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Determinants of rapid adaptation in species with large variance in offspring production

Kevin Korfmann[1] | Marie Temple-Boyer[1] | Thibaut Sellinger[1,2] | Aurélien Tellier[1]

[1]Professorship for Population Genetics, Department of Life Science Systems, Technical University of Munich, Freising, Germany

[2]Department of Environment and Biodiversity, Paris Lodron University of Salzburg, Salzburg, Austria

Correspondence
Aurélien Tellier, Professorship for Population Genetics, Department of Life Science Systems, Technical University of Munich, Freising, Germany.
Email: aurelien.tellier@tum.de

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Abstract

The speed of population adaptation to changing biotic and abiotic environments is determined by the interaction between genetic drift, positive selection and linkage effects. Many marine species (fish, crustaceans), invertebrates and pathogens of humans and crops, exhibit sweepstakes reproduction characterized by the production of a very large amount of offspring (fecundity phase) from which only a small fraction may survive to the next generation (viability phase). Using stochastic simulations, we investigate whether the occurrence of sweepstakes reproduction affects the efficiency of a positively selected unlinked locus, and thus, the speed of adaptation since fecundity and/or viability have distinguishable consequences on mutation rate, probability and fixation time of advantageous alleles. We observe that the mean number of mutations at the next generation is always the function of the population size, but the variance increases with stronger sweepstakes reproduction when mutations occur in the parents. On the one hand, stronger sweepstakes reproduction magnifies the effect of genetic drift thus increasing the probability of fixation of neutral allele and decreasing that of selected alleles. On the other hand, the time to fixation of advantageous (as well as neutral) alleles is shortened by stronger sweepstakes reproduction. Importantly, fecundity and viability selection exhibit different probabilities and times to fixation of advantageous alleles under intermediate and weak sweepstakes reproduction. Finally, alleles under both strong fecundity and viability selection display a synergistic efficiency of selection. We conclude that measuring and modelling accurately fecundity and/or viability selection are crucial to predict the adaptive potential of species with sweepstakes reproduction.

KEYWORDS
adaptation, multiple merger coalescent, population genetics, selection

1 | INTRODUCTION

Starting from the seminal work of Darwin, evolution and adaptation of species/populations to their environment through a particular phenotype or trait have been traditionally assumed to be occurring at a slow pace and be beyond the direct observation of evolutionary biologists. However, numerous counter-examples recently challenge this view and demonstrate that adaptation to environmental change can be fast, which is occurring over few generations (Zhou et al., 2019). To name but a few, rapid adaptation is observed in

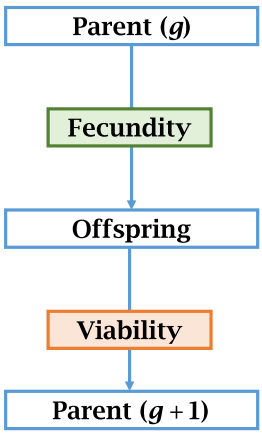
natural settings during colonization of novel habitats (Hu et al., 2019; Losos & Ricklefs, 2009), but also in response to human activities: in plants (Anderson et al., 2012) and fish (Crotti et al., 2021) responding to anthropogenic changes and destruction of habitats, in insects colonizing new urban habitats (Diamond et al., 2022), in bacteria resisting antibiotics (Barbosa et al., 2021), in fungi resistant to fungicides (Fisher et al., 2022) or in crop pathogens overcoming new plant resistance (Persoons et al., 2017). We define here rapid adaptation as occurring over few tens (up to hundred) generations thus including the effect of generation time.

With advances in sequencing technology, it becomes feasible to dissect the genetic architecture of the trait underpinning rapid adaptation, namely to decipher whether one or few genes with major effects or many loci with small effects are involved. In the former case, so-called selective sweeps occur at the given genes by the selection of an advantageous allele (Maynard Smith & Haigh, 1974; Stephan, 2019), while in the latter case, there is so-called polygenic selection driven by simultaneous changes in allele frequencies across many loci (Barghi et al., 2020; Jain & Stephan, 2017). Arguably, these both types of selection processes and models represent two extreme in a continuum of possible genetic architectures (number of genes involved, epistatic and pleiotropic interactions) and distribution of selection coefficients across loci (Barghi et al., 2020; Jain & Stephan, 2017; Stephan, 2016). Based on the current climate and global change accompanied by loss of biodiversity, as well as the importance of adaptive mechanisms for medicine and agriculture, there is a tremendous interest in measuring the speed of adaptation of species and uncovering the underlying genetic (coding genes, gene expression change, gene duplication, genome rearrangement, transposable elements, …) or epigenetic (RNA silencing, methylation, …) mechanisms. However, we suggest here that for evolutionary genomics of rapid adaptation to move into a predictive science, that is to be able to assess the adaptive potential of species and predict how and when adaptation may occur, it is important to account for the variability in life cycles and specificity of the life-history traits of each species. Indeed, a potential pitfall lies in the relative inadequacy of classic population genetics theory to describe the diversity of life cycles and life-history traits found in nature (Ellegren & Galtier, 2016). To date, analyses and predictions of adaptation (rapid or not) are mostly biased by the use of mathematical models with simplifying assumptions (e.g. assuming a Wright-Fisher model), which are violated in many species of bacteria, viruses, fish, invertebrates, fungi or plants, which exhibit clonal reproduction, large variance in offspring production (sweepstakes reproduction) and dormancy/quiescence (Eldon, 2020; Ellegren & Galtier, 2016; Lennon et al., 2021; Sabin et al., 2022; Tellier, 2019; Tellier & Lemaire, 2014).

In this study, we chose to focus on adaptation provided by one locus with a significant positive fitness effect. As a result, this allele may spread and become fixed in the population, generating a so-called selective sweep at the locus under selection (Maynard Smith & Haigh, 1974; Stephan, 2016, 2019). The speed of rapid adaptation depends on three distinct processes (Charlesworth, 2020; Charlesworth & Charlesworth, 2010): (1) the probability that a given advantageous allele appears by mutation at this locus; (2) the probability of fixation of this allele; and (3) the time to fixation of that advantageous allele. First, an advantageous allele needs to appear by random mutation. This process is quantified by the population mutation rate $\theta = 4N_e\mu$, where N_e is the inbreeding effective population size and μ the mutation rate (per site or per locus). In general, the time for new mutations to appear is only small enough to play an important role in rapid adaptation when both the mutation rate and population size are high such as in viruses, bacteria or fungi (especially crop pathogens; Stam & McDonald, 2018). Conversely, in most animal or plant species, mutation rates are too small to promote new mutations over few generations, and it suffices to analyse rapid adaptation based on standing variation (Eldon & Stephan, 2018, 2023). Second, a new advantageous allele (mutant) has a probability to reach fixation (P_{fix}) or to be lost, as genetic drift may counter-act the effect of positive selection. To assess the efficiency of selection, the probability of fixation of an advantageous allele should be compared with the probability of fixation of a neutral allele. Third, if the advantageous allele reaches fixation, it can do so more or less rapidly (measured in generations). This is termed as the time to fixation (T_{fix}) and to measure the effectiveness of selection it ought to be compared with that of a neutral allele. While we focus, for simplicity, on rapid adaptation due to positive selection at one locus, note that our predictions are affected in the genomic context by the effect of linked selection at neighbouring sites.

As mentioned above, population genetics theory is built on a mathematical framework, which models these three processes and is historically based on the so-called Wright-Fisher (WF) model of population evolution (see description in textbooks such as Charlesworth & Charlesworth, 2010). The Wright-Fisher model was rapidly extended to continuous-time diffusion and coalescent models (Charlesworth & Charlesworth, 2010). In its simplest version, the WF neutral model of evolution assumes a simplified life cycle in which each of the N haploid parents at generation g produces more than enough offspring (an infinite number), in order for N of them to constitute the next reproducing generation ($g + 1$). There is no overlap between generations, and offsprings choose their parent at random from generation g following a binomial sampling. An emerging property resulting from this random sampling scheme is that parents exhibit a distribution of offspring number, which is well approximated by a Poisson distribution with mean (and variance) equals to one (Charlesworth & Charlesworth, 2010). In other words, the variance in offspring production is small as most parents produce zero, one or two offspring, which become the next reproducing generation ($g + 1$).

To explicit the limitations of the WF model, we draw in Figure 1 a simplified life cycle starting from parents at generation g producing offspring regrouping various developmental stages: Plants produce seeds germinating into seedlings; fish but also invertebrates such as nematodes, crustaceans or insects produce eggs developing into juveniles; fungi produce various forms of spores; and bacteria can produce dormant/quiescent spores. The production of offspring



Processes		
Genetic drift	Mutation	Selection
Variance in offspring production among parents	Mutation in parent and/or mutation in offspring	Fecundity selection = mean production of of offspring per parent
Life span of offspring (dormancy, quiescence)	Mutation during the life span of offspring	Viability selection = mean viability of offspring

FIGURE 1 Schematic view of species life cycle. The cycle has two phases: fecundity and production of developmental stages (green), and viability (orange) with the growth and development to become a reproducing parent at generation $g + 1$. Each phase has neutral, mutational and selective processes associated.

constitutes the fecundity phase. These produced offspring hatch, germinate and/or grow to form potential parents, which are mature for reproduction, and constitute the next generation ($g + 1$). The survival of the produced offspring is termed the viability phase of the cycle. At each phase, life-history traits determine the rate of genetic drift, as well as mutational and selective processes, which can potentially result in different expectations from the Wright-Fisher model for θ, P_{fix} and T_{fix}. First, some species present a very large fecundity meaning that parents can produce a number of offspring/developmental stages much larger than the population size of adults (number of offsprings $\gg$ number of parents N), which can generate a large variance in offspring production (and/or survival) between parents (Árnason et al., 2023; Arnason & Halldorsdottir, 2015; Eldon et al., 2015; Eldon & Stephan, 2023; Eldon & Wakeley, 2006; Hedgecock & Pudovkin, 2011; Menardo et al., 2020; Sabin et al., 2022 and reviewed in Eldon, 2020; Tellier & Lemaire, 2014) resulting in a neutral sweepstakes reproduction life cycle. The neutral sweepstakes reproduction life cycle can be qualified as a specific case of "boom-and-bust" population dynamics within a generation.

Furthermore, under the explicit life cycle of Figure 1, defining the mutational process can be important as new mutations can occur in (1) the parental germ lines and are inherited by all produced offspring or (2) in the offspring. Additionally, fecundity selection occurs if a parent with an advantageous allele produces on average a larger number of offspring than other genotypes (Figure 1). Second, once the offspring are produced, their viability and life span can exhibit large variance within and between population/species. Dormancy is a common life-history trait of plants (seeds), invertebrates (eggs) or fungi and bacteria (also called quiescence or covert infections for human diseases), which increases the life span of the offspring, generating overlap of generations (Charlesworth, 1994; Charlesworth & Charlesworth, 2010; Kaj et al., 2001; Lennon et al., 2021; Tellier, 2019). Defining the mutational process is also here non-trivial as mutations may or may not occur in the dormant stage (Lennon et al., 2021; Tellier, 2019). Viability selection occurs when the survival of offspring carrying an advantageous allele increases compared with other genotypes (Figure 1). When adding mutations in the population model, the fecundity and viability phases are not distinguished nor distinguishable under the assumptions of the WF model. As a result, for an advantageous allele, the probability of fixation and the time to fixation are identical for fecundity and viability selection (He et al., 2017).

Recent studies have chiefly investigated the effect of sweepstakes reproduction on the polymorphism of neutral alleles with the aim to infer the strength of the skew in offspring production (Árnason et al., 2023; Eldon et al., 2015; Eldon & Wakeley, 2006; Freund, 2020; Irwin et al., 2016; Korfmann et al., 2022; Koskela, 2018; Koskela & Berenguer, 2019; Sackman et al., 2019; Schweinsberg, 2003; Vendrami et al., 2021), while the influence of sweepstakes reproduction on selected alleles is not yet fully understood. It is shown in Der et al., 2011 that selection should act more deterministically under sweepstakes reproduction than under the WF model though under a peculiar model of reproduction (the Dirac model). Further, the time to fixation of an advantageous allele is much faster than expected under the WF model under a sweepstakes reproduction model with viability selection (Eldon & Stephan, 2018). A complementary analysis of the effect of sweepstakes reproduction with viability selection including the effect of allele dominance and random demographic changes is concomitantly available to the present study (Eldon & Stephan, 2023). These studies suggest that strong sweepstakes reproduction may, on the one hand, increase the effectiveness of positive selection and speed up adaptation by shortening the time to fixation of an advantageous allele (T_{fix} conditioned on fixation). On the other hand, when observing all allele trajectories (supplementary results in Eldon & Stephan, 2018, 2023), there is a high chance that advantageous alleles get lost under sweepstakes reproduction. This means that the efficiency of viability selection, that is the probability of fixation (P_{fix}), may be decreased under sweepstakes reproduction. These studies mostly consider constant population size (but see Eldon & Stephan, 2023) and constant selection in time, while

varying population size and fluctuating selection are shown to be also key determinants of the fate of advantageous alleles. Indeed, such non-constant conditions affect the outcome of the interaction between genetic drift and selection under the WF model (Devi & Jain, 2020; Kaushik & Jain, 2021).

Our study is unique in disentangling the effect of viability and fecundity effect on genetic drift (sweepstakes reproduction under boom-and-bust cycle) and selection. We first investigate the effect of sweepstakes reproduction on the three components of speed of adaptation θ, P_{fix} and T_{fix} by comparing neutral and advantageous alleles and considering fecundity and/or viability selection under constant and varying population size, as well as under fluctuating selection. Second, we also investigate the effect of joint viability and fecundity selection on P_{fix} and T_{fix}. We rely on the Cannings model (Cannings, 1974), which allows us to model the life cycle depicted in Figure 1. We use simple analytical derivations to provide intuitions on the main results and then use stochastic forward-in-time simulations, to assess the effectiveness and efficiency of positive selection under a wide range of biologically plausible life cycles and scenarios. We conclude on the importance of taking into account life cycles, including neutral sweepstakes, when predicting the potential of species for rapid adaptation in medicine or agriculture.

2 | MATERIALS AND METHODS

2.1 | Model description

With the idea to focus on sweepstakes reproduction in invertebrates, fungi, viruses or bacteria, we consider a population of haploid individuals of constant size N evolving under a Cannings model (Cannings, 1974). We furthermore assume in our population the existence of a bi-allelic locus (with alleles A or a). We begin by setting up the definitions of the neutral Cannings model following the model of Schweinsberg (2003) in which allele A and a have an identical fitness value.

> **Definition** 1 (Neutral Cannings model of reproduction). Let $(X_i)_{1\le i\le N}$ be identical independent $\mathbb{N}$-valued random variables such that $\mathbb{E}(X_1) > 1$.
> For each $1 \le i \le N$, the number of offspring of the ith parental individual is X_i. The N surviving offspring are then drawn without replacement amongst the $X_1 + \cdots + X_N$ offspring ($\mathbb{N}$ is the set of natural numbers).

The hypothesis $\mathbb{E}(X_1) > 1$ guarantees there will be more than N offspring generated at each generation assuring at least N surviving offspring when N goes to infinity as required in mathematical models (Eldon & Stephan, 2018, 2023; Schweinsberg, 2003). As we wish to investigate sweepstakes reproduction, we assume throughout this manuscript that the number of offspring produced by each parent to be independent and identically distributed as in Schweinsberg (2003). Hence the distribution of the number of produced offspring is shaped by a unique parameter α (dropping the scaling constant C). More precisely, the distribution of the number of produced offspring by a parent i (i.e. X_i), given the parameter α, is:

$$\begin{aligned} P(X_i = 0) &= 0 \\ P(X_i \ge k) &= \frac{1}{k^\alpha} \text{ with } k \ge 1 \end{aligned} \tag{1}$$

Let us define now a Cannings model with selection with the allele of type A exhibiting a selection advantage with coefficient s. Under fecundity selection individuals with allele A produce on average more offspring than a individuals.

> **Definition** 2 (Reproduction with fecundity selection). Let $(X_i)_{1\le i\le N}$ be identical independent $\mathbb{N}$-valued random variables such that $\mathbb{E}(X_i) > 1$. Let s be the selection coefficient of the type A. Let $(Y_i)_{1\le i\le N}$ be identical independent $\mathbb{N}$-valued random variable such that $\mathbb{E}(Y_i) > 1$ and $\mathbb{E}(Y_i) = (1+s)\mathbb{E}(X_i)$.
> For each $1 \le i \le N$, the number of offspring of the ith parental individual is X_i if the ith individual has the type a and Y_i otherwise.
> The N surviving offspring are then drawn without replacement amongst all produced offspring.

We first assume that parental individuals with allele A produce on average $1 + s$ more (or less is if $s < 0$) offspring than parents with allele a. Yet, each produced offspring has the same probability to be drawn for the next generation (viability). We define an advantageous allele for fecundity, as an allele that increases on average the number of produced offspring by a factor s ($s > 0$).

In other words, the expected number of produced offspring by parent with the allele A is $(1 + s)$ times of the number of offspring produced by parents with allele a. Additionally, there is no limit to the total number of offspring produced. This definition, referred to as the model F1 for fecundity selection, is our fecundity selection default model. Our F1 fecundity model is implemented by applying the *inverse transform sampling* method (see Appendix S1 and Equation 1), multiplying the number of offspring produced by the selection component $(1 + s)$ and flooring the resulting number of type A offspring for each generation.

However, we also suggest that alleles might affect the fecundity in a different way than in the model F1 (i.e. scaling the average of the offspring distribution for individuals carrying allele A). We wish to investigate an alternative fecundity selection model F2, in which the distribution of produced offspring by parents with allele A is possibly more skewed (towards high values) than that of parents with allele a . This effect takes place in addition to producing on average $(1 + s)$ times the expected number of offspring produced by parents with allele a. Such a model might be a more realistic model for selection in species already displaying skewed offspring distribution. In this alternative fecundity selection scenario (F2), the advantageous (A) allele increases on average the number of produced offspring by a factor

s as well compared to individuals with allele a (as in F1). However, individuals with the allele a produce offspring with the parameter of the Cannings model α_a, whereas the individuals with the allele A produce their offspring with a modified α_A (where $\alpha_A < \alpha_a$). Hence, in our fecundity F2 model, α_A is obtained by the following formula:

$$\alpha_A = \alpha_a / (1 + s) \tag{2}$$

Definition 3 (Reproduction with viability selection). Let $(X_i)_{1 \le i \le N}$ be identical independent $\mathbb{N}$-valued random variables such that $\mathbb{E}(X_i) > 1$. Let $s \ge 0$ be the selection coefficient of the type A.

For each $1 \le i \le N$, the number of offspring of the ith individual is X_i.

The N surviving offspring are the draw according to the Wallenius noncentral hypergeometric distribution where the weight of an offspring is $w = 1 + s$ if it has the type A and $w = 1$ otherwise.

Here, viability selection increases the probability of offspring with allele A to be drawn to constitute the next generation $g + 1$ (similar to Eldon & Stephan, 2018). In Appendix S1, we present a cursory analysis of our discrete time Cannings model with and without selection. We provide some useful general expressions for the expectation and variance of the number of offspring (of allele A) at a given generation. These analytical results generate the insight that fecundity and viability selection do differ in their mean and variance of the number of offspring produced under our sweepstakes reproduction model. However, this formalism does not allow to compute further analytical results because the precise distribution of offspring would need to be specified. We therefore use simulations to generate quantitative results on the comparison of neutral and selection models.

2.2 | Stochastic simulations

2.2.1 | Simulating offspring production

The neutral and selection Cannings models are implemented in *Julia*. As defined above (Equation 1), under neutrality we assume the number of offspring produced by each parent to be independent and identically distributed as defined in (Schweinsberg, 2003). The main parameter α determines the distribution of offspring produced (Schweinsberg, 2003), with α close to one meaning a large variance in offspring production with some individuals producing extremely large numbers of offspring (on the order of N). When α is close to two, there is a small variance (of one) in offspring production between parents. Note that as described in (Eldon & Stephan, 2018, 2023), due to scaling of large offspring production under the Cannings model, a value of $\alpha = 2$ does not generate exactly a WF model. In order to obtain the WF model, we specify in our Cannings model a Poisson distribution of offspring (with parameter λ). Further details of the implementation are found in Appendix S1. Implementations and scripts to run simulations can be found at https://github.com/kevinkorfmann/CanningsSimulator.

2.2.2 | Simulating selection and demography

Each α parameter setting is coupled with viability selection and/or fecundity selection model under the influence of weak and strong selection coefficient, namely $s = [0,0.01,0.1]$ ($s = 0$ being the neutral case). We use population sizes N of 500, 1000, 5000, so that the effective selection coefficients are $N_s = ([0,0,0,], [5,10,50], [50,100,500])$, respectively.

We follow previous work to model time-dependent sinus functions with varying amplitudes and periods for the population size (Devi & Jain, 2020) or selection coefficient (Kaushik & Jain, 2021) (Figures S1 and S2). As environmental conditions change, so can the fitness provided by alleles. To model this fluctuating effect, we now assume population size to be constant, but the selective advantage provided by the allele A to be changing through time. To simplify our approach (as in Kaushik & Jain, 2021), we assume the average value of the selection coefficient to be 0 over a period of fluctuating selection, but the amplitude of the selective coefficient s ranges up to 0.01 or 0.1 (i.e. maximum fitness provided by the allele A).

We test the effects on the probability of fixation and time to fixation regarding the initial introduction phase of the allele (initially advantageous or deleterious) and the speed at which the selection coefficient changes through time (slow period ~1000 generations or fast period ~100 generations, see Figure S2).

We analyse the allele fixation probabilities and fixation times under different scenarios: constant population size, fluctuating population size and fluctuating selection. The obtained results are based on 5×10^5 simulations to compute the probability of fixation, while the time to fixation simulations are conditioned on fixation. Thus, simulations are run until 5000 fixation events have occurred. Simulations start with time-independent constant population size and selection coefficient. Finally, to produce simulations under the WF model, we use a Poisson distribution with $\lambda = 1.2$ (based on empirical simulation). We perform simulations demonstrating that we recover the known expectations for the probability of fixation and time to fixation of neutral and advantageous alleles under the WF model (Table S1). Furthermore, the probabilities and times to fixation are found to be identical for viability and fecundity selection (Table S1) as expected under the WF model (He et al., 2017).

2.3 | Mutation process

Mutations may occur during the life cycle of the parent (in the cells of the germ line) and can be heritable, so that all offsprings produced by this parent share these mutations. Mutations can occur during the gamete production and are thus offspring specific, with independence

between mutations. Hence the total number of occurring mutations M in the produced offspring at generation g can be decomposed as:

$$M = L \times (\mu_p \times N_p + \mu_o \times N_o), \quad (3)$$

where L is the sequence length (or number of loci), μ_p is the mutation rate per generation per site/locus during the life cycle of the parent, N_p the number of parents (in our case, $N_p = N$), μ_o the mutation rate per generation per site/locus during gamete production and N_o the number of produced offspring.

We simulate two different models. In the first model, parents mutate at a rate of 0.01 (i.e. $\mu_p = 0.01$ and $\mu_o = 0$), while in the second model, the offspring mutate (and not the parents) individually and independently under the same mutation rate (i.e. $\mu_p = 0$ and $\mu_o = 0.01$). We then simulate mutations under the two models and compare the observed diversity, that is the number of A alleles produced in one generation. Each replicate consists of a population of size $N = 10{,}000$ (starting with all individuals of type a allele) and only one generation is simulated. The number of offspring produced is simulated under the distribution described above (Equation 1) for different values of the α parameter. We then randomly sample amongst the produced offspring, N_p surviving individuals to assess the diversity at the next generation ($g + 1$).

3 | RESULTS

3.1 | Distribution of new mutations

We first focus on the distribution of new alleles obtained by mutations under a parental or offspring mutational process and as a function of the α parameter. As expected from Equation (3), the average number of new alleles is very similar for the parental and offspring mutational model and all values of α, with a mean of 100 (as $N_p \times \mu_p = N_o \times \mu_o = 1000 \times 0.01 = 100$, Figure 2). However, if mutations occur in the parents the variance in the number of new mutations across simulation replicates is higher than if mutations occur in offspring. Furthermore, the variance across replicates in the number of new alleles increases with diminishing α when mutations occur in parents, while α has a negligible effect on the variance of a number of new alleles when mutations occur in the offspring (Figure 2). These first results indicate that in a population of fixed size N, species with mutation in parents or in offspring would exhibit an average similar speed of adaptation based on the average rate of appearance of novel advantageous mutations, but species with mutations in offspring are more likely to consistently produce this number at each generation.

3.2 | Constant population size and constant selection

3.2.1 | Viability and F1 fecundity selection

We first estimate the probability for alleles to reach fixation for different α values under constant population size (Figure 3 with $N = 1000$, $N = 500$ in Figure S3 and $N = 5000$ in Figure S4). The fixation probability of a neutral allele, i.e. $s = 0$ in Figure 3a, diminishes from 0.001 to 0.0002 with increasing α values. Hence, neutral stronger sweepstakes reproduction increases the probability of a neutral allele to become fixed. As expected from classic theoretical results under the WF model, the probability of fixation of a neutral allele diminishes with increasing population size (compare Figure 3a,d with Figures S3 and S4). Furthermore, viability and fecundity have a similar effect on the probability of fixation (advantageous alleles

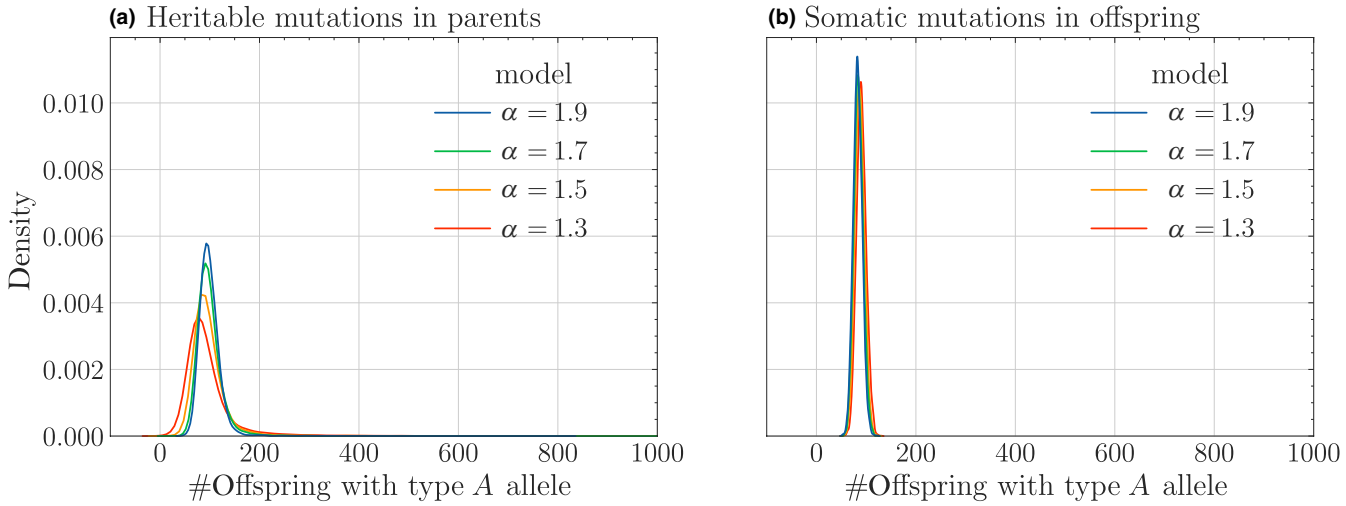


FIGURE 2 Density distribution of new mutants (individuals with type A allele) after one generation for two different mutation models. Density distribution of individuals with type A allele after one generation under our Cannings model of offspring distribution with α measures of 1.3, 1.5, 1.7 and 1.9 for two different mutation models. In (a) parents mutate, and the mutation is heritable for all offspring of a given parent, in (b) mutations occur in each offspring individually. Population size is $N_p = N_o = 10^4$ and mutation rate $\mu_p = \mu_o = 0.01$. The density estimation is the result of 5×10^3 repetitions per α value.

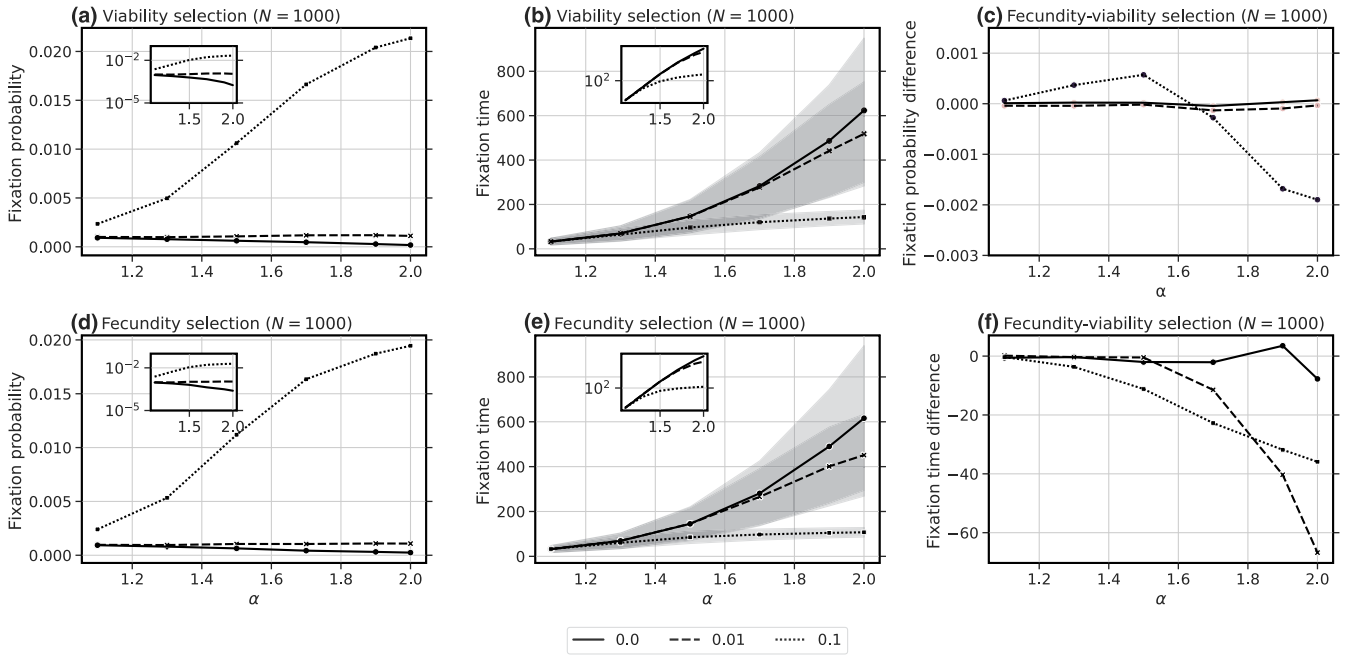


FIGURE 3 Allele fixation probability and average time to fixation of alleles under constant population size. Fixation probability (a, d) and average fixation times (b, e) under different sweepstakes strength (α ranging from 1.1 to 2.0) for (a, b) viability selection and (d, e) fecundity selection (F1). Three selection coefficients are shown ($s = 0; 0.01; 0.1$) and $N = 1000$. Probabilities are obtained from 5×10^5 simulations, while fixation times are estimated based on 5×10^3 simulations conditioned on fixation. Shaded areas correspond to 95% confidence intervals. Panels (c) and (f) present the difference between the probability of fixation (c) and time to fixation (f) for fecundity compared with viability selection.

for viability in Figure 3a, or for fecundity, Figure 3d). As could be expected, under weaker selection ($s = 0.01$), the probability of fixation of the advantageous allele is similar to that under neutrality, while stronger selection ($s = 0.1$) increases the fixation probability (Figure 3a,d). Note that in contrast to the neutral allele, stronger sweepstakes reproduction decreases the probability of fixation of an advantageous allele (from ca. 0.005 for $\alpha = 1.1$ to 0.02 for $\alpha = 2$). This means that sweepstakes reproduction is equivalent to stronger genetic drift, which can counter-act the action of selection, thus decreasing the probability of advantageous allele to be fixed by up to a factor 4. Under strong sweepstakes reproduction (low α values), viability and fecundity advantageous alleles exhibit ultimately similar probabilities of fixation as neutral alleles (Figure 3c,f). To better assess the dissimilarity between viability and fecundity selection, we compute the difference of fixation probability between allele providing a fecundity and viability advantage (Figure 3c). When an allele provides no or only a small advantage, the difference is equal to zero for all α values and population sizes (Figures S3 and S4). However under strong selection for α smaller than 1.7, fecundity selection yields higher probabilities of fixation than viability selection, a trend that reverses for higher α values (Figure 3c).

We provide estimates of the fixation time (in generation) of a neutral or advantageous allele (Figure 3b,e). As expected from the classic theory under the WF, the time to fixation decreases with the strength of selection and with population size (Figures S3b,e and S4b,e). As reported before (Eldon & Stephan, 2018), the time to fixation of advantageous alleles increases with increasing α values (the effect being more apparent for large population size $N = 5000$ in Figure S4b,e). Yet under neutrality ($s = 0$ in Figure 3e), the time to fixation (and its variance) increases exponentially with α, while under strong selection the time to fixation increases almost linearly with α. Overall, neutral alleles tend to reach fixation as fast as advantageous alleles under strong sweepstakes reproduction (low α values), i.e. confirming the stronger effect of genetic drift with diminishing α (note that the neutral case is not shown in Eldon & Stephan, 2018). We assess the difference in time to fixation between fecundity or viability selection (Figure 3f) and observe, as expected, no difference under neutrality. Under selection, the time to fixation of an allele providing fecundity advantage is shorter than an allele providing viability advantage, while this difference tends to zero when α tends to one.

3.2.2 | Joint fecundity and viability selection

We now generalize the previous results by considering that the advantageous allele affects simultaneously fecundity (F1) with weak $s = 0.01$ or strong $s = 0.1$ coefficient and viability with weak $s = 0.01$ or strong $s = 0.1$ effect. As above, for an allele with strong effect for both types of selection (i.e. $s = 0.1$), the probability of allele fixation increases with increasing α. However, the probability of fixation under joint strong selection (blue line in Figure 4a) can become greater than the additive effect of viability and fecundity as measured by summing up the probability for strong viability and strong fecundity obtained separately (solid black line in Figure 4a). This synergistic effect

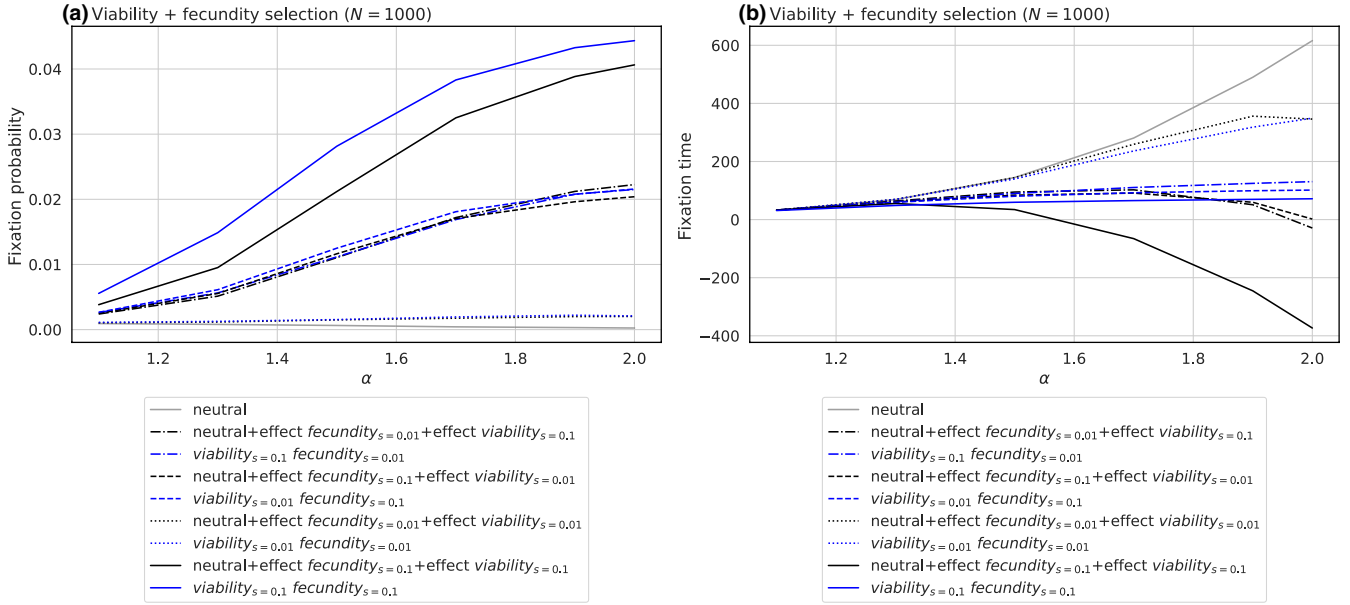


FIGURE 4 Allele fixation probability and average fixation time under constant population size and additive selection models. (a) Probability of fixation under simultaneous viability and fecundity selection (F1, blue) in comparison to neutral fixation probability with added effect (net contribution) of fecundity (F1) and viability selection, when simulated individually (black). (b) Average time to fixation of alleles under simultaneous selection models (blue) in comparison to neutral estimates of time to fixation summed up with the effect (net contribution) of each selection type (black). Probabilities are obtained from 5×10^5 simulations, while fixation times are estimated based on 5×10^3 simulations conditioned on fixation.

is also observed for the time to fixation when comparing the time to fixation under joint strong selection with the sum of each strong selection measured independently (blue line versus solid black line in Figure 4b). When both selection coefficients are smaller ($s = 0.01$) or sweepstakes reproduction is strong (small α), this synergistic effect diminishes so the probability of fixation and time to fixation is close to the weak combined effect (see Figure 4). These results hold for all tested population sizes (Figures S5 and S6). We therefore demonstrate that as we decouple fecundity and viability selection in our model of offspring production, a synergistic effect appears for simultaneous strong fecundity and strong viability selection.

3.2.3 | Fecundity selection (F2) model

We then estimate the probability (Figure 5a) and time to fixation (Figure 5b) of neutral and advantageous alleles under the fecundity selection F2 model and compare with previous results under F1 fecundity selection. The probability of fixation under model F2 is at least five times greater than that under model F1 (Figure 5a), and the time of fixation is at least twice as fast than under F1 (Figure 5b).

3.3 | Fluctuating conditions

3.3.1 | Fluctuating population sizes

Under fluctuating population sizes (Figure S1), the probability of fixation of an allele under fecundity F1 or under viability selection is similar as that under constant population size (Figures S7 and S8). When comparing two different demographic scenarios, namely with different amplitude and period of oscillations, the probability of fixation only slightly vary. Similarly, the times to fixation of an advantageous allele with fecundity or viability selection under fluctuating population sizes, are slightly shorter and with higher variance than those obtained under constant population size (Figures S9 and S10). This confirms the intuition and previous theoretical results under the WF model that varying population size around the mean N does increase genetic drift and decrease the time to fixation of alleles. Overall, the difference in time to fixation and in fixation probability between the two selection models (fecundity F1 and viability) also follow those under constant population size (Figures S11–S14).

3.3.2 | Fluctuating selection

Under a slow variation of s through time, the probability of fixation of the A allele depends strongly on whether the initial fitness of that allele is beneficial or deleterious (Figure 6). Comparing these two situations, when the A allele is initially advantageous, the fixation probability is higher (less chance for the allele to be lost) and time to fixation is smaller (Figures S15–S17). Furthermore, we observe no noticeable difference between the probability of fixation under viability or fecundity selection. The probability of fixation is increasing with α (for all population sizes Figures S18 and S19) when the allele is initially highly beneficial, otherwise in other cases, the probability of fixation is decreasing with α when

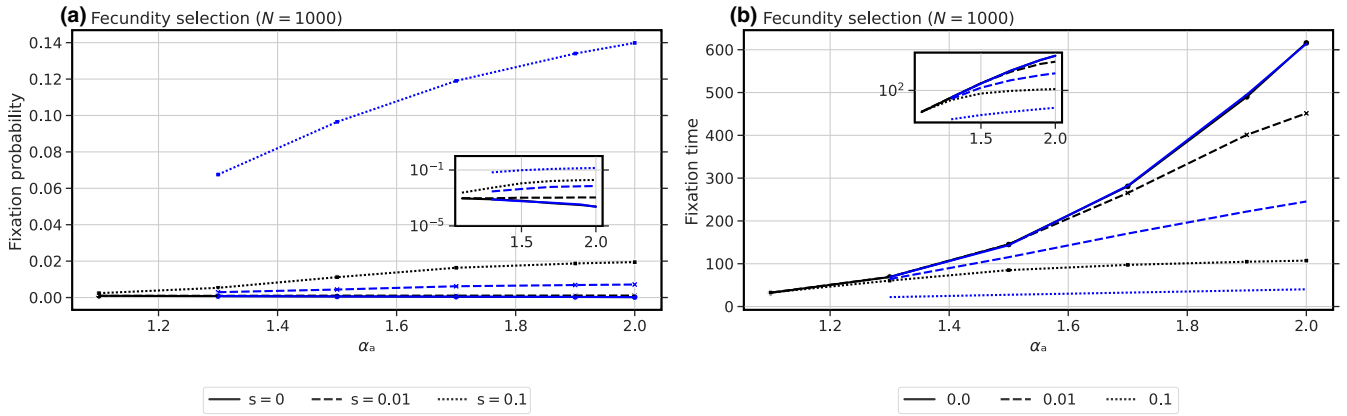


FIGURE 5 Allele fixation probability and average fixation time under constant population size and two constant selection fecundity models. (a) Probability of fixation and (b) fixation time for two positive selection fecundity models. In black fecundity is modelled by increasing the offspring number (F1) and in blue the fecundity F2 selection. Probabilities are obtained from 5×10^5 simulations, and fixation times are estimated based on 5×10^3 simulations.

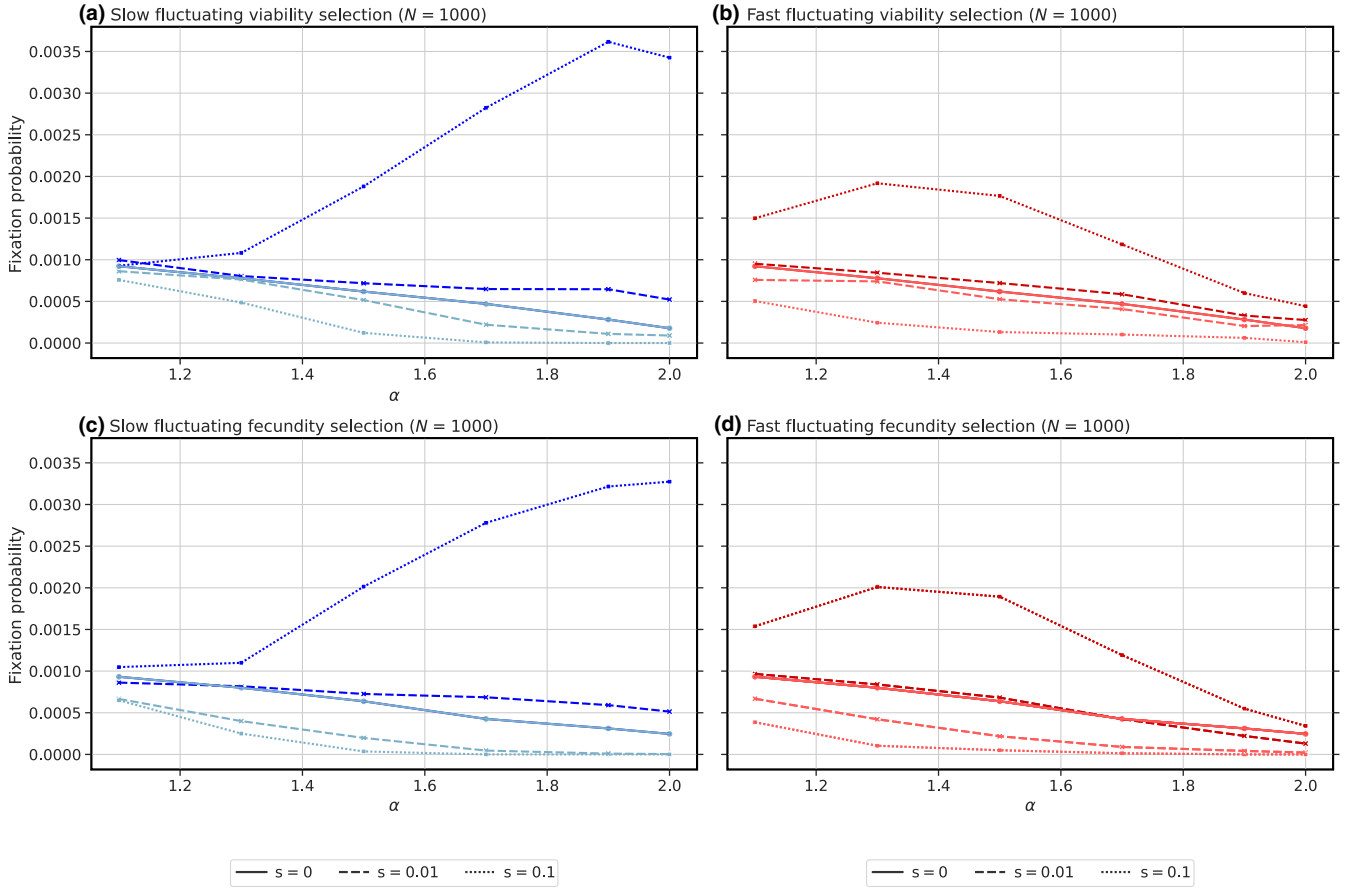


FIGURE 6 Allele fixation probability under constant population size and fluctuating selection coefficients. Fixation probability under different sweepstakes strength (α ranging from 1.1 to 2.0) for (a) slow fluctuating viability selection with initial positive selection s (dark blue) or starting with a negative selection coefficient (light blue). (b) Fast fluctuating viability selection starting with allele A being advantageous (dark red) and allele A starting being deleterious (light red). The same colour code is used for slow (c) and fast (d) fluctuating fecundity selection (F1). Estimates were obtained from 5×10^5 simulations.

we consider slow fluctuating selection (Figure 6a,c). A new result emerges when varying the speed of the fluctuating fitness (Figure 6b,d). When the speed of fitness variation increases (fast fluctuations), the probability of fixation becomes non-monotonic and is maximized at intermediate values of α (at high amplitude of fitness).

For small amplitude of fitness variation, the results are similar to slow variation of fitness (Figure 6). If the allele is initially deleterious (disadvantageous, light curves Figure 6a–d), the probability to loose this allele is higher when the amplitude of fitness variation increases. Similar results are obtained if the speed of fitness variation is increased (Figure 6). This demonstrates that there is an interaction between the speed and amplitude of fitness fluctuation on one hand, and the occurrence of sweepstakes reproduction events on the other hand. When selection is fast and strong enough, it can counter-act the stronger genetic drift generated by sweepstakes reproduction (intermediate values of α), increasing thus the probability of fixation for advantageous alleles.

4 | DISCUSSION

Throughout this manuscript, we investigate the effect of sweepstakes reproduction on the three components of speed of adaptation θ, P_{fix} and T_{fix}. Our results are in line with previous results under viability selection regarding P_{fix} becoming higher and T_{fix} becoming shorter, when decreasing the parameter α (Eldon & Stephan, 2018, 2023). In the following, we highlight few far-reaching implications of our results. We focus on pathogens of crops and plant species where sweepstakes reproduction may occur (Tellier & Lemaire, 2014) to complement the abundant literature on already investigated biological systems such as fish and marine organisms, or bacteria and viruses parasites of humans (Árnason et al., 2023; Irwin et al., 2016; Matuszewski et al., 2017; Menardo et al., 2020; Morales-Arce et al., 2020; Sabin et al., 2022; Sackman et al., 2019; Vendrami et al., 2021). On a technical note of caution, our model assumes that the potential maximum number of produced offspring is unbounded (as in Schweinsberg, 2003). As we intend to keep our model generally applicable to many species, from fish to fungi, we refrain to fix a species-specific boundary, although we are aware that this may be biologically unrealistic. Investigating the effect of different boundary values for the number of offspring produced is beyond the scope of this study and will be part of future work focusing on given species of interest.

4.1 | Mutational process under sweepstakes reproduction

We first analyse the number of new mutations produced either in the parental germ lines giving rise to the gametes or in the offspring. Species with a short life span and with strong sweepstakes reproduction, such as fungi (e.g. of crop pathogens), viruses, bacteria, invertebrates and vertebrates (fish) presenting a typical type-III survivorship ecological strategy (i.e. life span is exponentially distributed), do benefit from mutations occurring in offspring (eggs, spores, particles). Indeed, the number of new alleles is proportional to the number of produced offspring (which is affected by α and can possibly be very large) and not to the number of parents, but the probability that individuals with new mutation survive the viability phase is very small. Nevertheless, in such sweepstakes reproducing species with mutations in offspring, a more consistent number of new (advantageous) mutations are observed than when mutations occur in the parents (centered around the expected mean $N \times \mu$). This small variance in the number of new mutations would reduce the variance for the waiting time for a new advantageous mutation to appear (the random variable θ), thereby likely speeding up rapid adaptation compared with the case where mutations occur in the parents. When mutations occur in offspring, even under large boom-and-bust cycle of population size, that is the production of the large amount of offspring that can mutate, the number of new mutants observed at the next generation is determined by the number of offspring surviving (N) and does not depend on the parameter α. Hence, for parasites, the effective population size depends on the number of spores/infectious particles that successfully land on, transmit to and infect a host (N). If we define the total number of offspring (spores, infectious particles) produced during the boom cycle of fecundity as the census size (N_{cs}), we obtain the following relationships: The inbreeding effective population size (N_e) is smaller than the number of surviving offspring (N), which is itself smaller than N_{cs}. These discrepancies between N_e, N and N_{cs} become larger as α becomes smaller, meaning that the sweepstakes reproduction model shows an increasing discrepancy with the WF model of population evolution in which $N = N_e = N_{cs}$ (Eldon, 2020; Hare et al., 2011; Waples, 2005 and references therein). In other words, sweepstakes reproduction, as well as dormancy in seed banks, disentangle the process of genetic drift and mutation as usually considered in the classic expression of the population mutation rate $\theta = 4N_e\mu$ (Figure 1) possibly explaining the so-called Lewontin's paradox in some species (Charlesworth & Jensen, 2022; Tellier, 2019).

We consequently draw two conclusions. First, the high stochastic processes of fecundity and viability under sweepstakes reproduction do generate different, but likely more realistic, predictions regarding the number of new mutations compared with average simple computations based on census size (N_{cs}) observations in the field. Indeed, the census size of the boom fecundity part of the life cycle is routinely assessed in plant pathology by measuring the spore production of fungal lesions (see computations in Stam & McDonald, 2018), while measuring the viability part of the infection cycle is more difficult but essential to define the value of the population size N (likely overestimated in Stam & McDonald, 2018). Conversely, the estimation of inbreeding effective population size (N_e) using polymorphism sequence data is likely biased and likely underestimates (N), meaning that predictions from N_e do not fully assess the full adaptive potential of crop pathogens (see, for example, McDonald & Linde, 2002). We suggest as a way forward to use full genome polymorphism data to estimate simultaneously N and α (Korfmann et al., 2022). Second, species with parents exhibiting long live life span (trees, mammals) and in which mutations occur in parental germ lines (generating the gametes) may be expected to show more variable amount of new (advantageous) mutations each generation. Our results show that this number of new mutations is

reduced under strong sweepstakes reproduction (α close to one). Nonetheless, as sweepstakes reproduction and a boom-and-bust life cycle are not common to species with type-I and type-II survivorship ecological strategy (e.g. mammals), we may expect our results to be relevant to explain the variance in the number of new mutations (and variance in waiting time for new advantageous mutations) in species such as long-lived plant species, which produce a large amount of seeds, few of which surviving to the next generation.

4.2 | Neutrality versus selection under sweepstakes reproduction

We study the probability of fixation of an allele providing fecundity and/or viability advantage. We first attempt to derive fixation probabilities analytically under a general reproduction model. Yet, those probabilities could not be obtained without the exact definition of offspring distributions. Hence, we use simulations. We quantify the effect of sweepstakes reproduction on increasing, respectively, decreasing, the fixation probabilities of neutral and, respectively, selected alleles. Under strong sweepstakes reproduction (α tends to one), the probability of fixation and the time to fixation of advantageous alleles tend to the probability of fixation of neutral alleles (namely a probability of 0.001 for $N = 1000$ when $\alpha = 1.1$ similar to $1/N$ under the WF model), while these quantities are not notably affected by population size or population size variations.

We draw two further conclusions. First, as the probability of fixation of neutral allele increases under stronger sweepstakes reproduction, we suggest that genomic divergence (substitution rate) is not any longer a sole function of the mutation rate (μ) as assumed under the classic population genetics neutral theory (Charlesworth & Charlesworth, 2010). Phylogenetic methods and dating of past events would need to account for the higher substitution rate in species with low α. We speculate that this effect of neutral sweepstakes may explain the large variance in substitution rates observed across bacteria species (Cui et al., 2013; Gibson & Eyre-Walker, 2019), especially as pervasive and strong recurrent selection generates sweepstakes in bacteria (Menardo et al., 2020; Neher & Hallatschek, 2013). As a follow-up, we speculate that classic methods to detect the action of positive selection based on divergence versus polymorphism analyses at synonymous and non-synonymous sites (the McDonald-Kreitman test, McDonald & Kreitman, 1991); and its derivatives (Stoletzki & Eyre-Walker, 2011) could be biased and could show low statistical power in species with sweepstakes. This is because neutral (synonymous) and selected (non-synonymous) allele exhibit similar probability and time to fixation. Second, we suggest to revise the previous claim that sweepstakes reproduction speed up rapid adaptation (Eldon & Stephan, 2018, but a slightly different model generates a significant decrease in the probability of fixation; Eldon & Stephan, 2023), because while we agree that time to fixation is faster, the probability of fixation of advantageous allele is significantly smaller for small values of α (see also the supplementary table A11 in Eldon & Stephan, 2018). Furthermore, the detection of selective sweeps is likely complicated by the fact that strong sweepstakes reproduction generates fixation (sweep) of neutral alleles as often as of positively selected alleles. It is therefore expected that genome scan for positive selection would overestimate the number of true selective events and show a high rate of false positives depending on the recombination rate in the genome, a small rate increasing the effect of linkage disequilibrium and pervasive sweepstakes signatures (possibly partially explaining the results in cod fish; Árnason et al., 2023; discussed in Eldon & Stephan, 2023).

4.3 | Fecundity and viability selection under sweepstakes reproduction

Our results suggest an interaction between the type of selection, fecundity and viability, and the strength of the sweepstakes reproduction. At intermediate sweepstakes reproduction fecundity selection is more efficient than viability, and the reverse is true at low sweepstakes reproduction. Note that as expected when our model is adjusted to fit a WF model, we find the probability and time to fixation of advantageous alleles to be the same for both types of selection (He et al., 2017). These results hold under varying population size. Population size variation only slightly shortens the time to fixation of beneficial alleles, likely because in contrast to (Devi & Jain, 2020), sweepstakes reproduction is the strongest determinant of the effect of genetic drift compared with the weaker effect of population size change with a random bottlenecks model (see also Eldon & Stephan, 2023). Furthermore, when an allele jointly affects fecundity and viability, the probability of fixation and time to fixation of weakly advantageous alleles are largely additive as opposed to multiplicative, but a synergistic effect is observed for strong selection coefficients. This demonstrates the non-additive interaction between the fecundity and viability phases of the life cycle for species with boom-and-bust dynamics, possibly explaining the high adaptive potential and rapid adaptation of crop or animal pathogens in response to drug/fungicide treatments (Barbosa et al., 2021; Fisher et al., 2022) or to new crop resistant varieties (Persoons et al., 2017). Additionally, we observe that the probability of fixation of a beneficial allele affecting fecundity is elevated if it jointly increases the mean and skewness of the offspring distribution (model F2) compared with only increasing the average fitness (model F1). Therefore, the effect and magnitude of selection can only be appreciated and measured in the light of the offspring distribution and life cycle. We speculate that our F2 selection model may be typical of species such as asexual bacteria (Neher & Hallatschek, 2013) or asexual fungi (pathogen of crops), possibly exhibiting some kind of "winner takes all" dynamics whereby one clone would invade the population extremely rapidly due to selection accelerated by neutral sweepstakes reproduction.

Finally, we also investigate the effect of fluctuating fecundity or viability selection. As stronger sweepstakes reproduction corresponds to a higher occurrence of strong genetic drift events, the

efficiency of selection depends on the period of selection variation. When the period of selection change is smaller (and with large amplitudes) than the occurrence of sweepstakes reproductive events, selection overruns drift. In other cases, selected alleles do not differ in their probability and time to fixation from the neutral alleles. As previously acknowledged (Kaushik & Jain, 2021), the initial phase of the cycle of selection is crucial to determine the fate of an allele: If the selection coefficient is initially positive, the allele can become fixed, if it is negative, the allele is lost from the population. In this respect, there is no difference between fecundity or viability selection, and the strength of sweepstakes reproduction does not influence this behaviour. As far as we are aware, our results may be the first to demonstrate the different effects of fecundity and viability selection on fitness under sweepstakes reproduction (Figure 1), and thus, further work is needed to explore the possible selection models and their biological implications, as well as how to test the predictions in empirical data. We highlight especially the cases where fecundity and viability selection occur simultaneously, or that of fluctuating selection, as testing and measuring each selection phase and varying the selection coefficient in time maybe be doable empirically under controlled laboratory conditions.

5 | CONCLUSION

As indicated in the introduction, we advocate to remain cautious regarding the applicability of our results for the analysis of genome-wide polymorphism data (see for example Johri et al., 2021, 2022). Indeed, our model considers only one single locus under positive selection. The speed of rapid adaptation in species with sweepstakes, and the signatures of selective sweeps, is realistically affected by linked (positive and negative) selection at neighbouring sites with various distribution of fitness effects (Eyre-Walker & Keightley, 2007; Hill & Robertson, 1966; Johri et al., 2022). Nevertheless, life-history traits, such as sweepstakes reproduction, dormancy and clonality are ubiquitous in many virus, bacteria, fungi, invertebrates and plant species and do impact the reproductive mechanism and consequently the relative importance of the various forces shaping genome evolution. We disentangle here the fecundity and viability phases of the life cycle (Figure 1) under sweepstakes reproduction. We note that similar observations have been made for seed dormancy disentangling fecundity and viability selection in dormant seeds (Heinrich et al., 2018). However, in nature, organisms may exhibit several peculiar life-history traits (dormancy, sweepstakes reproduction) such that there is a large variance in produced offspring, some of which remain dormant for more than one generation before they become activated and can reproduce. Hence, it may be important to consider more complex but realistic models of evolution for species with peculiar life cycles to assess the limits of current population genetics theory and better predict the evolutionary potential of such species possibly important for medicine or agriculture.

AUTHOR CONTRIBUTIONS

MTB and TS conceptualized the project with support from AT. KK and MTB wrote the code, and KK performed all simulations. KK and TS wrote the manuscript with support from AT. All authors reviewed and approved the final manuscript.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

The simulated data that support the findings of this study are openly available at: https://github.com/kevinkorfmann/CanningsSimulator.

ORCID

Thibaut Sellinger https://orcid.org/0000-0002-8538-7800
Aurélien Tellier https://orcid.org/0000-0002-8895-0785

REFERENCES

Anderson, J. T., Panetta, A. M., & Mitchell-Olds, T. (2012). Evolutionary and ecological responses to anthropogenic climate change: Update on anthropogenic climate change. *Plant Physiology*, *160*(4), 1728–1740.

Arnason, E., & Halldorsdottir, K. (2015). Nucleotide variation and balancing selection at the Ckma gene in Atlantic cod: Analysis with multiple merger coalescent models. *PeerJ*, *3*, e786.

Árnason, E., Koskela, J., Halldórsdóttir, K., & Eldon, B. (2023). Sweepstakes reproductive success via pervasive and recurrent selective sweeps. *eLife*, *12*, e80781.

Barbosa, C., Mahrt, N., Bunk, J., Graßer, M., Rosenstiel, P., Jansen, G., & Schulenburg, H. (2021). The genomic basis of rapid adaptation to antibiotic combination therapy in *Pseudomonas aeruginosa*. *Molecular Biology and Evolution*, *38*(2), 449–464.

Barghi, N., Hermisson, J., & Schlötterer, C. (2020). Polygenic adaptation: A unifying framework to understand positive selection. *Nature Reviews Genetics*, *21*(12), 769–781.

Cannings, C. (1974). The latent roots of certain Markov chains arising in genetics: A new approach, I. Haploid models. *Advances in Applied Probability*, *6*(2), 260–290.

Charlesworth, B. (1994). *Evolution in age-structured populations* (Vol. *2*). Cambridge University Press Cambridge.

Charlesworth, B. (2020). How long does it take to fix a favorable mutation, and why should we care? *The American Naturalist*, *195*(5), 753–771.

Charlesworth, B., & Charlesworth, D. (2010). *Elements of evolutionary genetics*.

Charlesworth, B., & Jensen, J. D. (2022). How can we resolve Lewontin's paradox? *Genome Biology and Evolution*, *14*(7), evac096.

Crotti, M., Yohannes, E., Winfield, I. J., Lyle, A. A., Adams, C. E., & Elmer, K. R. (2021). Rapid adaptation through genomic and epigenomic responses following translocations in an endangered salmonid. *Evolutionary Applications*, *14*(10), 2470–2489.

Cui, Y., Yu, C., Yan, Y., Li, D., Li, Y., Jombart, T., Weinert, L. A., Wang, Z., Guo, Z., Xu, L., Zhang, Y., Zheng, H., Qin, N., Xiao, X., Wu, M., Wang, X., Zhou, D., Qi, Z., Du, Z., … Yang, R. (2013). Historical variations in mutation rate in an epidemic pathogen, *Yersinia pestis*. *Proceedings of the National Academy of Sciences*, *110*(2), 577–582.

Der, R., Epstein, C. L., & Plotkin, J. B. (2011). Generalized population models and the nature of genetic drift. *Theoretical Population Biology*, *80*(2), 80–99.

Devi, A., & Jain, K. (2020). The impact of dominance on adaptation in changing environments. *Genetics*, *216*(1), 227–240.

Diamond, S. E., Prileson, E. G., & Martin, R. A. (2022). Adaptation to urban environments. *Current Opinion in Insect Science*, *51*, 100893.

Eldon, B. (2020). Evolutionary genomics of high fecundity. *Annual Review of Genetics*, *54*, 213–236.

Eldon, B., Birkner, M., Blath, J., & Freund, F. (2015). Can the site-frequency spectrum distinguish exponential population growth from multiple-merger coalescents? *Genetics*, *199*(3), 841–856.

Eldon, B., & Stephan, W. (2018). Evolution of highly fecund haploid populations. *Theoretical Population Biology*, *119*, 48–56.

Eldon, B., & Stephan, W. (2023). Sweepstakes reproduction facilitates rapid adaptation in highly fecund populations. *Molecular Ecology*, 1–15. https://doi.org/10.1111/mec.16903

Eldon, B., & Wakeley, J. (2006). Coalescent processes when the distribution of offspring number among individuals is highly skewed. *Genetics*, *172*(4), 2621–2633.

Ellegren, H., & Galtier, N. (2016). Determinants of genetic diversity. *Nature Reviews Genetics*, *17*(7), 422–433.

Eyre-Walker, A., & Keightley, P. D. (2007). The distribution of fitness effects of new mutations. *Nature Reviews Genetics*, *8*(8), 610–618.

Fisher, M. C., Alastruey-Izquierdo, A., Berman, J., Bicanic, T., Bignell, E. M., Bowyer, P., Bromley, M., Brüggemann, R., Garber, G., Cornely, O. A., Gurr, S. J., Harrison, T. S., Kuijper, E., Rhodes, J., Sheppard, D. C., Warris, A., White, P. L., Xu, J., Zwaan, B., & Verweij, P. E. (2022). Tackling the emerging threat of antifungal resistance to human health. *Nature Reviews Microbiology*, *20*, 1–15.

Freund, F. (2020). Cannings models, population size changes and multiple-merger coalescents. *Journal of Mathematical Biology*, *80*(5), 1497–1521.

Gibson, B., & Eyre-Walker, A. (2019). Investigating evolutionary rate variation in bacteria. *Journal of Molecular Evolution*, *87*(9–10), 317–326.

Hare, M. P., Nunney, L., Schwartz, M. K., Ruzzante, D. E., Burford, M., Waples, R. S., Ruegg, K., & Palstra, F. (2011). Understanding and estimating effective population size for practical application in marine species management. *Conservation Biology*, *25*(3), 438–449.

He, Z., Beaumont, M., & Yu, F. (2017). Effects of the ordering of natural selection and population regulation mechanisms on wright-fisher models. *G3: Genes, Genomes, Genetics*, *7*(7), 2095–2106.

Hedgecock, D., & Pudovkin, A. I. (2011). Sweepstakes reproductive success in highly fecund marine fish and shellfish: A review and commentary. *Bulletin of Marine Science*, *87*(4), 971–1002.

Heinrich, L., Mueller, J., Tellier, A., & Zivkovic, D. (2018). Effects of population- and seed bank size fluctuations on neutral evolution and efficacy of natural selection. *Theoretical Population Biology*, *123*, 45–69.

Hill, W. G., & Robertson, A. (1966). The effect of linkage on limits to artificial selection. *Genetics Research*, *8*(3), 269–294.

Hu, J., Askary, A. M., Thurman, T. J., Spiller, D. A., Palmer, T. M., Pringle, R. M., & Barrett, R. D. (2019). The epigenetic signature of colonizing new environments in anolis lizards. *Molecular Biology and Evolution*, *36*(10), 2165–2170.

Irwin, K. K., Laurent, S., Matuszewski, S., Vuilleumier, S., Ormond, L., Shim, H., Bank, C., & Jensen, J. D. (2016). On the importance of skewed offspring distributions and background selection in virus population genetics. *Heredity*, *117*(6), 393–399.

Jain, K., & Stephan, W. (2017). Modes of rapid polygenic adaptation. *Molecular Biology and Evolution*, *34*(12), 3169–3175.

Johri, P., Aquadro, C. F., Beaumont, M., Charlesworth, B., Excoffier, L., Eyre-Walker, A., Keightley, P. D., Lynch, M., McVean, G., Payseur, B. A., Pfeifer, S. P., Stephan, W., & Jensen, J. D. (2022). Recommendations for improving statistical inference in population genomics. *PLoS Biology*, *20*(5), e3001669.

Johri, P., Riall, K., Becher, H., Excoffier, L., Charlesworth, B., & Jensen, J. D. (2021). The impact of purifying and background selection on the inference of population history: Problems and prospects. *Molecular Biology and Evolution*, *38*(7), 2986–3003.

Kaj, I., Krone, S., & Lascoux, M. (2001). Coalescent theory for seed bank models. *Journal of Applied Probability*, *38*(2), 285–300.

Kaushik, S., & Jain, K. (2021). Time to fixation in changing environments. *Genetics*, *219*(3), iyab148.

Korfmann, K., Sellinger, T., Freund, F., Fumagalli, M., & Tellier, A. (2022). Simultaneous inference of past demography and selection from the ancestral recombination graph under the beta coalescent. *bioRxiv*. https://doi.org/10.1101/2022.09.28.508873

Koskela, J. (2018). Multi-locus data distinguishes between population growth and multiple merger coalescents. *Statistical Applications in Genetics and Molecular Biology*, *17*(3), 20170011.

Koskela, J., & Berenguer, M. W. (2019). Robust model selection between population growth and multiple merger coalescents. *Mathematical Biosciences*, *311*, 1–12.

Lennon, J. T., den Hollander, F., Wilke-Berenguer, M., & Blath, J. (2021). Principles of seed banks and the emergence of complexity from dormancy. *Nature Communications*, *12*(1), 1–16.

Losos, J. B., & Ricklefs, R. E. (2009). Adaptation and diversification on islands. *Nature*, *457*(7231), 830–836.

Matuszewski, S., Hildebrandt, M. E., Achaz, G., & Jensen, J. D. (2017). Coalescent processes with skewed offspring distributions and non-equilibrium demography. *Genetics*, *208*(1), 323–338.

Maynard Smith, J., & Haigh, J. (1974). The hitch-hiking effect of a favourable gene. *Genetics Research*, *23*(1), 23–35.

McDonald, B. A., & Linde, C. (2002). Pathogen population genetics, evolutionary potential, and durable resistance. *Annual Review of Phytopathology*, *40*(1), 349–379.

McDonald, J. H., & Kreitman, M. (1991). Adaptive protein evolution at the *Adh* locus in *Drosophila*. *Nature*, *351*(6328), 652–654.

Menardo, F., Gagneux, S., & Freund, F. (2020). Multiple merger genealogies in out-breaks of *Mycobacterium tuberculosis*. *Molecular Biology and Evolution*, *38*(1), 290–306.

Morales-Arce, A. Y., Harris, R. B., Stone, A. C., & Jensen, J. D. (2020). Evaluating the contributions of purifying selection and progeny-skew in dictating within-host *Mycobacterium tuberculosis* evolution. *Evolution*, *74*(5), 992–1001.

Neher, R. A., & Hallatschek, O. (2013). Genealogies of rapidly adapting populations. *Proceedings of the National Academy of Sciences*, *110*(2), 437–442.

Persoons, A., Hayden, K. J., Fabre, B., Frey, P., De Mita, S., Tellier, A., & Halkett, F. (2017). The escalatory Red Queen: Population extinction and replacement following arms race dynamics in poplar rust. *Molecular Ecology*, *26*(7), 1902–1918.

Sabin, S., Morales-Arce, A. Y., Pfeifer, S. P., & Jensen, J. D. (2022). The impact of frequently neglected model violations on bacterial recombination rate estimation: A case study in *Mycobacterium canettii* and *Mycobacterium tuberculosis*. *G3*, *12*(5), jkac055.

Sackman, A. M., Harris, R. B., & Jensen, J. D. (2019). Inferring demography and selection in organisms characterized by skewed offspring distributions. *Genetics*, *211*(3), 1019–1028.

Schweinsberg, J. (2003). Coalescent processes obtained from supercritical Galton-Watson processes. *Stochastic Processes and their Applications*, *106*(1), 107–139.

Stam, R., & McDonald, B. A. (2018). When resistance gene pyramids are not durable—The role of pathogen diversity. *Molecular Plant Pathology*, *19*(3), 521–524.

Stephan, W. (2016). Signatures of positive selection: From selective sweeps at individual loci to subtle allele frequency changes in polygenic adaptation. *Molecular Ecology*, *25*(1), 79–88.

Stephan, W. (2019). Selective sweeps. *Genetics*, *211*(1), 5–13.

Stoletzki, N., & Eyre-Walker, A. (2011). Estimation of the neutrality index. *Molecular Biology and Evolution*, *28*(1), 63–70.

Tellier, A. (2019). Persistent seed banking as eco-evolutionary determinant of plant nucleotide diversity: Novel population genetics insights. *New Phytologist*, *221*(2), 725–730.

Tellier, A., & Lemaire, C. (2014). Coalescence 2.0: A multiple branching of recent theoretical developments and their applications. *Molecular Ecology*, *23*(11), 2637–2652.

Vendrami, D. L., Peck, L. S., Clark, M. S., Eldon, B., Meredith, M., & Hoffman, J. I. (2021). Sweepstake reproductive success and collective dispersal produce chaotic genetic patchiness in a broadcast spawner. *Science Advances*, *7*(37), eabj4713.

Waples, R. S. (2005). Genetic estimates of contemporary effective population size: To what time periods do the estimates apply? *Molecular Ecology*, *14*(11), 3335–3352.

Zhou, M., Sng, N. J., LeFrois, C. E., Paul, A.-L., & Ferl, R. J. (2019). Epigenomics in an extraterrestrial environment: Organ-specific alteration of DNA methylation and gene expression elicited by spaceflight in *Arabidopsis thaliana*. *BMC Genomics*, *20*(1), 1–17.

SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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