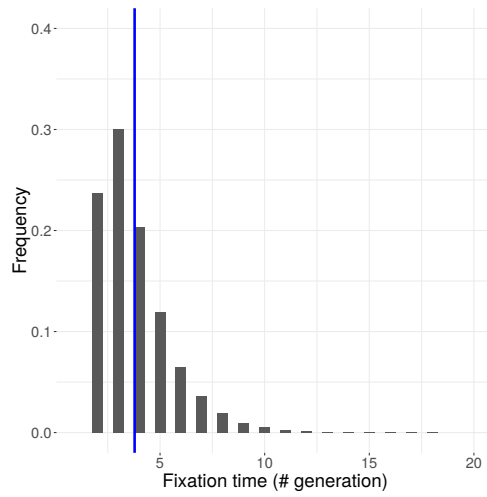
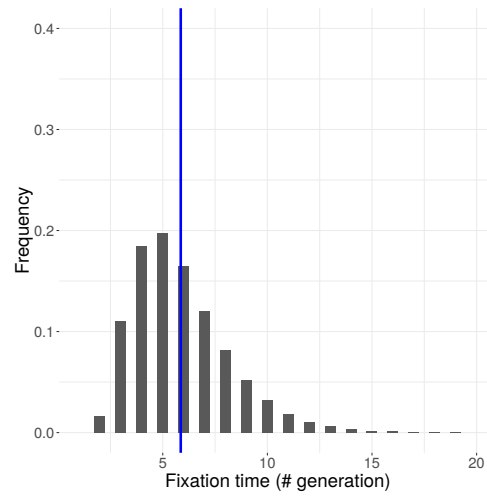


Figure S6 Evolution through time of the per-family mean number of polymorphic loci, under HDHS (a), LDHS (b), HDNS (c), LDNS (d). The black line represents the median value over 2000 simulations. The shaded area corresponds to the 5th-95th percentile (light blue) and to the 25th-75th percentile (dark blue). Four randomly chosen simulated families are represented with dotted line.

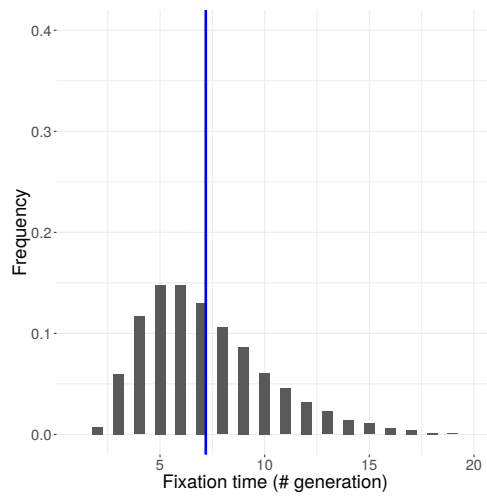
(a) High Drift-High Selection



(b) Low Drift-High Selection



(c) High Drift-No Selection



(d) Low Drift-No Selection

Figure S7 Frequency distribution of mutation fixation times over all simulated families under HDHS (a), LDHS (b), HDNS (c), LDNS (d). Note that under LDNS, we obtained very few fixed mutation so that we were unable to draw the corresponding distribution. Blue vertical lines represent the interpolated median.

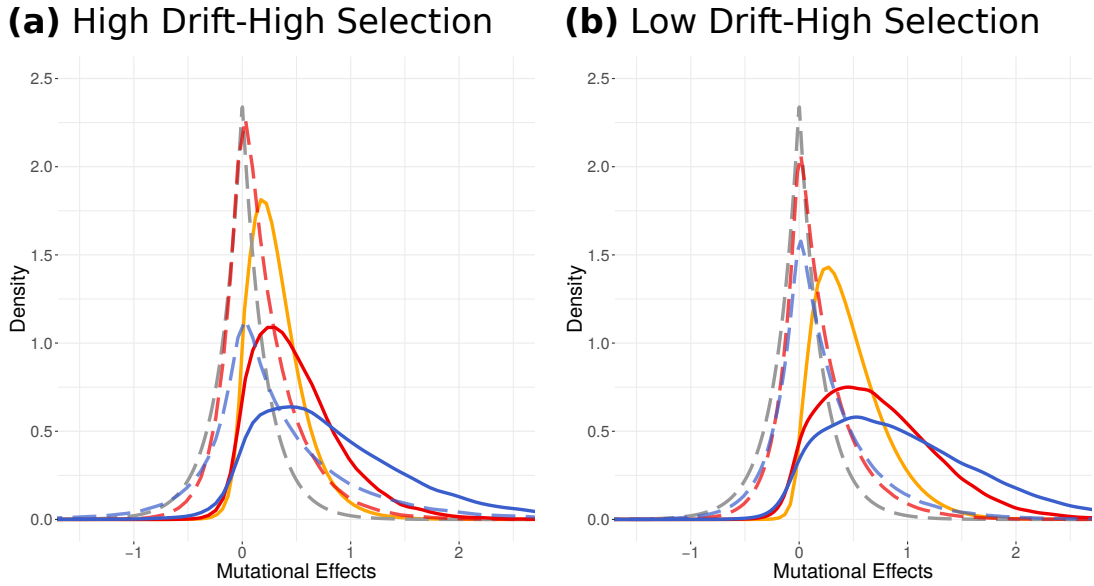


Figure S8 Distribution of mutation effects under HDHS (a), LDHS (b). The dotted lines indicate the distribution of effects (DFE) of incoming *de novo* mutations considering raw effects in all individuals (grey), in selected individuals (red), and effects normalized by environmental variation in selected individuals (blue). The plain lines indicate DFE of fixed mutations following the same colour code. The golden line represents the expected DFE of fixed mutations according to Eq: 16.

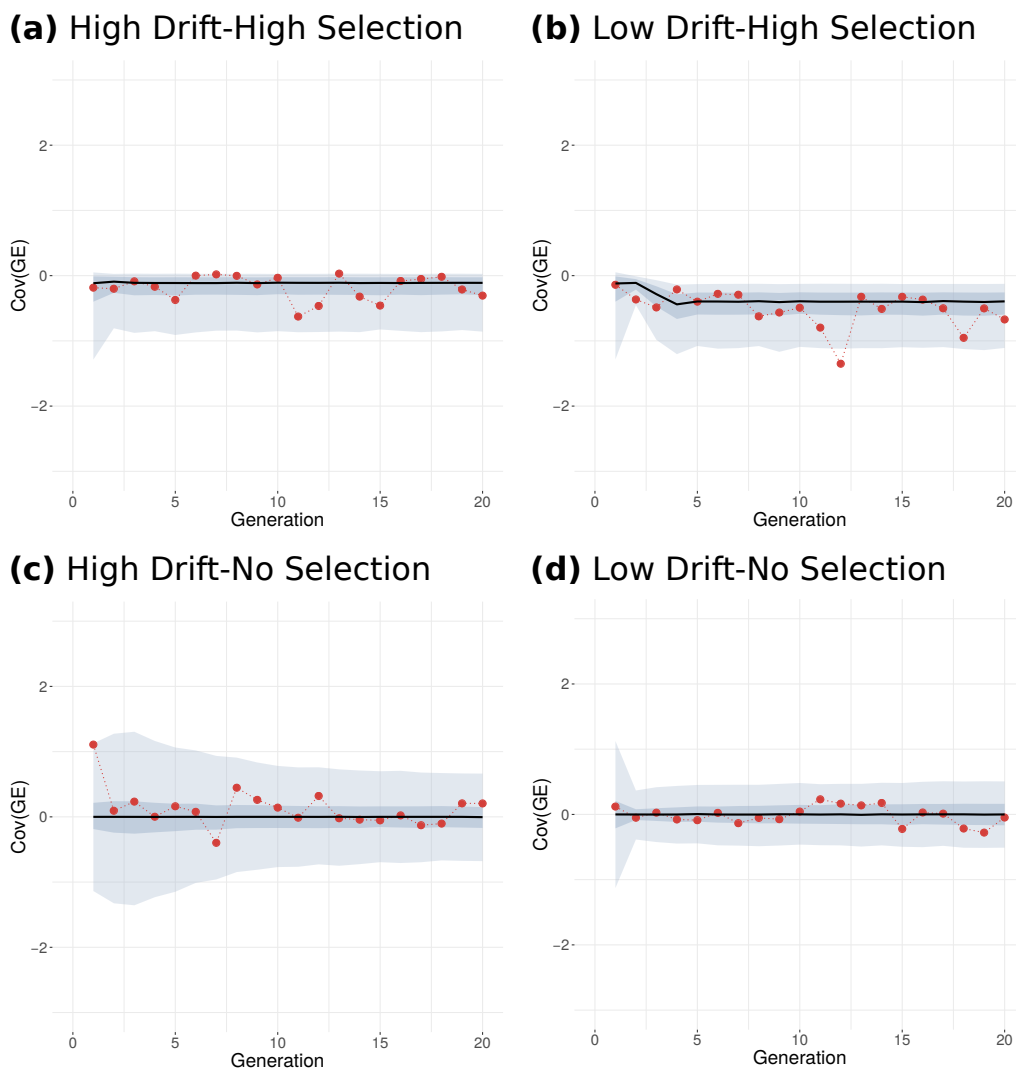


Figure S9 Evolution through time of the per-family covariance between environmental and genotypic values of the selected individuals, under our four simulated regimes. The black line represents the evolution of the median value over 2000 simulations in HDHS (a), LDHS (b), HDNS (c), LDNS (d). The shaded area corresponds to the 5th-95th percentile (light blue) and to the 25th-75th percentile (dark blue). One randomly chosen simulated family is represented with red dotted line, to highlight the inter-generation stochasticity. No significant autocorrelation was found.

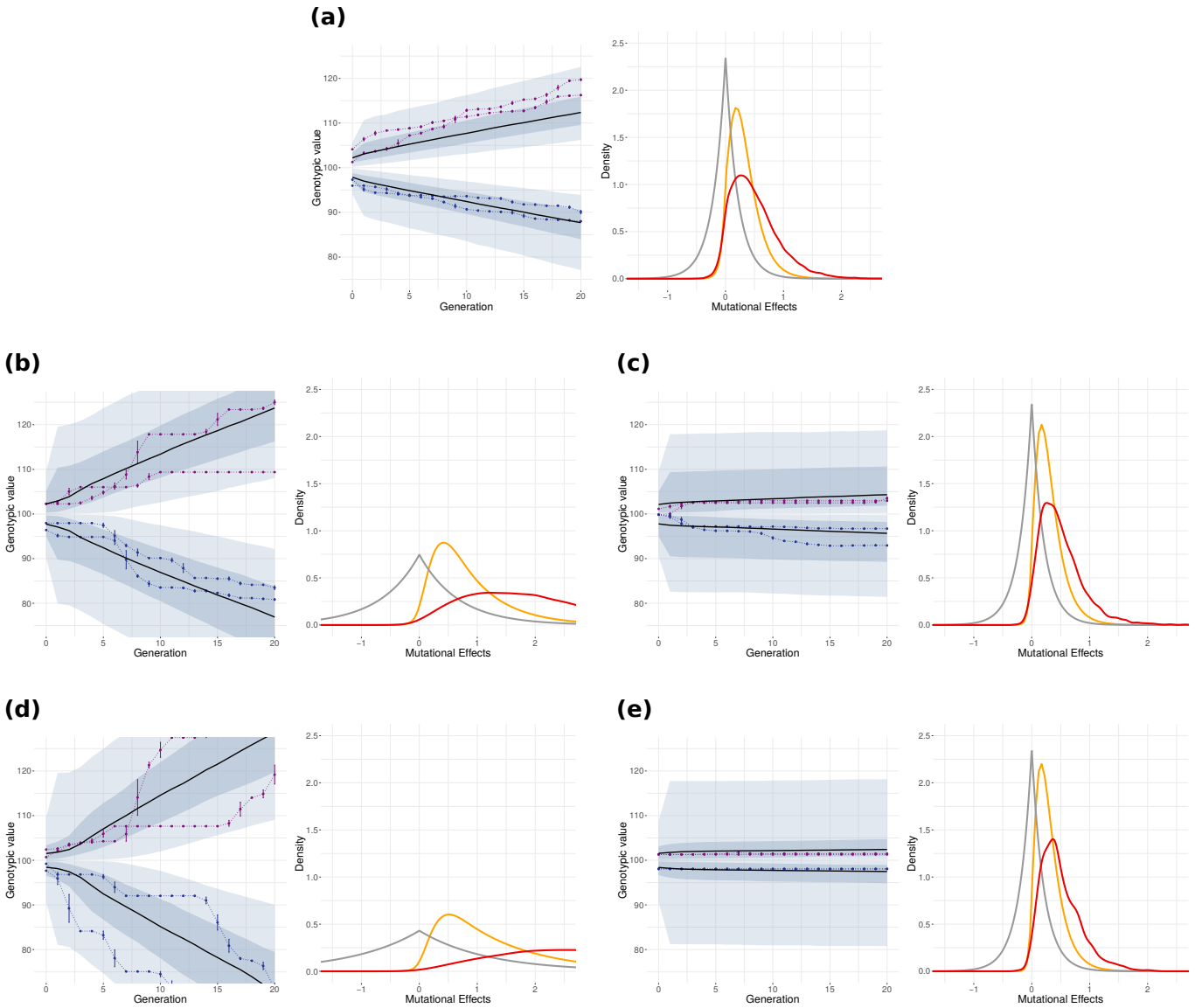


Figure S10 Comparison between simulated HDHS regime under various mutational parameters. Each panel (a) to (e) replicates Fig. 1 on the left and Fig. 4 on the right. The left side of each panel represents the mean genotypic values of the selected progenitors per family (expressed in Days To Flowering, DTF) across generations, violet/blue color identifies the late/ early population. In each population, the black line represents the evolution of the median value over 2000 simulations of the family genotypic mean. The shaded area corresponds to the 5th-95th percentile (light blue) and to the 25th-75th percentile (dark blue). In addition, two randomly chosen simulations are shown with dotted lines. The right side of each panel represents the distribution of effects of incoming *de novo* and fixed mutations under HDHS. Density distributions are shown for all incoming *de novo* mutational effects in grey — reflected exponential distribution —, and fixed mutations over 2000 simulations in red. Theoretical expectations from (Eq: 16) are plotted in gold. Panel (a) corresponds to the main text simulation parameters, so that HDHS: $U = 1000 \times 6000 \times 30 \times 10^{-9} = 0.18$, $E(\lambda_M) = 4.69$, $E(\sigma_M^2) = 0.033$. (b) and (c) correspond to simulations with 100 loci and the same mutation rate per locus $\mu = 6000 \times 30 \times 10^{-9} = 0.018$, while (d) and (e) correspond to simulations with 1000 loci but a mutation rate per locus $\mu = 6000 \times 1 \times 10^{-9} = 0.006$. Panels (b) and (d) were obtained with the same total mutational variance $E(\sigma_M^2) = 0.033$ as HDHS but smaller λ_M , ($E(\lambda_M) = 1.50$ and $E(\lambda_M) = 0.86$ respectively). (c) and (e) were obtained with the same mutational variance per locus as HDHS ($E(\lambda_M) = 4.69$) but smaller total mutational variance than HDHS ($E(\sigma_M^2) = 0.0033$ and $E(\sigma_M^2) = 0.001$ respectively). Overall we have :

(b) $U = 100 \times 6000 \times 30 \times 10^{-9} = 0.018$, $E(\lambda_M) = 1.50$, $E(\sigma_M^2) = 0.033$

(c) $U = 100 \times 6000 \times 30 \times 10^{-9} = 0.018$, $E(\lambda_M) = 4.69$, $E(\sigma_M^2) = 0.0033$

(d) $U = 1000 \times 6000 \times 1 \times 10^{-9} = 0.006$, $E(\lambda_M) = 0.86$, $E(\sigma_M^2) = 0.033$

(e) $U = 1000 \times 6000 \times 1 \times 10^{-9} = 0.006$, $E(\lambda_M) = 4.69$, $E(\sigma_M^2) = 0.001$.

Note that while the distributions of incoming *de novo* and fixed mutational effects are similar among panels (a), (c), (e), the number of fixed mutations in (c) and (e) is much lower than in (a) accounting for the lack of selection response observed in those panels.

Negative $\text{Cov}(G_{\text{selected}}, E_{\text{selected}})$ schematic

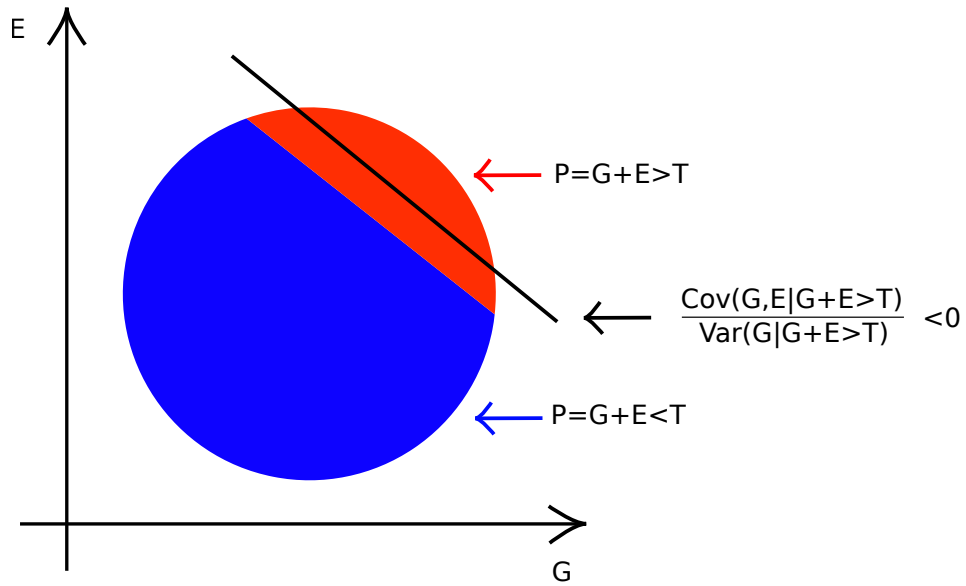


Figure S11 Schematic representation of the impact of selection on $\text{Cov}(G, E)$. For illustration purposes, let P the sum of two independent and identically distributed random variables, G and E , such that both G and E follow a standard normal distribution, *i.e.* $P = G + E$ with $G \sim \mathcal{N}(0, 1)$ and $E \sim \mathcal{N}(0, 1)$. The black line represent the regression of E_{selected} on G_{selected} with a negative slope $\frac{\text{Cov}(G_{\text{selected}}, E_{\text{selected}})}{\text{Var}(G_{\text{selected}})} \leq 0$.

1 **Negative** $\text{Cov}(G_{|\text{selected}}, E_{|\text{selected}})$ **and its stochasticity**

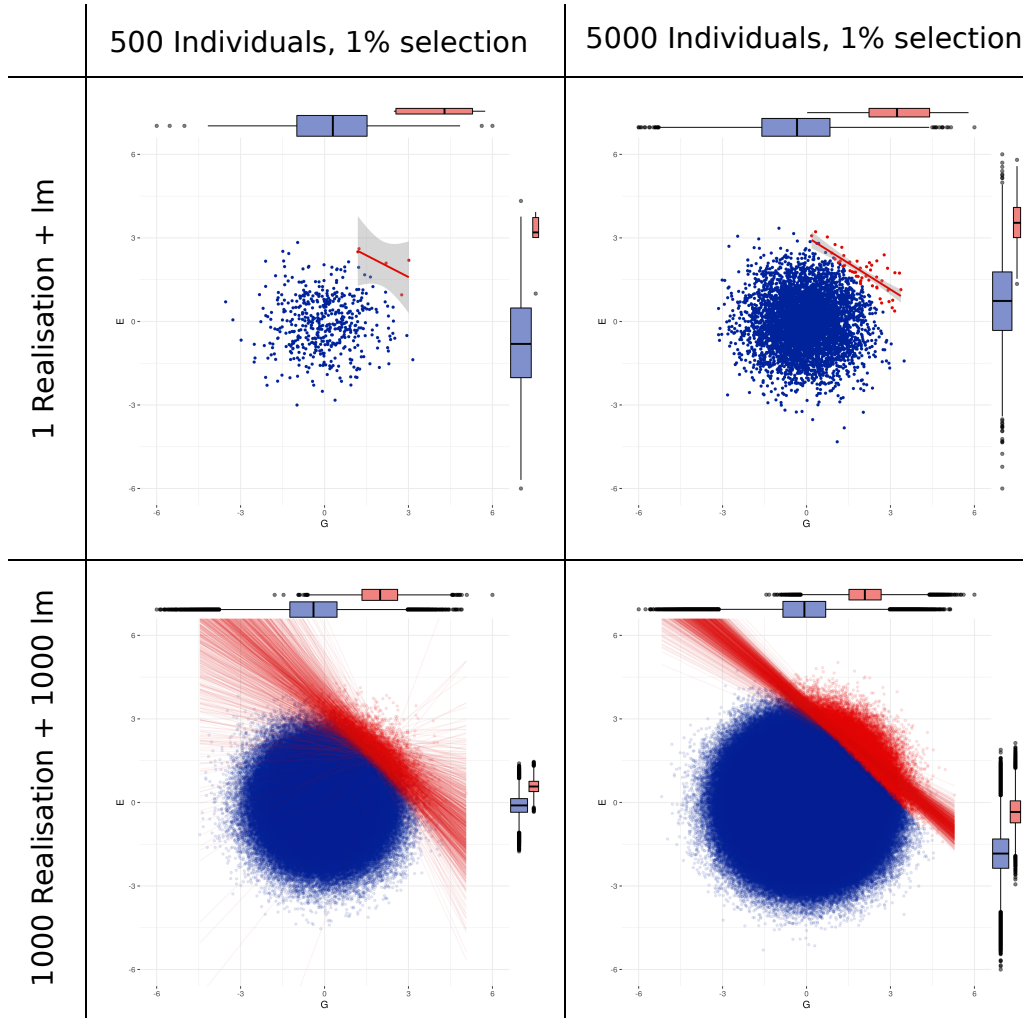


Figure S12 Schematic representation of the impact of selection and drift on $\text{Cov}(G, E)$. Let P the sum of two independent random variables, G and E , such that both G and E follow a standard normal distribution, *i.e.* $P = G + E$ with $G \sim \mathcal{N}(0, 1)$ and $E \sim \mathcal{N}(0, 1)$. Let sample 500 individuals from P and plot $E = f(G)$ (right columns), respectively 5000 (left columns) and select (red dots) the best 1% based on P . The upper row represents one realisation, with the red line corresponding to the regression of $E_{|\text{selected}}$ on $G_{|\text{selected}}$ with a negative slope $\frac{\text{Cov}(G_{|\text{selected}}, E_{|\text{selected}})}{\text{Var}(G_{|\text{selected}})} \leq 0$. The lower row represents the realisation of 1000 independent sampling of 500 and 5000 individuals, with the corresponding linear regressions. We observe a lower lesser exploration of possible values (red plus blue area) under low population size and a high stochasticity in the values of $\text{Cov}(G_{|\text{selected}}, E_{|\text{selected}})$